

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805778	5249	27405	198	65

Description

GTC ORF with score 186 to: (fn:translocates inorganic phosphate into the) (sr:spruce budworm) (db:genpept-inv) (de:choristoneura fumiferana phosphate transport protein mrna, nucleargene encoding mitochondrial protein, complete cds.) (nt:mitochondrial ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805780	5250	27406	456	151

Description

GTC ORF with score 394 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome v cosmid 9379, 9581, and lambda clone 4678.) (nt:similar to mitochondrial phosphate carrier protein) (le:40977) (re:41879) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805781	5251	27407	348	115

Description

5000689284 hypothetical protein:hypothetical 15.7 kd protein in rpsu-phoh intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfB yqfB Bacillus subtilis 1423 -11531453 115871 yqfB (de:hypothetical 15.7 kd protein in rpsu-phoh intergenic region) (db:swissprot) YQFB\_BACSU P54467 BACILLUS SUBTILIS 1423 -11531453 7000688371 yqfB hypothetical protein yqfB (db:pir2.dat) B69953 B69953 Bacillus subtilis 1423 -11531453 216062 yqfB (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:102181) (re:102600) (di:direct) BACJH642 D84432 g1303818 Bacillus subtilis 1423 -11531453 7500952416 yqfB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (le:16830) (re:17249) (di:complement) BSUB0014 Z99117 g2634983 Bacillus subtilis 1423 -11531453 6500727595 hypothetical protein:hypothetical 15.7 kd protein in rpsu-phoh intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfB yqfB Bacillus subtilis 1423 -11531453

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805782	5252	27408	270	89

Description

5000689283 hypothetical protein:hypothetical 35.6 kd protein in rpsu-phoh interegenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfA yqfA Bacillus subtilis 1423 -11531454 115870 yqfa (de:hypothetical 35.6 kd protein in rpsu-phoh interegenic region) (db:swissprot) YQFA\_BACSU P54466 BACILLUS SUBTILIS 1423 -11531454 7000688370 yqfa hypothetical protein yqfa (db:pir2.dat) A69953 A69953 Bacillus subtilis 1423 -11531454 216061 yqfa (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:101161) (re:102156) (di:direct) BACJH642 D84432 g1303817 Bacillus subtilis 1423 -11531454 7500952415 yqfa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:17274) (re:18269) (di:complement) BSUB0014 Z99117 g2634984 Bacillus subtilis 1423 -11531454 6500727596 hypothetical protein:hypothetical 35.6 kd protein in rpsu-phoh interegenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfA yqfA Bacillus subtilis 1423 -11531454

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805794	5253	27409	378	125

Description

5000689282 hypothetical protein:hypothetical 46.5 kd protein in rpsu-phoh interegenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeZ yqeZ Bacillus subtilis 1423 -11531455 115868 yqez (de:hypothetical 46.5 kd protein in rpsu-phoh interegenic region) (db:swissprot) YQEZ\_BACSU P54465 BACILLUS SUBTILIS 1423 -11531455 7000688369 yqez hypothetical protein yqez (db:pir2.dat) H69952 H69952 Bacillus subtilis 1423 -11531455 216060 yqez (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:99826) (re:101139) (di:direct) BACJH642 D84432 g1303816 Bacillus subtilis 1423 -11531455 7500952414 yqez (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:18291) (re:19604) (di:complement) BSUB0014 Z99117 g2634985 Bacillus subtilis 1423 -11531455 6500727597 hypothetical protein:hypothetical 46.5 kd protein in rpsu-phoh interegenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeZ yqeZ Bacillus subtilis 1423 -11531455



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805812	5254	27410	411	136

#### Description

5000689281 hypothetical protein:hypothetical 16.8 kd protein in rpsu-phoh interegenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeY yqeY Bacillus subtilis 1423 -11531456 115867 yqey (de:hypothetical 16.8 kd protein in rpsu-phoh interegenic region) (db:swissprot) YQEY\_BACSU P54464 BACILLUS SUBTILIS 1423 -11531456 7000688368 yqey conserved hypothetical protein yqey (db:pir2.dat) G69952 G69952 Bacillus subtilis 1423 -11531456 216059 yqey (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:99249) (re:99695) (di:direct) BACJH642 D84432 g1303815 Bacillus subtilis 1423 -11531456 7500952413 yqey (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:19735) (re:20181) (di:complement) BSUB0014 Z99117 g2634986 Bacillus subtilis 1423 -11531456 6500727598 hypothetical protein:hypothetical 16.8 kd protein in rpsu-phoh interegenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeY yqeY Bacillus subtilis 1423 -11531456

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805813	5255	27411	258	85

#### Description

5000689280 hypothetical protein:hypothetical 33.4 kd protein in dnaj-rpsu interegenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeW yqeW Bacillus subtilis 1423 -11531457 115866 yqew (de:hypothetical 33.4 kd protein in dnaj-rpsu interegenic region) (db:swissprot) YQEW\_BACSU P54463 BACILLUS SUBTILIS 1423 -11531457 7000688367 yqew na+/pi cotransporter homolog yqew (db:pir2.dat) F69952 F69952 Bacillus subtilis 1423 -11531457 216057 yqew (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:97965) (re:98897) (di:complement) BACJH642 D84432 g1303813 Bacillus subtilis 1423 -11531457 302936 yqew (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to na+/pi cotransporter) (le:20533) (re:21465) (di:direct) BSUB0014 Z99117 g2634988 Bacillus subtilis 1423 -11531457 7500952412 yqew (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna for dnaj, yqet, yqeu, yqev, yqew, yqex, yqey, complete and partial cds.) (nt:similar to 59.6 kda protein (yjbb) of e. coli) (le:3496) (re:4428) (di:compl... D83717 D83717 g1890062 Bacillus subtilis 1423 -11531457 6500727599 hypothetical protein:hypothetical 33.4 kd protein in dnaj-rpsu interegenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeW yqeW Bacillus subtilis 1423 -11531457

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805823	5256	27412	306	101

Description

5000689279 hypothetical protein:hypothetical 51.7 kd protein in dnaj-rpsu interegenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeV yqeV Bacillus subtilis 1423 -11531458 115865 yqev (de:hypothetical 51.7 kd protein in dnaj-rpsu interegenic region) (db:swissprot) YQEV\_BACSU P54462 BACILLUS SUBTILIS 1423 -11531458 7000688366 yqev conserved hypothetical protein yqev (cl:conserved hypothetical protein hi0019) (db:pir2.dat) E69952 E69952 Bacillus subtilis 1423 -11531458 216056 yqev (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:96573) (re:97928) (di:direct) BACJH642 D84432 g1303812 Bacillus subtilis 1423 -11531458 302935 yqev (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:21502) (re:22857) (di:complement) BSUB0014 Z99117 g2634989 Bacillus subtilis 1423 -11531458 7500952411 yqev (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna for dnaj, yqet, yqeu, yqev, yqew, yqex, yqey, complete and partial cds.) (le:2104) (re:3459) (di:direct) D83717 D83717 g1890061 Bacillus subtilis 1423 -11531458 6500727600 hypothetical protein:hypothetical 51.7 kd protein in dnaj-rpsu interegenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeV yqeV Bacillus subtilis 1423 -11531458

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501805826	5257	27413	240	79

Description

5000689278 hypothetical protein:hypothetical 28.8 kd protein in dnaj-rpsu interegenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeU yqeU Bacillus subtilis 1423 -11531459 115864 yqeU (de:hypothetical 28.8 kd protein in dnaj-rpsu interegenic region) (db:swissprot) YQEU\_BACSU P54461 BACILLUS SUBTILIS 1423 -11531459 7000688365 yqeU conserved hypothetical protein yqeU (db:pir2.dat) D69952 D69952 Bacillus subtilis 1423 -11531459 216055 yqeU (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:95803) (re:96573) (di:direct) BACJH642 D84432 g1303811 Bacillus subtilis 1423 -11531459 302934 yqeU (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:22857) (re:23627) (di:complement) BSUB0014 Z99117 g2634990 Bacillus subtilis 1423 -11531459 7500952410 yqeU (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna for dnaj, yqet, yqeU, yqev, yqew, yqex, yqey,complete and partial cds.) (nt:similar to 26.9 kda protein (yggj) of e. coli) (le:1334) (re:2104) (di:direct) D83717 D83717 g1890060 Bacillus subtilis 1423 -11531459 6500727601 hypothetical protein:hypothetical 28.8 kd protein in dnaj-rpsu interegenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeU yqeU Bacillus subtilis 1423 -11531459

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805830	5258	27414	459	152

Description

6500727602 hypothetical protein:probable methyltransferase (gtcfc:14.1) (ec:2.1.1.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeT yqeT Bacillus subtilis 1423 -11531460 115863 yqeT (ec:2.1.1.-) (de:probable methyltransferase,) (db:swissprot) PRMA\_BACSU P54460 BACILLUS SUBTILIS 1423 -11531460 7000686179 yqeT ribosomal protein l11 methyltransferase homolog yqeT (cl:ribosomal protein l11 methyltransferase:bioc homology) (db:pir2.dat) C69952 C69952 Bacillus subtilis 1423 -11531460 216054 yqeT (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:94845) (re:95780) (di:direct) BACJH642 D84432 g1303810 Bacillus subtilis 1423 -11531460 302933 yqeT (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to ribosomal protein l11 methyltransferase) (le:23650) (re:24585) (di:complement) BSUB0014 Z99117 g2634991 Bacillus subtilis 1423 -11531460 7500888510 yqeT (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna for dnaj, yqeT, yqeu, yqev, yqew, yqex, yqey,complete and partial cds.) (nt:similar to ribosomal protein l11 methyltransferase) (le:376) (re:1311) (di:d... D83717 D83717 g1890059 Bacillus subtilis 1423 -11531460 5000689277 (de:(yqeT) (pn:hypothetical 34) (gtcfc:13.07) (ec:) (yqeT\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yqeT yqeT Bacillus subtilis 1423 10057589



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501805834	5259	27415	960	319

Description

6500727603 yqep:yqxa hypothetical protein:hypothetical 12.5 kd protein in spoiiip-lepa intergenic region:orf79 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqxA yqxA Bacillus subtilis 1423 -11531461 116026 yqxa:yqep (de:hypothetical 12.5 kd protein in spoiiip-lepa intergenic region (orf79)) (db:swissprot) YQXA\_BACSU P38425 BACILLUS SUBTILIS 1423 -11531461 7000688492 yqxa hypothetical protein yqxa (db:pir2.dat) F69967 F69967 Bacillus subtilis 1423 -11531461 215797 orf79 protein (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis gpr gene for spore protease partial sequence and 3'downstream region.) (le:1963) (re:2301) (di:direct) BACGPR D17650 g436035 Bacillus subtilis 1423 -11531461 216047 yqep (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:86394) (re:86732) (di:direct) BACJH642 D84432 g1303803 Bacillus subtilis 1423 -11531461 7500952569 yqxa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yqep) (le:32698) (re:33036) (di:complement) BSUB0014 Z99117 g2634998 Bacillus subtilis 1423 -11531461 5000689676 (de:(yqxa) (pn:hypothetical 12) (gn:yqep) (gtcfc:13.07) (ec:) (yqxa\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yqxA yqxA Bacillus subtilis 1423 10057752

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501805843	5260	27416	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501805850	5261	27417	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501805855	5262	27418	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805856	5263	27419	282	93

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805859	5264	27420	708	235

Description

5000689276 hypothetical protein:hypothetical 40.5 kd protein in come-rpst intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeN yqeN Bacillus subtilis 1423 -11531462 115862 yqen (de:hypothetical 40.5 kd protein in come-rpst intergenic region) (db:swissprot) YQEN\_BACSU P54459 BACILLUS SUBTILIS 1423 -11531462 7000688364 yqen conserved hypothetical protein yqen (db:pir2.dat) B69952 B69952 Bacillus subtilis 1423 -11531462 216043 yqen (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:82475) (re:83518) (di:direct) BACJH642 D84432 g1303799 Bacillus subtilis 1423 -11531462 7500952409 yqen (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:35912) (re:36955) (di:complement) BSUB0014 Z99117 g2635002 Bacillus subtilis 1423 -11531462 6500727604 hypothetical protein:hypothetical 40.5 kd protein in come-rpst intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeN yqeN Bacillus subtilis 1423 -11531462

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805866	5265	27421	471	156

Description

5000689275 hypothetical protein:hypothetical 28.3 kd protein in arod-comer intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqem yqem Bacillus subtilis 1423 -11531463 115861 yqem (de:hypothetical 28.3 kd protein in arod-comer intergenic region) (db:swissprot) YQEM\_BACSU P54458 BACILLUS SUBTILIS 1423 -11531463 7000688363 yqem conserved hypothetical protein yqem (cl:bioc homology) (db:pir2.dat) A69952 A69952 Bacillus subtilis 1423 -11531463 216038 yqem (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:76770) (re:77513) (di:direct) BACJH642 D84432 g1303794 Bacillus subtilis 1423 -11531463 7500952408 yqem (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:41917) (re:42660) (di:complement) BSUB0014 Z99117 g2635007 Bacillus subtilis 1423 -11531463 6500727605 hypothetical protein:hypothetical 28.3 kd protein in arod-comer intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqem yqem Bacillus subtilis 1423 -11531463

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805877	5266	27422	555	184

Description

5000689274 hypothetical protein:hypothetical 13.3 kd protein in arod-comer intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeL yqeL Bacillus subtilis 1423 -11531464 115860 yqeL (de:hypothetical 13.3 kd protein in arod-comer intergenic region) (db:swissprot) YQEL\_BACSU P54457 BACILLUS SUBTILIS 1423 -11531464 7000688362 yqeL ybeb protein homolog yqeL (cl:escherichia coli ybeb protein) (db:pir2.dat) H69951 H69951 Bacillus subtilis 1423 -11531464 216037 yqeL (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:76417) (re:76773) (di:direct) BACJH642 D84432 g1303793 Bacillus subtilis 1423 -11531464 7500952407 yqeL (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:42657) (re:43013) (di:complement) BSUB0014 Z99117 g2635008 Bacillus subtilis 1423 -11531464 6500727606 hypothetical protein:hypothetical 13.3 kd protein in arod-comer intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeL yqeL Bacillus subtilis 1423 -11531464

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501805890	5267	27423	1062	354

Description

5000689273 hypothetical protein:hypothetical 21.3 kd protein in arod-comer intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeK yqeK Bacillus subtilis 1423 -11531465 115859 yqeK (de:hypothetical 21.3 kd protein in arod-comer intergenic region) (db:swissprot) YQEK\_BACSU P54456 BACILLUS SUBTILIS 1423 -11531465 7000688360 yqeK conserved hypothetical protein yqeK (cl:hypothetical protein yqeK) (db:pir2.dat) G69951 G69951 Bacillus subtilis 1423 -11531465 216036 yqeK (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:75839) (re:76399) (di:direct) BACJH642 D84432 g1303792 Bacillus subtilis 1423 -11531465 7500952405 yqeK (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:43031) (re:43591) (di:complement) BSUB0014 Z99117 g2635009 Bacillus subtilis 1423 -11531465 6500727607 hypothetical protein:hypothetical 21.3 kd protein in arod-comer intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeK yqeK Bacillus subtilis 1423 -11531465

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501805907	5268	27424	624	207

Description

5000689272 hypothetical protein:hypothetical 22.2 kd protein in arod-comer intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeJ yqeJ Bacillus subtilis 1423 -11531466 115858 yqeJ (de:hypothetical 22.2 kd protein in arod-comer intergenic region) (db:swissprot) YQEJ\_BACSU P54455 BACILLUS SUBTILIS 1423 -11531466 7000688358 yqeJ conserved hypothetical protein yqeJ (db:pir2.dat) F69951 F69951 Bacillus subtilis 1423 -11531466 216035 yqeJ (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:75280) (re:75849) (di:direct) BACJH642 D84432 g1303791 Bacillus subtilis 1423 -11531466 7500952403 yqeJ (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:43581) (re:44150) (di:complement) BSUB0014 Z99117 g2635010 Bacillus subtilis 1423 -11531466 6500727608 hypothetical protein:hypothetical 22.2 kd protein in arod-comer intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeJ yqeJ Bacillus subtilis 1423 -11531466



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805909	5269	27425	411	137

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805922	5270	27426	729	242

Description

5000689271 hypothetical protein: hypothetical 10.8 kd protein in arod-comer intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeI yqeI Bacillus subtilis 1423 -11531467 115857 yqeI (de: hypothetical 10.8 kd protein in arod-comer intergenic region) (db:swissprot) YQEI\_BACSU P54454 BACILLUS SUBTILIS 1423 -11531467 7000688355 yqeI dihydrodipicolinate reductase homolog yqeI (cl: methanococcus jannaschii conserved hypothetical protein mj0652) (db:pir2.dat) E69951 E69951 Bacillus subtilis 1423 -11531467 216034 yqeI (sr: bacillus subtilis (strain: jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de: bacillus subtilis dna, 283 kb region containing skin element.) (le:74978) (re:75268) (di:direct) BACJH642 D84432 g1303790 Bacillus subtilis 1423 -11531467 7500952401 yqeI (fn:unknown) (db:genpept-bct1) (de: bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt: similar to dihydrodipicolinate reductase) (le:44162) (re:44452) (di: complement) BSUB0014 Z99117 g2635011 Bacillus subtilis 1423 -11531467 6500727609 hypothetical protein: hypothetical 10.8 kd protein in arod-comer intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeI yqeI Bacillus subtilis 1423 -11531467

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805931	5271	27427	264	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805961	5272	27428	1467	488
<u>Description</u>				
5000689270 hypothetical protein:hypothetical 41.0 kd protein in nucb-arod intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeH yqeH Bacillus subtilis 1423 -11531468 115856 yqeh (de:hypothetical 41.0 kd protein in nucb-arod intergenic region) (db:swissprot) YQEH_BACSU P54453 BACILLUS SUBTILIS 1423 -11531468 7000688352 yqeh conserved hypothetical protein yqeh (db:pir2.dat) D69951 D69951 Bacillus subtilis 1423 -11531468 216032 yqeh (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:73024) (re:74124) (di:direct) BACJH642 D84432 g1303788 Bacillus subtilis 1423 -11531468 7500952399 yqeh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:45306) (re:46406) (di:complement) BSUB0014 Z99117 g2635013 Bacillus subtilis 1423 -11531468 6500727610 hypothetical protein:hypothetical 41.0 kd protein in nucb-arod intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeH yqeH Bacillus subtilis 1423 -11531468				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805963	5273	27429	348	115
<u>Description</u>				
5000689269 hypothetical protein:hypothetical 20.1 kd protein in nucb-arod intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeG yqeG Bacillus subtilis 1423 -11531469 115855 yqeg (de:hypothetical 20.1 kd protein in nucb-arod intergenic region) (db:swissprot) YQEG_BACSU P54452 BACILLUS SUBTILIS 1423 -11531469 7000688351 yqeg conserved hypothetical protein yqeg (db:pir2.dat) C69951 C69951 Bacillus subtilis 1423 -11531469 216031 yqeg (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:72502) (re:73020) (di:direct) BACJH642 D84432 g1303787 Bacillus subtilis 1423 -11531469 7500952398 yqeg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:46410) (re:46928) (di:complement) BSUB0014 Z99117 g2635014 Bacillus subtilis 1423 -11531469 6500727611 hypothetical protein:hypothetical 20.1 kd protein in nucb-arod intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeG yqeG Bacillus subtilis 1423 -11531469				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805975	5274	27430	264	87
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805980	5275	27431	417	138
<u>Description</u>				

5000689268 hypothetical protein:hypothetical 27.6 kd lipoprotein in nucb-arod intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeF yqeF Bacillus subtilis 1423 -11531470 115854 yqeF (de:precursor) (db:swissprot) YQEF\_BACSU P54451 BACILLUS SUBTILIS 1423 -11531470 7000688349 yqeF hypothetical protein yqeF (db:pir2.dat) B69951 B69951 Bacillus subtilis 1423 -11531470 216030 yqeF (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:70963) (re:71694) (di:direct) BACJH642 D84432 g1303786 Bacillus subtilis 1423 -11531470 7500952396 yqeF (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:47736) (re:48467) (di:complement) BSUB0014 Z99117 g2635015 Bacillus subtilis 1423 -11531470 6500727612 hypothetical protein:hypothetical 27.6 kd lipoprotein in nucb-arod intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeF yqeF Bacillus subtilis 1423 -11531470

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805987	5276	27432	441	146
<u>Description</u>				

5000689267 hypothetical protein:hypothetical 22.9 kd protein in nucb-arod intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeD yqeD Bacillus subtilis 1423 -11531471 115852 yqeD (de:hypothetical 22.9 kd protein in nucb-arod intergenic region) (db:swissprot) YQED\_BACSU P54449 BACILLUS SUBTILIS 1423 -11531471 7000688347 yqeD conserved hypothetical protein yqeD (db:pir2.dat) H69950 H69950 Bacillus subtilis 1423 -11531471 216028 yqeD (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:69146) (re:69772) (di:complement) BACJH642 D84432 g1303784 Bacillus subtilis 1423 -11531471 7500952394 yqeD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:49658) (re:50284) (di:direct) BSUB0014 Z99117 g2635017 Bacillus subtilis 1423 -11531471 6500727613 hypothetical protein:hypothetical 22.9 kd protein in nucb-arod intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeD yqeD Bacillus subtilis 1423 -11531471

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805990	5277	27433	963	320

Description

GTC ORF with score 163 to: (fn:converts arachidonic acid to an allene oxide) (db:genpept-inv) (de:plexaura homomalla 8r-lipoxygenase-allene oxide synthase fusionprotein mrna, complete cds.) (nt:peroxidase-lipoxygenase fusion protein; naturally) (le:97)...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501805995	5278	27434	621	206

Description

5000689266 hypothetical protein:hypothetical 32.8 kd protein in nucb-arod intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeC yqeC Bacillus subtilis 1423 -11531472 115851 yqeC (de:hypothetical 32.8 kd protein in nucb-arod intergenic region) (db:swissprot) YQEC\_BACSU P54448 BACILLUS SUBTILIS 1423 -11531472 7000688346 yqeC 6-phosphogluconate dehydrogenase pentose homolog yqeC (cl:3-hydroxyisobutyrate dehydrogenase homology) (db:pir2.dat) G69950 G69950 Bacillus subtilis 1423 -11531472 216027 yqeC (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:68234) (re:69127) (di:direct) BACJH642 D84432 g1303783 Bacillus subtilis 1423 -11531472 7500952393 yqeC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to 6-phosphogluconate dehydrogenase) (le:50303) (re:51196) (di:complement) BSUB0014 Z99117 g2635018 Bacillus subtilis 1423 -11531472 6500727614 hypothetical protein:hypothetical 32.8 kd protein in nucb-arod intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeC yqeC Bacillus subtilis 1423 -11531472

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806014	5279	27435	1782	593

Description

5000689265 hypothetical protein:hypothetical 27.6 kd protein in nucb-arod intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeB yqeB Bacillus subtilis 1423 -11531473 115850 yqeb (de:hypothetical 27.6 kd protein in nucb-arod intergenic region) (db:swissprot) YQEB\_BACSU P54447 BACILLUS SUBTILIS 1423 -11531473 7000688345 yqeb hypothetical protein yqeb (db:pir2.dat) F69950 F69950 Bacillus subtilis 1423 -11531473 216026 yqeb (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:67257) (re:67982) (di:complement) BACJH642 D84432 g1303782 Bacillus subtilis 1423 -11531473 7500952392 yqeb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:51448) (re:52173) (di:direct) BSUB0014 Z99117 g2635019 Bacillus subtilis 1423 -11531473 6500727615 hypothetical protein:hypothetical 27.6 kd protein in nucb-arod intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeB yqeB Bacillus subtilis 1423 -11531473

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806026	5280	27436	639	212

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806033	5281	27437	633	210
<u>Description</u>				
5000689675 hypothetical protein:hypothetical 38.3 kd protein in cwla-cisa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqcL yqcL Bacillus subtilis 1423 -11531474 115846 yqcL (de:hypothetical 38.3 kd protein in cwla-cisa intergenic region) (db:swissprot) YQCL_BACSU P45946 BACILLUS SUBTILIS 1423 -11531474 7000688342 yqcL conserved hypothetical protein yqcL (cl:conserved hypothetical protein mth900) (db:pir2.dat) B69950 B69950 Bacillus subtilis 1423 -11531474 216021 yqcL (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:62818) (re:63858) (di:direct) BACJH642 D84432 g1303777 Bacillus subtilis 1423 -11531474 216808 orf1 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiiic.) (nt:similarity to arsenic efflux pump protein (arsb) of) (le:44573) (re:... BACSKIN D32216 g1217884 Bacillus subtilis 1423 -11531474 7500952387 yqcL (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to hypothetical proteins) (le:55572) (re:56612) (di:complement) BSUB0014 Z99117 g2635024 Bacillus subtilis 1423 -11531474 6500727616 hypothetical protein:hypothetical 38.3 kd protein in cwla-cisa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqcL yqcL Bacillus subtilis 1423 -11531474				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501806035	5282	27438	825	274

Description

5000689674 hypothetical protein:hypothetical 16.6 kd protein in cwla-cisa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqck yqck Bacillus subtilis 1423 -11531475 115845 yqck (de:hypothetical 16.6 kd protein in cwla-cisa intergenic region) (db:swissprot) YQCK\_BACSU P45945 BACILLUS SUBTILIS 1423 -11531475 7000688341 yqck conserved hypothetical protein yqck (db:pir2.dat) A69950 A69950 Bacillus subtilis 1423 -11531475 216020 yqck (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:62355) (re:62795) (di:direct) BACJH642 D84432 g1303776 Bacillus subtilis 1423 -11531475 216807 orf2 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiic.) (le:44110) (re:44550) (di:direct) BACSKIN D32216 g1217883 Bacillus subtilis 1423 -11531475 7500952386 yqck (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to hypothetical proteins) (le:56635) (re:57075) (di:complement) BSUB0014 Z99117 g2635025 Bacillus subtilis 1423 -11531475 6500727617 hypothetical protein:hypothetical 16.6 kd protein in cwla-cisa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqck yqck Bacillus subtilis 1423 -11531475

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806051	5283	27439	360	119

Description

5000689673 hypothetical protein:hypothetical 12.3 kd protein in cwla-cisa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqcJ yqcJ Bacillus subtilis 1423 -11531476 115844 yqcj (de:hypothetical 12.3 kd protein in cwla-cisa intergenic region) (db:swissprot) YQCJ\_BACSU P45949 BACILLUS SUBTILIS 1423 -11531476 7000688340 yqcj transcription regulator arsr family homolog yqcj (cl:arsenical resistance operon repressor) (db:pir2.dat) H69949 H69949 Bacillus subtilis 1423 -11531476 216019 yqcj (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:61977) (re:62294) (di:direct) BACJH642 D84432 g1303775 Bacillus subtilis 1423 -11531476 216806 orf3 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiiic.) (nt:similarity to arsenical resistance operon) (le:43732) (re:44049) (di... BACSKIN D32216 g1217882 Bacillus subtilis 1423 -11531476 7500952385 yqcj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to transcriptional regulator (arsr family)) (le:57136) (re:57453) (di:complement) BSUB0014 Z99117 g2635026 Bacillus subtilis 1423 -11531476 6500727618 hypothetical protein:hypothetical 12.3 kd protein in cwla-cisa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqcJ yqcJ Bacillus subtilis 1423 -11531476

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806053	5284	27440	240	79

Description

GTC ORF with score 96 to: (or:Mus musculus) (sr:mus musculus (strain balb/c, sub\_species domesticus) brain dna) (db:genpept-rod) (de:mouse brain-1 pou-domain protein, complete cds.) (nt:brain-1 class iii pou-domain protein) (le:2001) (re:3488) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806067	5285	27441	546	181

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806075	5286	27442	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806087	5287	27443	471	156

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806103	5288	27444	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806116	5289	27445	360	120

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806117	5290	27446	261	86

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806125	5291	27447	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806141	5292	27448	1344	447

Description

5000689672 hypothetical protein:hypothetical 30.1 kd protein in cwla-cisa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqcI yqcI Bacillus subtilis 1423 -11531477  
 115843 yqci (de:hypothetical 30.1 kd protein in cwla-cisa intergenic region) (db:swissprot) YQCI\_BACSU P45944 BACILLUS SUBTILIS 1423 -11531477  
 7000688339 yqci conserved hypothetical protein yqci (db:pir2.dat) G69949 G69949 Bacillus subtilis 1423 -11531477 216018 yqci (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:60841) (re:61605) (di:direct) BACJH642 D84432 g1303774 Bacillus subtilis 1423 -11531477 216805 orf4 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiic.) (le:42596) (re:43360) (di:direct) BACSKIN D32216 g1217881 Bacillus subtilis 1423 -11531477 7500952384 yqci (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins from b. subtilis) (le:57825) (re:58589) (di:complement) BSUB0014 Z99117 g2635027 Bacillus subtilis 1423 -11531477 6500727619 hypothetical protein:hypothetical 30.1 kd protein in cwla-cisa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqcI yqcI Bacillus subtilis 1423 -11531477

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806142	5293	27449	222	73

Description

6500727620 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqzI yqzI Bacillus subtilis 1423 -11531478  
 7000693851 yqzi hypothetical protein yqzi (db:pir2.dat) H69969 H69969 Bacillus subtilis 1423 -11531478 7500964664 yqzi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:60394) (re:60552) (di:direct) BSUB0014 Z99117 g2635030 Bacillus subtilis 1423 -11531478

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501806146	5294	27450	486	161

Description

5000689670 hypothetical protein:hypothetical 59.7 kd protein in cwla-cisa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqcG yqcG Bacillus subtilis 1423 -11531479 115841 yqcG (de:hypothetical 59.7 kd protein in cwla-cisa intergenic region) (db:swissprot) YQCG\_BACSU P45942 BACILLUS SUBTILIS 1423 -11531479 7000688337 yqcG conserved hypothetical protein yqcG (db:pir2.dat) F69949 F69949 Bacillus subtilis 1423 -11531479 216016 yqcG (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:56913) (re:58508) (di:complement) BACJH642 D84432 g1303772 Bacillus subtilis 1423 -11531479 216803 orf94 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiic.) (le:38668) (re:40263) (di:complement) BACSKIN D32216 g1217879 Bacillus subtilis 1423 -11531479 7500952383 yqcG (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to hypothetical proteins from b. subtilis) (le:60922) (re:62517) (di:direct) BSUB0014 Z99117 g2635031 Bacillus subtilis 1423 -11531479 6500727621 hypothetical protein:hypothetical 59.7 kd protein in cwla-cisa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqcG yqcG Bacillus subtilis 1423 -11531479

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806147	5295	27451	528	175

Description

5000689669 hypothetical protein:hypothetical 21.5 kd protein in cwla-cisa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqcF yqcF Bacillus subtilis 1423 -11531480 115840 yqcf (de:hypothetical 21.5 kd protein in cwla-cisa intergenic region) (db:swissprot) YQCF\_BACSU P45941 BACILLUS SUBTILIS 1423 -11531480 7000688336 yqcf hypothetical protein yqcf (db:pir2.dat) E69949 E69949 Bacillus subtilis 1423 -11531480 216015 yqcf (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:56320) (re:56898) (di:complement) BACJH642 D84432 g1303771 Bacillus subtilis 1423 -11531480 216802 orf95 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiic.) (le:38075) (re:38653) (di:complement) BACSKIN D32216 g1217878 Bacillus subtilis 1423 -11531480 7500952382 yqcf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (le:62532) (re:63110) (di:direct) BSUB0014 Z99117 g2635032 Bacillus subtilis 1423 -11531480 6500727622 hypothetical protein:hypothetical 21.5 kd protein in cwla-cisa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqcF yqcF Bacillus subtilis 1423 -11531480

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806184	5296	27452	576	191

Description

GTC ORF with score 134 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k02g10.) (nt:similar to the dna-j domain found in dnaj) (le:35350:35411:36666) (re:35356:35884:36832) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806187	5297	27453	474	157

Description

6500727623 yqdf:yqxj hypothetical protein:hypothetical 14.3 kd protein in cwla-cisa intergenic region:orf5 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqxJ yqxJ Bacillus subtilis 1423 -11531481  
 116033 yqxj:yqdf (de:hypothetical 14.3 kd protein in cwla-cisa intergenic region (orf5)) (db:swissprot) YQXJ\_BACSU P24809 BACILLUS SUBTILIS 1423 -11531481 7000688498 yqxj hypothetical protein yqxj (db:pir2.dat) D69968 D69968 Bacillus subtilis 1423 -11531481 215458 (sr:bacillus subtilis (strain 168) dna, clone lambda pe3) (db:genpept-bct1) (de:bacillus subtilis n-acetylmuramoyl-l-alanine amidase (cwla) gene,complete cds.) (nt:open reading frame 5) (le:2491) (re:2853) (di:direct) BACCWLAA M59232 g551700 Bacillus subtilis 1423 -11531481 216014 yqdf (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:55697) (re:56059) (di:direct) BACJH642 D84432 g1303770 Bacillus subtilis 1423 -11531481 216801 orf119 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiic.) (le:37452) (re:37814) (di:direct) BACSKIN D32216 g1217877 Bacillus subtilis 1423 -11531481 7500952575 yqxj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:alternate gene name: yqdf) (le:63371) (re:63733) (di:complement) BSUB0014 Z99117 g2635033 Bacillus subtilis 1423 -11531481 5000689682 (de:(yqxj) (pn:hypothetical 14) (gn:yqdf) (gtcfc:13.07) (ec:) (yqxj\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yqxJ yqxJ Bacillus subtilis 1423 10057759

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806193	5298	27454	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501806200	5299	27455	408	135

Description

6500727624 yqde:yqxi hypothetical protein:hypothetical 17.0 kd protein in cwla-cisa intergenic region:orf4 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqxI yqxI Bacillus subtilis 1423 -11531482

116032 yqxi:yqde (de:hypothetical 17.0 kd protein in cwla-cisa intergenic region (orf4)) (db:swissprot) YQXI\_BACSU P24812 BACILLUS SUBTILIS 1423 -11531482 7000688497 yqxi hypothetical protein yqxi (db:pir2.dat) D44816 D44816 Bacillus subtilis 1423 -11531482 7500952574 (sr:bacillus subtilis (strain 168) dna, clone lambda pe3) (db:genpept-bct1) (de:bacillus subtilis n-acetylmuramoyl-l-alanine amidase (cwla) gene,complete cds.) (nt:open reading frame 4) (le:1996) (re:2475) (di:direct) BACCWLAA M59232 g142803 Bacillus subtilis 1423 -11531482 215457 yqde (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:55202) (re:55681) (di:direct) BACJH642 D84432 g1303769 Bacillus subtilis 1423 -11531482 216013 orf120 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which islocated between spoivcb and spoiiiic.) (le:36957) (re:37436) (di:direct) BACSKIN D32216 g1217876 Bacillus subtilis 1423 -11531482 216800 yqxi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yqde) (le:63749) (re:64228) (di:complement) BSUB0014 Z99117 g2635034 Bacillus subtilis 1423 -11531482 170401 yqxi hypothetical protein yqxi (db:pir) D44816 D44816 Bacillus subtilis 1423 -11531482 5000689681 (de:(yqxi) (pn:hypothetical 17) (gn:yqde) (gtcfc:13.07) (ec:) (yqxi\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yqxI yqxI Bacillus subtilis 1423 10057758

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501806205	5300	27456	207	69

Description

6500727625 yqdd:yqxh hypothetical protein:hypothetical 15.7 kd protein in spoiiiic-cwla intergenic region:orf2 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqxH yqxH Bacillus subtilis 1423 -11531483 116031 yqxh:yqdd (de:hypothetical 15.7 kd protein in spoiiiic-cwla intergenic region (orf2)) (db:swissprot) YQXH\_BACSU P24811 BACILLUS SUBTILIS 1423 -11531483 7000688496 yqxh holin homolog yqxh (db:pir2.dat) B44816 B44816 Bacillus subtilis 1423 -11531483 7500952573 (sr:bacillus subtilis (strain 168) dna, clone lambda pe3) (db:genpept-bct1) (de:bacillus subtilis n-acetylmuramoyl-l-alanine amidase (cwla) gene,complete cds.) (nt:open reading frame 2) (le:546) (re:968) (di:direct) BACCWLAA M59232 g142801 Bacillus subtilis 1423 -11531483 215455 yqdd (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:53752) (re:54174) (di:direct) BACJH642 D84432 g1303767 Bacillus subtilis 1423 -11531483 216011 orf121 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which islocated between spoivcb and spoiiiic.) (le:35507) (re:35929) (di:direct) BACSKIN D32216 g1217874 Bacillus subtilis 1423 -11531483 216798 yqxh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yqdd; similar to holin) (le:65256) (re:65678) (di:complement) BSUB0014 Z99117 g2635036 Bacillus subtilis 1423 -11531483 170398 yqxh holin homolog yqxh (db:pir) B44816 B44816 Bacillus subtilis 1423 -11531483 5000689680 (de:(yqxh) (pn:hypothetical 15) (gn:yqdd) (gtcfc:13.07) (ec:) (yqxh\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yqxH yqxH Bacillus subtilis 1423 10057757

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501806211	5301	27457	1539	512

Description

6500727626 yqdc:yqxg hypothetical protein:hypothetical 32.5 kd protein in spoiiic-cwla intergenic region:orf1 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqxG yqxG Bacillus subtilis 1423 -11531484 116030 yqxg:yqdc (de:hypothetical 32.5 kd protein in spoiiic-cwla intergenic region (orf1)) (db:swissprot) YQXG\_BACSU P24810 BACILLUS SUBTILIS 1423 -11531484 7000688495 yqxg phage-related lytic exoenzyme homolog yqxg (db:pir2.dat) A69968 A69968 Bacillus subtilis 1423 -11531484 216010 yqdc (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:52814) (re:53707) (di:direct) BACJH642 D84432 g1303766 Bacillus subtilis 1423 -11531484 216797 orf122 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which islocated between spoivcb and spoiiic.) (le:34569) (re:35462) (di:direct) BACSKIN D32216 g1217873 Bacillus subtilis 1423 -11531484 7500952572 yqxg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yqdc; similar to phage-related) (le:65723) (re:66616) (di:complement) BSUB0014 Z99117 g2635037 Bacillus subtilis 1423 -11531484 5000689679 (de:(yqxg) (pn:hypothetical 32) (gn:yqdc) (gtcfc:13.07) (ec:) (yqxg\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yqxG yqxG Bacillus subtilis 1423 10057756



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806230	5302	27458	393	130

Description

5000689668 hypothetical protein:hypothetical 6.3 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqcE yqcE Bacillus subtilis 1423 -11531485 115839 yqcE (de:hypothetical 6.3 kd protein in spoiiic-cwla intergenic region) (db:swissprot) YQCE\_BACSU P45940 BACILLUS SUBTILIS 1423 -11531485 7000688334 yqcE phage-related protein homolog yqcE (db:pir2.dat) D69949 D69949 Bacillus subtilis 1423 -11531485 216009 yqcE (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:52562) (re:52726) (di:direct) BACJH642 D84432 g1303765 Bacillus subtilis 1423 -11531485 216796 orf128 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiic.) (le:34317) (re:34481) (di:direct) BACSKIN D32216 g1217872 Bacillus subtilis 1423 -11531485 7500952380 yqcE (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to phage-related protein) (le:66704) (re:66868) (di:complement) BSUB0014 Z99117 g2635038 Bacillus subtilis 1423 -11531485 6500727627 hypothetical protein:hypothetical 6.3 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqcE yqcE Bacillus subtilis 1423 -11531485

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806245	5303	27459	216	72

Description

5000689667 hypothetical protein:hypothetical 12.4 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqcD yqcD Bacillus subtilis 1423 -11531486 115838 yqcD (de:hypothetical 12.4 kd protein in spoiii-cwla intergenic region) (db:swissprot) YQCD\_BACSU P45939 BACILLUS SUBTILIS 1423 -11531486 7000688332 yqcD phage-related protein homolog yqcD (db:pir2.dat) C69949 C69949 Bacillus subtilis 1423 -11531486 216008 yqcD (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:52230) (re:52565) (di:direct) BACJH642 D84432 g1303764 Bacillus subtilis 1423 -11531486 216795 orf129 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiii-cwla) (le:33985) (re:34320) (di:direct) BACSKIN D32216 g1217871 Bacillus subtilis 1423 -11531486 7500952377 yqcD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to phage-related protein) (le:66865) (re:67200) (di:complement) BSUB0014 Z99117 g2635039 Bacillus subtilis 1423 -11531486 6500727628 hypothetical protein:hypothetical 12.4 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqcD yqcD Bacillus subtilis 1423 -11531486

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806246	5304	27460	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806253	5305	27461	456	151

Description

5000689666 hypothetical protein:hypothetical 41.5 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqcC yqcC Bacillus subtilis 1423 -11531487  
115837 yqcc (de:hypothetical 41.5 kd protein in spoiiic-cwla intergenic region) (db:swissprot) YQCC\_BACSU P45938 BACILLUS SUBTILIS 1423 -11531487  
7000688331 yqcc phage-related protein homolog yqcc (db:pir2.dat) B69949 B69949 Bacillus subtilis 1423 -11531487 216007 yqcc (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:51120) (re:52220) (di:direct) BACJH642 D84432 g1303763 Bacillus subtilis 1423 -11531487 216794 orf131 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiic.) (le:32875) (re:33975) (di:direct) BACSKIN D32216 g1217870 Bacillus subtilis 1423 -11531487  
7500952369 yqcc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to phage-related protein) (le:67210) (re:68310) (di:complement) BSUB0014 Z99117 g2635040 Bacillus subtilis 1423 -11531487 6500727629 hypothetical protein:hypothetical 41.5 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqcC yqcC Bacillus subtilis 1423 -11531487

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501806268	5306	27462	837	278

Description

5000689665 hypothetical protein:hypothetical 10.4 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqCB yqCB Bacillus subtilis 1423 -11531488  
115836 yqcb (de:hypothetical 10.4 kd protein in spoiii-cwla intergenic region) (db:swissprot) YQCB\_BACSU P45937 BACILLUS SUBTILIS 1423 -11531488  
7000688329 yqcb hypothetical protein yqcb (db:pir2.dat) A69949 A69949 Bacillus subtilis 1423 -11531488 216006 yqcb (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:50845) (re:51117) (di:direct) BACJH642 D84432 g1303762 Bacillus subtilis 1423 -11531488  
216793 orf130 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiii-cwla) (le:32600) (re:32872) (di:direct) BACSKIN D32216 g1217869 Bacillus subtilis 1423 -11531488  
7500952367 yqcb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (le:68313) (re:68585) (di:complement) BSUB0014 Z99117 g2635041 Bacillus subtilis 1423 -11531488 6500727630 hypothetical protein:hypothetical 10.4 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqCB yqCB Bacillus subtilis 1423 -11531488

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806274	5307	27463	639	212

Description

5000689664 hypothetical protein:hypothetical 22.3 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqca yqca Bacillus subtilis 1423 -11531489 115835 yqca (de:hypothetical 22.3 kd protein in spoiii-cwla intergenic region) (db:swissprot) YQCA\_BACSU P45936 BACILLUS SUBTILIS 1423 -11531489 7000688328 yqca phage-related protein homolog yqca (db:pir2.dat) H69948 H69948 Bacillus subtilis 1423 -11531489 216005 yqca (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:50270) (re:50848) (di:direct) BACJH642 D84432 g1303761 Bacillus subtilis 1423 -11531489 216792 orf123 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiii.) (le:32025) (re:32603) (di:direct) BACSKIN D32216 g1217868 Bacillus subtilis 1423 -11531489 7500952366 yqca (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to phage-related protein) (le:68582) (re:69160) (di:complement) BSUB0014 Z99117 g2635042 Bacillus subtilis 1423 -11531489 6500727631 hypothetical protein:hypothetical 22.3 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqca yqca Bacillus subtilis 1423 -11531489

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806275	5308	27464	765	254

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806310	5309	27465	198	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806311	5310	27466	612	203

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806312	5311	27467	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806321	5312	27468	834	277

Description

5000689663 hypothetical protein: hypothetical 35.0 kd protein in spoiiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbT yqbT Bacillus subtilis 1423 -11531490 115834 yqbt (de: hypothetical 35.0 kd protein in spoiiiic-cwla intergenic region) (db:swissprot) YQBT\_BACSU P45935 BACILLUS SUBTILIS 1423 -11531490 7000688327 yqbt phage-related protein homolog yqbt (db:pir2.dat) G69948 G69948 Bacillus subtilis 1423 -11531490 216004 yqbt (sr: bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de: bacillus subtilis dna, 283 kb region containing skin element.) (le:49240) (re:50286) (di:direct) BACJH642 D84432 g1303760 Bacillus subtilis 1423 -11531490 216791 orf89 (sr: bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de: bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiiic.) (le:30995) (re:32041) (di:direct) BACSKIN D32216 g1217867 Bacillus subtilis 1423 -11531490 7500952365 yqbt (fn:unknown) (db:genpept-bct1) (de: bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt: similar to phage-related protein) (le:69144) (re:70190) (di:complement) BSUB0014 Z99117 g2635043 Bacillus subtilis 1423 -11531490 6500727632 hypothetical protein: hypothetical 35.0 kd protein in spoiiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbT yqbT Bacillus subtilis 1423 -11531490

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806322	5313	27469	207	68

Description

5000689662 hypothetical protein:hypothetical 16.2 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbS yqbS Bacillus subtilis 1423 -11531491  
115833 yqbs (de:hypothetical 16.2 kd protein in spoiii-cwla intergenic region) (db:swissprot) YQBS\_BACSU P45934 BACILLUS SUBTILIS 1423 -11531491  
7000688326 yqbs phage-related protein homolog yqbs (db:pir2.dat) F69948 F69948 Bacillus subtilis 1423 -11531491 216003 yqbs (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:48822) (re:49247) (di:direct) BACJH642 D84432 g1303759 Bacillus subtilis 1423 -11531491 216790 orf88 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiii-cwla) (le:30577) (re:31002) (di:direct) BACSKIN D32216 g1217866 Bacillus subtilis 1423 -11531491  
7500952364 yqbs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to phage-related protein) (le:70183) (re:70608) (di:complement) BSUB0014 Z99117 g2635044 Bacillus subtilis 1423 -11531491 6500727633 hypothetical protein:hypothetical 16.2 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbS yqbS Bacillus subtilis 1423 -11531491

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806325	5314	27470	564	187

Description

5000689661 hypothetical protein:hypothetical 9.5 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqBR yqBR Bacillus subtilis 1423 -11531492 115832 yqbr (de:hypothetical 9.5 kd protein in spoiiic-cwla intergenic region) (db:swissprot) YQBR\_BACSU P45933 BACILLUS SUBTILIS 1423 -11531492 7000688325 yqbr phage-related protein homolog yqbr (db:pir2.dat) E69948 E69948 Bacillus subtilis 1423 -11531492 216002 yqbr (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:48546) (re:48809) (di:direct) BACJH642 D84432 g1303758 Bacillus subtilis 1423 -11531492 216789 orf87 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiic.) (le:30301) (re:30564) (di:direct) BACSKIN D32216 g1217865 Bacillus subtilis 1423 -11531492 7500952363 yqbr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to phage-related protein) (le:70621) (re:70884) (di:complement) BSUB0014 Z99117 g2635045 Bacillus subtilis 1423 -11531492 6500727634 hypothetical protein:hypothetical 9.5 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqBR yqBR Bacillus subtilis 1423 -11531492

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501806326	5315	27471	855	284

Description

5000689660 hypothetical protein:hypothetical 37.0 kd protein in spoiiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbQ yqbQ Bacillus subtilis 1423 -11531493 115831 yqbq (de:hypothetical 37.0 kd protein in spoiiiic-cwla intergenic region) (db:swissprot) YQBQ\_BACSU P45950 BACILLUS SUBTILIS 1423 -11531493 7000688324 yqbq phage-related protein homolog yqbq (db:pir2.dat) D69948 D69948 Bacillus subtilis 1423 -11531493 216001 yqbq (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:47569) (re:48549) (di:direct) BACJH642 D84432 g1303757 Bacillus subtilis 1423 -11531493 216788 orf86 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which islocated between spoivcb and spoiiiic.) (le:29324) (re:30304) (di:direct) BACSKIN D32216 g1217864 Bacillus subtilis 1423 -11531493 7500952362 yqbq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to phage-related protein) (le:70881) (re:71861) (di:complement) BSUB0014 Z99117 g2635046 Bacillus subtilis 1423 -11531493 6500727635 hypothetical protein:hypothetical 37.0 kd protein in spoiiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbQ yqbQ Bacillus subtilis 1423 -11531493

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806336	5316	27472	669	223

Description

5000689659 hypothetical protein:hypothetical 25.3 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbP yqbP Bacillus subtilis 1423 -11531494  
115830 yqbp (de:hypothetical 25.3 kd protein in spoiii-cwla intergenic region) (db:swissprot) YQBP\_BACSU P45932 BACILLUS SUBTILIS 1423 -11531494  
7000688323 yqbp phage-related protein homolog yqbp (db:pir2.dat) C69948 C69948 Bacillus subtilis 1423 -11531494 216000 yqbp (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:46897) (re:47556) (di:direct) BACJH642 D84432 g1303756 Bacillus subtilis 1423 -11531494  
216787 orf85 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiii-cwla) (le:28652) (re:29311) (di:direct) BACSKIN D32216 g1217863 Bacillus subtilis 1423 -11531494  
7500952361 yqbp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to phage-related protein) (le:71874) (re:72533) (di:complement) BSUB0014 Z99117 g2635047 Bacillus subtilis 1423 -11531494 6500727636 hypothetical protein:hypothetical 25.3 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbP yqbP Bacillus subtilis 1423 -11531494

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806356	5317	27473	210	69

Description

5000689658 hypothetical protein:hypothetical 171.0 kd protein in spoiiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbO yqbO Bacillus subtilis 1423 -11531495  
 115829 yqbO (de:hypothetical 171.0 kd protein in spoiiiic-cwla intergenic region) (db:swissprot) YQBO\_BACSU P45931 BACILLUS SUBTILIS 1423 -11531495  
 7000688322 yqbO phage-related protein homolog yqbO (db:pir2.dat) B69948 B69948 Bacillus subtilis 1423 -11531495 215999 yqbO (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:42147) (re:46904) (di:direct) BACJH642 D84432 g1303755 Bacillus subtilis 1423 -11531495  
 216786 orf54 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which islocated between spoivcb and spoiiiic.) (le:23902) (re:28659) (di:direct) BACSKIN D32216 g1217862 Bacillus subtilis 1423 -11531495  
 7500952360 yqbO (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to phage-related protein) (le:72526) (re:77283) (di:complement) BSUB0014 Z99117 g2635048 Bacillus subtilis 1423 -11531495 6500727637 hypothetical protein:hypothetical 171.0 kd protein in spoiiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbO yqbO Bacillus subtilis 1423 -11531495

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806359	5318	27474	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806363	5319	27475	243	80

Description

5000689657 hypothetical protein:hypothetical 17.1 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbN yqbN Bacillus subtilis 1423 -11531496 115828 yqbN (de:hypothetical 17.1 kd protein in spoiii-cwla intergenic region) (db:swissprot) YQBN\_BACSU P45930 BACILLUS SUBTILIS 1423 -11531496 7000688321 yqbn phage-related protein homolog yqbn (db:pir2.dat) A69948 A69948 Bacillus subtilis 1423 -11531496 215998 yqbn (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:41516) (re:41965) (di:direct) BACJH642 D84432 g1303754 Bacillus subtilis 1423 -11531496 216785 orf55 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiii-cwla) (le:23271) (re:23720) (di:direct) BACSKIN D32216 g1217861 Bacillus subtilis 1423 -11531496 7500952359 yqbn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to phage-related protein) (le:77465) (re:77914) (di:complement) BSUB0014 Z99117 g2635049 Bacillus subtilis 1423 -11531496 6500727638 hypothetical protein:hypothetical 17.1 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbN yqbN Bacillus subtilis 1423 -11531496

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806367	5320	27476	270	89

Description

6500727639 yqcr:yqdb hypothetical protein:hypothetical 6.7 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqdB yqdB Bacillus subtilis 1423 -11531497 115849 yqdB (de:hypothetical 6.7 kd protein in spoiii-cwla intergenic region) (db:swissprot) YQDB\_BACSU P54373 BACILLUS SUBTILIS 1423 -11531497 7000688344 yqdb hypothetical protein yqdb (db:pir2.dat) E69950 E69950 Bacillus subtilis 1423 -11531497 215997 yqdb (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:41191) (re:41370) (di:complement) BACJH642 D84432 g1303753 Bacillus subtilis 1423 -11531497 7500952391 yqdb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:alternate gene name: yqcr) (le:78060) (re:78239) (di:direct) BSUB0014 Z99117 g2635050 Bacillus subtilis 1423 -11531497 5000689264 (de:(yqdb) (pn:hypothetical 6) (gtcfc:13.07) (ec:) (yqdb\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yqdB yqdB Bacillus subtilis 1423 10057575

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806368	5321	27477	249	83

Description

5000689656 hypothetical protein:hypothetical 16.3 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbM yqbM Bacillus subtilis 1423 -11531498 115827 yqbM (de:hypothetical 16.3 kd protein in spoiii-cwla intergenic region) (db:swissprot) YQBM\_BACSU P45929 BACILLUS SUBTILIS 1423 -11531498 7000688320 yqbM phage-related protein homolog yqbM (db:pir2.dat) H69947 H69947 Bacillus subtilis 1423 -11531498 215996 yqbM (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:40025) (re:40468) (di:direct) BACJH642 D84432 g1303752 Bacillus subtilis 1423 -11531498 216784 orf71 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiii-cwla.) (le:21780) (re:22223) (di:direct) BACSKIN D32216 g1217860 Bacillus subtilis 1423 -11531498 7500952358 yqbM (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to phage-related protein) (le:78962) (re:79405) (di:complement) BSUB0014 Z99117 g2635051 Bacillus subtilis 1423 -11531498 6500727640 hypothetical protein:hypothetical 16.3 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbM yqbM Bacillus subtilis 1423 -11531498

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806370	5322	27478	1464	487
<u>Description</u>				
5000689655 hypothetical protein:hypothetical 15.0 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbL yqbL Bacillus subtilis 1423 -11531499 115826 yqbl (de:hypothetical 15.0 kd protein in spoiiic-cwla intergenic region) (db:swissprot) YQBL_BACSU P45928 BACILLUS SUBTILIS 1423 -11531499 7000688319 yqbl phage-related protein homolog yqbl (db:pir2.dat) G69947 G69947 Bacillus subtilis 1423 -11531499 215995 yqbl (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:39618) (re:40022) (di:direct) BACJH642 D84432 g1303751 Bacillus subtilis 1423 -11531499 216783 orf70 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which islocated between spoivcb and spoiiic.) (le:21373) (re:21777) (di:direct) BACSKIN D32216 g1217859 Bacillus subtilis 1423 -11531499 7500952357 yqbl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to phage-related protein) (le:79408) (re:79812) (di:complement) BSUB0014 Z99117 g2635052 Bacillus subtilis 1423 -11531499 6500727641 hypothetical protein:hypothetical 15.0 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbL yqbL Bacillus subtilis 1423 -11531499				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806371	5323	27479	279	92
<u>Description</u>				
Hypothetical protein				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501806373	5324	27480	384	127

Description

5000689654 hypothetical protein:hypothetical 32.7 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbK yqbK Bacillus subtilis 1423 -11531500  
 115825 yqbk (de:hypothetical 32.7 kd protein in spoiiic-cwla intergenic region) (db:swissprot) YQBK\_BACSU P45927 BACILLUS SUBTILIS 1423 -11531500  
 7000688318 yqbk phage-related protein homolog yqbk (db:pir2.dat) F69947 F69947 Bacillus subtilis 1423 -11531500 215994 yqbk (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:38623) (re:39540) (di:direct) BACJH642 D84432 g1303750 Bacillus subtilis 1423 -11531500  
 7500952356 yqbk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to phage-related protein) (le:79890) (re:80807) (di:complement) BSUB0014 Z99117 g2635053 Bacillus subtilis 1423 -11531500 6500727642 hypothetical protein:hypothetical 32.7 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbK yqbK Bacillus subtilis 1423 -11531500

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501806384	5325	27481	210	69

Description

5000689653 hypothetical protein:hypothetical 16.8 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbJ yqbJ Bacillus subtilis 1423 -11531501  
 115824 yqbj (de:hypothetical 16.8 kd protein in spoiiic-cwla intergenic region) (db:swissprot) YQBJ\_BACSU P45926 BACILLUS SUBTILIS 1423 -11531501  
 7000688317 yqbj phage-related protein homolog yqbj (db:pir2.dat) E69947 E69947 Bacillus subtilis 1423 -11531501 215993 yqbj (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:37997) (re:38434) (di:direct) BACJH642 D84432 g1303749 Bacillus subtilis 1423 -11531501  
 216781 orf68 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiic.) (le:19753) (re:20190) (di:direct) BACSKIN D32216 g1217857 Bacillus subtilis 1423 -11531501  
 7500952355 yqbj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to phage-related protein) (le:80996) (re:81433) (di:complement) BSUB0014 Z99117 g2635054 Bacillus subtilis 1423 -11531501 6500727643 hypothetical protein:hypothetical 16.8 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbJ yqbJ Bacillus subtilis 1423 -11531501

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806388	5326	27482	855	284

#### Description

5000689652 hypothetical protein:hypothetical 19.9 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbI yqbI Bacillus subtilis 1423 -11531502  
 115823 yqbi (de:hypothetical 19.9 kd protein in spoiii-cwla intergenic region) (db:swissprot) YQBI\_BACSU P45925 BACILLUS SUBTILIS 1423 -11531502  
 7000688316 yqbi phage-related protein homolog yqbi (db:pir2.dat) D69947 D69947 Bacillus subtilis 1423 -11531502 215992 yqbi (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:37481) (re:37984) (di:direct) BACJH642 D84432 g1303748 Bacillus subtilis 1423 -11531502  
 216780 orf67 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiic.) (le:19237) (re:19740) (di:direct) BACSKIN D32216 g1217856 Bacillus subtilis 1423 -11531502  
 7500952354 yqbi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to phage-related protein) (le:81446) (re:81949) (di:complement) BSUB0014 Z99117 g2635055 Bacillus subtilis 1423 -11531502 6500727644 hypothetical protein:hypothetical 19.9 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbI yqbI Bacillus subtilis 1423 -11531502

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806390	5327	27483	522	173

#### Description

5000689651 hypothetical protein:hypothetical 14.3 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbH yqbH Bacillus subtilis 1423 -11531503  
 115822 yqbh (de:hypothetical 14.3 kd protein in spoiii-cwla intergenic region) (db:swissprot) YQBH\_BACSU P45924 BACILLUS SUBTILIS 1423 -11531503  
 7000688315 yqbh phage-related protein homolog yqbh (db:pir2.dat) C69947 C69947 Bacillus subtilis 1423 -11531503 215991 yqbh (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:37122) (re:37484) (di:direct) BACJH642 D84432 g1303747 Bacillus subtilis 1423 -11531503  
 7500952353 yqbh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to phage-related protein) (le:81946) (re:82308) (di:complement) BSUB0014 Z99117 g2635056 Bacillus subtilis 1423 -11531503 6500727645 hypothetical protein:hypothetical 14.3 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbH yqbH Bacillus subtilis 1423 -11531503



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501806399	5328	27484	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501806411	5329	27485	1431	477

Description

5000689650 hypothetical protein: hypothetical 14.7 kd protein in spoiiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbG yqbG Bacillus subtilis 1423 -11531504 115821 yqbg (de: hypothetical 14.7 kd protein in spoiiiic-cwla intergenic region) (db:swissprot) YQBG\_BACSU P45923 BACILLUS SUBTILIS 1423 -11531504 7000688314 yqbg hypothetical protein yqbg (db:pir2.dat) B69947 B69947 Bacillus subtilis 1423 -11531504 215990 yqbg (sr: bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de: bacillus subtilis dna, 283 kb region containing skin element.) (le:36730) (re:37125) (di:direct) BACJH642 D84432 g1303746 Bacillus subtilis 1423 -11531504 216779 orf76 (sr: bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de: bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiiic.) (le:18486) (re:18881) (di:direct) BACSKIN D32216 g1217855 Bacillus subtilis 1423 -11531504 7500952352 yqbg (fn:unknown) (db:genpept-bct1) (de: bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (le:82305) (re:82700) (di:complement) BSUB0014 Z99117 g2635057 Bacillus subtilis 1423 -11531504 6500727646 hypothetical protein: hypothetical 14.7 kd protein in spoiiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbG yqbG Bacillus subtilis 1423 -11531504

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806418	5330	27486	687	228

Description

5000689649 hypothetical protein:hypothetical 11.8 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbF yqbF Bacillus subtilis 1423 -11531505  
115820 yqbf (de:hypothetical 11.8 kd protein in spoiii-cwla intergenic region) (db:swissprot) YQBF\_BACSU P45922 BACILLUS SUBTILIS 1423 -11531505  
7000688313 yqbf hypothetical protein yqbf (db:pir2.dat) A69947 A69947 Bacillus subtilis 1423 -11531505 215989 yqbf (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:36415) (re:36726) (di:direct) BACJH642 D84432 g1303745 Bacillus subtilis 1423 -11531505 216778 orf77 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiii-c.) (le:18171) (re:18482) (di:direct) BACSKIN D32216 g1217854 Bacillus subtilis 1423 -11531505 7500952351 yqbf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (le:82704) (re:83015) (di:complement) BSUB0014 Z99117 g2635058 Bacillus subtilis 1423 -11531505 6500727647 hypothetical protein:hypothetical 11.8 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbF yqbF Bacillus subtilis 1423 -11531505

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806419	5331	27487	615	204

Description

5000689648 hypothetical protein:hypothetical 34.5 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbE yqbE Bacillus subtilis 1423 -11531506  
115819 yqbe (de:hypothetical 34.5 kd protein in spoiiic-cwla intergenic region) (db:swissprot) YQBE\_BACSU P45921 BACILLUS SUBTILIS 1423 -11531506  
7000688312 yqbe phage-related protein homolog yqbe (db:pir2.dat) H69946 H69946 Bacillus subtilis 1423 -11531506 215988 yqbe (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:35469) (re:36404) (di:direct) BACJH642 D84432 g1303744 Bacillus subtilis 1423 -11531506  
216777 orf53 (sr:bacillus subtilis (strain:jh642 (trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiic.) (le:17225) (re:18160) (di:direct) BACSKIN D32216 g1217853 Bacillus subtilis 1423 -11531506  
7500952350 yqbe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to phage-related protein) (le:83026) (re:83961) (di:complement) BSUB0014 Z99117 g2635059 Bacillus subtilis 1423 -11531506 6500727648 hypothetical protein:hypothetical 34.5 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbE yqbE Bacillus subtilis 1423 -11531506

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806420	5332	27488	573	190

Description

5000689647 hypothetical protein:hypothetical 36.2 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbD yqbD Bacillus subtilis 1423 -11531507 115818 yqbD (de:hypothetical 36.2 kd protein in spoiii-cwla intergenic region) (db:swissprot) YQBD\_BACSU P45920 BACILLUS SUBTILIS 1423 -11531507 7000688311 yqbD phage-related protein homolog yqbD (db:pir2.dat) G69946 G69946 Bacillus subtilis 1423 -11531507 215987 yqbD (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:34482) (re:35450) (di:direct) BACJH642 D84432 g1303743 Bacillus subtilis 1423 -11531507 216776 orf52 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiii-cwla) (le:16238) (re:17206) (di:direct) BACSKIN D32216 g1217852 Bacillus subtilis 1423 -11531507 7500952349 yqbD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to phage-related protein) (le:83980) (re:84948) (di:complement) BSUB0014 Z99117 g2635060 Bacillus subtilis 1423 -11531507 6500727649 hypothetical protein:hypothetical 36.2 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbD yqbD Bacillus subtilis 1423 -11531507

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806426	5333	27489	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501806430	5334	27490	582	193

Description

5000689646 hypothetical protein:hypothetical 25.3 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbc yqbc Bacillus subtilis 1423 -11531508 115817 yqbc (de:hypothetical 25.3 kd protein in spoiiic-cwla intergenic region) (db:swissprot) YQBC\_BACSU P45919 BACILLUS SUBTILIS 1423 -11531508 7000688310 yqbc hypothetical protein yqbc (db:pir2.dat) F69946 F69946 Bacillus subtilis 1423 -11531508 215986 yqbc (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:33796) (re:34449) (di:direct) BACJH642 D84432 g1303742 Bacillus subtilis 1423 -11531508 216775 orf84 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which islocated between spoivcb and spoiiic.) (le:15552) (re:16205) (di:direct) BACSKIN D32216 g1217851 Bacillus subtilis 1423 -11531508 7500952348 yqbc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:84981) (re:85634) (di:complement) BSUB0014 Z99117 g2635061 Bacillus subtilis 1423 -11531508 6500727650 hypothetical protein:hypothetical 25.3 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbc yqbc Bacillus subtilis 1423 -11531508

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501806439	5335	27491	462	153

Description

GTC ORF with score 458 to: (sr:aspergillus niger transposon ant1 chlorate-resistant mutant 46) (db:genpept-pln1) (de:orf1 3' of ant1 5' insertion site {niad insertion site}(aspergillus niger, chlorate-resistant mutant 46, transposon ant1,transposon, ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806452	5336	27492	315	104

Description

5000689645 hypothetical protein:hypothetical 34.9 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yqbB yqbB Bacillus subtilis 1423 -11531509  
115816 yqbb (de:hypothetical 34.9 kd protein in spoiiic-cwla intergenic region) (db:swissprot) YQBB\_BACSU P45918 BACILLUS SUBTILIS 1423 -11531509  
7000688309 yqbb hypothetical protein yqbb (db:pir2.dat) E69946 E69946  
Bacillus subtilis 1423 -11531509 215985 yqbb (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:32838) (re:33755)  
(di:direct) BACJH642 D84432 g1303741 Bacillus subtilis 1423 -11531509  
216774 orf66 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which islocated between spoivcb and spoiiic.) (le:14594) (re:15511)  
(di:direct) BACSKIN D32216 g1217850 Bacillus subtilis 1423 -11531509  
7500952347 yqbb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:85675) (re:86592) (di:complement) BSUB0014 Z99117 g2635062 Bacillus subtilis 1423 -11531509 6500727651 hypothetical protein:hypothetical 34.9 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbB yqbB Bacillus subtilis 1423 -11531509

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806453	5337	27493	510	169

Description

5000689644 hypothetical protein:hypothetical 58.5 kd protein in spoiiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbA yqbA Bacillus subtilis 1423 -11531510  
115815 yqbA (de:hypothetical 58.5 kd protein in spoiiiic-cwla intergenic region) (db:swissprot) YQBA\_BACSU P45917 BACILLUS SUBTILIS 1423 -11531510  
7000688308 yqbA phage-related protein homolog yqbA (db:pir2.dat) D69946  
D69946 Bacillus subtilis 1423 -11531510 215984 yqbA (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:31309) (re:32841) (di:direct) BACJH642 D84432 g1303740 Bacillus subtilis 1423 -11531510  
216773 orf51 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiiic.) (le:13065) (re:14597) (di:direct) BACSKIN D32216 g1217849 Bacillus subtilis 1423 -11531510  
7500952346 yqbA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to phage-related protein) (le:86589) (re:88121) (di:complement) BSUB0014 Z99117 g2635063 Bacillus subtilis 1423 -11531510 6500727652 hypothetical protein:hypothetical 58.5 kd protein in spoiiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqbA yqbA Bacillus subtilis 1423 -11531510

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806478	5338	27494	849	282

Description

5000689643 hypothetical protein:hypothetical 50.9 kd protein in spoiii-cwla intergenic region:orf50 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaT yqaT Bacillus subtilis 1423 -11531511 115814 yqat (de:(orf50)) (db:swissprot) YQAT\_BACSU P45916 BACILLUS SUBTILIS 1423 -11531511 7000688307 yqat phage-related terminase large subunit homolog yqat (db:pir2.dat) C69946 C69946 Bacillus subtilis 1423 -11531511 215983 yqat (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:30010) (re:31305) (di:direct) BACJH642 D84432 g1303739 Bacillus subtilis 1423 -11531511 216772 orf50 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiic.) (nt:similarity to spp1 terminase) (le:11766) (re:13061) (di:direct) BACSKIN D32216 g1217848 Bacillus subtilis 1423 -11531511 7500952345 yqat (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to phage-related terminase large subunit) (le:88125) (re:89420) (di:complement) BSUB0014 Z99117 g2635064 Bacillus subtilis 1423 -11531511 6500727653 hypothetical protein:hypothetical 50.9 kd protein in spoiii-cwla intergenic region:orf50 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaT yqaT Bacillus subtilis 1423 -11531511

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806491	5339	27495	216	71

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806492	5340	27496	666	221

Description

5000689642 hypothetical protein:hypothetical 27.7 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yqas yqas Bacillus subtilis 1423 -11531512  
115813 yqas (de:hypothetical 27.7 kd protein in spoiii-cwla intergenic region) (db:swissprot) YQAS\_BACSU P45915 BACILLUS SUBTILIS 1423 -11531512  
7000688306 yqas phage-related terminase small subunit homolog yqas  
(db:pir2.dat) B69946 B69946 Bacillus subtilis 1423 -11531512 215982 yqas  
(sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1)  
(de:bacillus subtilis dna, 283 kb region containing skin element.)  
(le:29298) (re:30017) (di:direct) BACJH642 D84432 g1303738 Bacillus subtilis 1423 -11531512 216771 orf43 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which islocated between spoivcb and spoiiic.) (le:11054) (re:11773) (di:direct) BACSKIN D32216 g1217847 Bacillus subtilis 1423 -11531512 7500952344 yqas (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to phage-related terminase small subunit) (le:89413) (re:90132) (di:complement) BSUB0014 Z99117 g2635065 Bacillus subtilis 1423 -11531512  
6500727654 hypothetical protein:hypothetical 27.7 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yqas yqas Bacillus subtilis 1423 -11531512

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806500	5341	27497	258	86

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806509	5342	27498	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806514	5343	27499	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501806517	5344	27500	258	85

Description

5000689641 hypothetical protein:hypothetical 18.1 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaR yqaR Bacillus subtilis 1423 -11531513 115812 yqaR (de:hypothetical 18.1 kd protein in spoiiic-cwla intergenic region) (db:swissprot) YQAR\_BACSU P45914 BACILLUS SUBTILIS 1423 -11531513 7000688305 yqaR hypothetical protein yqaR (db:pir2.dat) A69946 A69946 Bacillus subtilis 1423 -11531513 215981 yqaR (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:28766) (re:29230) (di:direct) BACJH642 D84432 g1303737 Bacillus subtilis 1423 -11531513 7500952343 yqaR (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:90200) (re:90664) (di:complement) BSUB0014 Z99117 g2635066 Bacillus subtilis 1423 -11531513 6500727655 hypothetical protein:hypothetical 18.1 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaR yqaR Bacillus subtilis 1423 -11531513

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501806523	5345	27501	438	145

Description

5000689640 hypothetical protein:hypothetical 17.9 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaQ yqaQ Bacillus subtilis 1423 -11531514 115811 yqaQ (de:hypothetical 17.9 kd protein in spoiiic-cwla intergenic region) (db:swissprot) YQAQ\_BACSU P45948 BACILLUS SUBTILIS 1423 -11531514 7000688304 yqaQ conserved hypothetical protein yqaQ (cl:hypothetical protein yjco) (db:pir2.dat) H69945 H69945 Bacillus subtilis 1423 -11531514 215980 yqaQ (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:28167) (re:28622) (di:direct) BACJH642 D84432 g1303736 Bacillus subtilis 1423 -11531514 216769 orf41 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which islocated between spoivcb and spoiiic.) (le:9923) (re:10378) (di:direct) BACSKIN D32216 g1217845 Bacillus subtilis 1423 -11531514 7500952342 yqaQ (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins from b. subtilis) (le:90808) (re:91263) (di:complement) BSUB0014 Z99117 g2635067 Bacillus subtilis 1423 -11531514 6500727656 hypothetical protein:hypothetical 17.9 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaQ yqaQ Bacillus subtilis 1423 -11531514

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501806524	5346	27502	282	93

Description

GTC ORF with score 95 to: (sr:mus sp. balb/c testes) (db:genpept-rod) (de:spot-1=nuclear localization signals (nls)-binding protein (mice,balb/c, testes, mrna, 1320 nt).) (nt:nuclear localization signals (nls)-binding protein;) (le:571) (re:990) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501806526	5347	27503	222	73

Description

5000689639 hypothetical protein:hypothetical 34.8 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaP yqaP Bacillus subtilis 1423 -11531515 115810 yqap (de:hypothetical 34.8 kd protein in spoiiic-cwla intergenic region) (db:swissprot) YQAP\_BACSU P45913 BACILLUS SUBTILIS 1423 -11531515 7000688303 yqap hypothetical protein yqap (db:pir2.dat) G69945 G69945 Bacillus subtilis 1423 -11531515 215979 yqap (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:27040) (re:27969) (di:complement) BACJH642 D84432 g1303735 Bacillus subtilis 1423 -11531515 216768 orf40 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which islocated between spoivcb and spoiiic.) (le:8796) (re:9725) (di:complement) BACSKIN D32216 g1217844 Bacillus subtilis 1423 -11531515 7500952341 yqap (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:91461) (re:92390) (di:direct) BSUB0014 Z99117 g2635068 Bacillus subtilis 1423 -11531515 6500727657 hypothetical protein:hypothetical 34.8 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaP yqaP Bacillus subtilis 1423 -11531515

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501806528	5348	27504	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501806533	5349	27505	861	286

Description

5000689638 hypothetical protein:hypothetical 7.6 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yqaO yqaO Bacillus subtilis 1423 -11531516  
115809 yqaO (de:hypothetical 7.6 kd protein in spoiii-cwla intergenic region) (db:swissprot) YQAO\_BACSU P45912 BACILLUS SUBTILIS 1423 -11531516  
7000688302 yqaO phage-related protein homolog yqaO (cl:hypothetical protein yqaO) (db:pir2.dat) F69945 F69945 Bacillus subtilis 1423 -11531516 215978  
yqaO (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna)  
(db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:26760) (re:26966) (di:direct) BACJH642 D84432 g1303734  
Bacillus subtilis 1423 -11531516 4000707469 hypothetical protein  
(sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1)  
(de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiic.) (le:8516) (re:8722) (di:direct) BACSKIN D32216  
g2252467 Bacillus subtilis 1423 -11531516 7500952340 yqaO (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to phage-related protein) (le:92464)  
(re:92670) (di:complement) BSUB0014 Z99117 g2635069 Bacillus subtilis 1423 -11531516 6500727658 hypothetical protein:hypothetical 7.6 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yqaO yqaO Bacillus subtilis 1423 -11531516

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806540	5350	27506	276	91

Description

5000689637 hypothetical protein:hypothetical 16.1 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaN yqaN Bacillus subtilis 1423 -11531517  
 115808 yqaN (de:hypothetical 16.1 kd protein in spoiii-cwla intergenic region) (db:swissprot) YQAN\_BACSU P45911 BACILLUS SUBTILIS 1423 -11531517  
 7000688301 yqaN hypothetical protein yqaN (db:pir2.dat) E69945 E69945 Bacillus subtilis 1423 -11531517 215977 yqaN (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:26250) (re:26678) (di:direct) BACJH642 D84432 G1303733 Bacillus subtilis 1423 -11531517  
 216767 orf39 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiii-cwla) (le:8006) (re:8434) (di:direct) BACSKIN D32216 G1217843 Bacillus subtilis 1423 -11531517  
 7500952339 yqaN (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (le:92752) (re:93180) (di:complement) BSUB0014 Z99117 G2635070 Bacillus subtilis 1423 -11531517 6500727659 hypothetical protein:hypothetical 16.1 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaN yqaN Bacillus subtilis 1423 -11531517

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806554	5351	27507	1041	346

Description

GTC ORF with score 144 to: (or:Sus scrofa) (fn:gel formation, gastric epithelial protection) (sr:pig) (db:genpept-mam) (de:sus scrofa yorkshire/chester white/hampshire clone pgm-ssz-9bgastric mucin mrna, partial cds.) (le:<1) (re:1584) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806559	5352	27508	918	306

Description

GTC ORF with score 588 to: (sr:acinetobacter sp. (strain ncib 9871) dna, clone puc2d3) (db:genpept-bct1) (de:acinetobacter sp. cyclohexanone monooxygenase gene, complete cds.) (nt:cyclohexanone monooxygenase) (le:391) (re:2022) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806563	5353	27509	318	106
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806579	5354	27510	435	144
<u>Description</u>				

5000689636 hypothetical protein: hypothetical 36.1 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqam yqam Bacillus subtilis 1423 -11531518 115807 yqam (de: hypothetical 36.1 kd protein in spoiiic-cwla intergenic region) (db:swissprot) YQAM\_BACSU P45910 BACILLUS SUBTILIS 1423 -11531518 7000688300 yqam phage-related protein homolog yqam (db:pir2.dat) D69945 D69945 Bacillus subtilis 1423 -11531518 215976 yqam (sr: bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de: bacillus subtilis dna, 283 kb region containing skin element.) (le:25073) (re:26014) (di:direct) BACJH642 D84432 g1303732 Bacillus subtilis 1423 -11531518 216766 orf34 (sr: bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de: bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiic.) (le:6829) (re:7770) (di:direct) BACSKIN D32216 g1217842 Bacillus subtilis 1423 -11531518 7500952338 yqam (fn:unknown) (db:genpept-bct1) (de: bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt: similar to phage-related protein) (le:93416) (re:94357) (di:complement) BSUB0014 Z99117 g2635071 Bacillus subtilis 1423 -11531518 6500727660 hypothetical protein: hypothetical 36.1 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqam yqam Bacillus subtilis 1423 -11531518

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806588	5355	27511	555	185
<u>Description</u>				

GTC ORF with score 473 to: (or:Caenorhabditis elegans) (db:genpept-inv) (de: caenorhabditis elegans cosmid r04b5, complete sequence.) (nt: similar to sorbitol dehydrogenase; cDNA est) (le:11086:11321:11598:11894) (re:11271:11547:11846:12008) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806593	5356	27512	276	91
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806597	5357	27513	564	187
<u>Description</u>				
5000689635 hypothetical protein:hypothetical 27.1 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaL yqaL Bacillus subtilis 1423 -11531519				
115806 yqaL (de:hypothetical 27.1 kd protein in spoiiic-cwla intergenic region) (db:swissprot) YQAL_BACSU P45909 BACILLUS SUBTILIS 1423 -11531519				
7000688299 yqaL hypothetical protein yqaL (db:pir2.dat) C69945 C69945 Bacillus subtilis 1423 -11531519 215975 yqaL (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:24490) (re:25191) (di:direct) BACJH642 D84432 g1303731 Bacillus subtilis 1423 -11531519				
216765 orf33 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which islocated between spoivcb and spoiiic.) (le:6246) (re:6947) (di:direct) BACSKIN D32216 g1217841 Bacillus subtilis 1423 -11531519				
7500952337 yqaL (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:94239) (re:94940) (di:complement) BSUB0014 Z99117 g2635072 Bacillus subtilis 1423 -11531519				
6500727661 hypothetical protein:hypothetical 27.1 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaL yqaL Bacillus subtilis 1423 -11531519				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806599	5358	27514	942	313

Description

5000689634 hypothetical protein:hypothetical 32.2 kd protein in spoiiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaK yqaK Bacillus subtilis 1423 -11531520 115805 yqaK (de:hypothetical 32.2 kd protein in spoiiiic-cwla intergenic region) (db:swissprot) YQAK\_BACSU P45908 BACILLUS SUBTILIS 1423 -11531520 7000688298 yqaK phage-related protein homolog yqaK (db:pir2.dat) B69945 B69945 Bacillus subtilis 1423 -11531520 215974 yqaK (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:23584) (re:24438) (di:direct) BACJH642 D84432 g1303730 Bacillus subtilis 1423 -11531520 216764 orf32 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiiic.) (le:5340) (re:6194) (di:direct) BACSKIN D32216 g1217840 Bacillus subtilis 1423 -11531520 7500952336 yqaK (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to phage-related protein) (le:94992) (re:95846) (di:complement) BSUB0014 Z99117 g2635073 Bacillus subtilis 1423 -11531520 6500727662 hypothetical protein:hypothetical 32.2 kd protein in spoiiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaK yqaK Bacillus subtilis 1423 -11531520

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501806607	5359	27515	384	127

Description

5000689633 hypothetical protein:hypothetical 37.0 kd protein in spoiiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaJ yqaJ Bacillus subtilis 1423 -11531521  
115804 yqaj (de:hypothetical 37.0 kd protein in spoiiiic-cwla intergenic region) (db:swissprot) YQAJ\_BACSU P45907 BACILLUS SUBTILIS 1423 -11531521  
7000688297 yqaj phage-related protein homolog yqaj (db:pir2.dat) A69945 A69945 Bacillus subtilis 1423 -11531521 215973 yqaj (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:22622) (re:23581) (di:direct) BACJH642 D84432 g1303729 Bacillus subtilis 1423 -11531521  
216763 orf21 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiiic.) (le:4378) (re:5337) (di:direct) BACSKIN D32216 g1217839 Bacillus subtilis 1423 -11531521  
7500952335 yqaj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to phage-related protein) (le:95849) (re:96808) (di:complement) BSUB0014 Z99117 g2635074 Bacillus subtilis 1423 -11531521 6500727663 hypothetical protein:hypothetical 37.0 kd protein in spoiiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaJ yqaJ Bacillus subtilis 1423 -11531521

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806610	5360	27516	888	295

Description

5000689632 hypothetical protein:hypothetical 7.6 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaI yqaI Bacillus subtilis 1423 -11531522  
115803 yqai (de:hypothetical 7.6 kd protein in spoiii-cwla intergenic region) (db:swissprot) YQAI\_BACSU P45906 BACILLUS SUBTILIS 1423 -11531522  
7000688296 yqai hypothetical protein yqai (db:pir2.dat) H69944 H69944 Bacillus subtilis 1423 -11531522 215972 yqai (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:22322) (re:22516) (di:direct) BACJH642 D84432 g1303728 Bacillus subtilis 1423 -11531522  
216762 orf20 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiic.) (le:4078) (re:4272) (di:direct) BACSKIN D32216 g1217838 Bacillus subtilis 1423 -11531522  
7500952334 yqai (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (le:96914) (re:97108) (di:complement) BSUB0014 Z99117 g2635075 Bacillus subtilis 1423 -11531522 6500727664 hypothetical protein:hypothetical 7.6 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaI yqaI Bacillus subtilis 1423 -11531522

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806617	5361	27517	312	103

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501806619	5362	27518	603	200

Description

5000689631 hypothetical protein:hypothetical 9.4 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaH yqaH Bacillus subtilis 1423 -11531523 115802 yqah (de:hypothetical 9.4 kd protein in spoiii-cwla intergenic region) (db:swissprot) YQAH\_BACSU P45905 BACILLUS SUBTILIS 1423 -11531523 7000688295 yqah hypothetical protein yqah (db:pir2.dat) G69944 G69944 Bacillus subtilis 1423 -11531523 215971 yqah (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:21935) (re:22192) (di:direct) BACJH642 D84432 g1303727 Bacillus subtilis 1423 -11531523 216761 orf19 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiii-cwla) (le:3691) (re:3948) (di:direct) BACSKIN D32216 g1217837 Bacillus subtilis 1423 -11531523 7500952333 yqah (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (le:97238) (re:97495) (di:complement) BSUB0014 Z99117 g2635076 Bacillus subtilis 1423 -11531523 6500727665 hypothetical protein:hypothetical 9.4 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaH yqaH Bacillus subtilis 1423 -11531523

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501806644	5363	27519	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501806647	5364	27520	462	153

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806649	5365	27521	468	155

Description

5000689630 hypothetical protein:hypothetical 21.4 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaG yqaG Bacillus subtilis 1423 -11531524  
115801 yqag (de:hypothetical 21.4 kd protein in spoiii-cwla intergenic region) (db:swissprot) YQAG\_BACSU P45904 BACILLUS SUBTILIS 1423 -11531524  
7000688294 yqag hypothetical protein yqag (db:pir2.dat) F69944 F69944 Bacillus subtilis 1423 -11531524 215970 yqag (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:21369) (re:21938) (di:direct) BACJH642 D84432 g1303726 Bacillus subtilis 1423 -11531524  
216760 orf18 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiic.) (le:3125) (re:3694) (di:direct) BACSKIN D32216 g1217836 Bacillus subtilis 1423 -11531524  
7500952332 yqag (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (le:97492) (re:98061) (di:complement) BSUB0014 Z99117 g2635077 Bacillus subtilis 1423 -11531524 6500727666 hypothetical protein:hypothetical 21.4 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaG yqaG Bacillus subtilis 1423 -11531524

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806655	5366	27522	192	63

Description

6500727667 yqcs:yqda hypothetical protein:hypothetical 5.3 kd protein in spoiiic-cwla intergenic region:orf8 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqda yqda Bacillus subtilis 1423 -11531525 115848 yqda (de:hypothetical 5.3 kd protein in spoiiic-cwla intergenic region (orf8)) (db:swissprot) YQDA\_BACSU P54372 BACILLUS SUBTILIS 1423 -11531525 7000688343 yqda hypothetical protein yqda (db:pir2.dat) D69950 D69950 Bacillus subtilis 1423 -11531525 215969 yqda (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:21155) (re:21295) (di:direct) BACJH642 D84432 g1303725 Bacillus subtilis 1423 -11531525 216759 orf17 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which islocated between spoivcb and spoiiic.) (le:2911) (re:3051) (di:direct) BACSKIN D32216 g1217835 Bacillus subtilis 1423 -11531525 7500952390 yqda (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yqcs) (le:98135) (re:98275) (di:complement) BSUB0014 Z99117 g2635078 Bacillus subtilis 1423 -11531525 5000689263 (de:(yqda) (pn:hypothetical 5) (gtcfc:13.07) (ec:) (yqda\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yqda yqda Bacillus subtilis 1423 10057574

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806657	5367	27523	318	105

Description

5000689629 hypothetical protein:hypothetical transcriptional regulator in spoiiiic-cwla intergenic region:orf8 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaF yqaF Bacillus subtilis 1423 -11531526 115800 yqaf (de:region (orf8)) (db:swissprot) YQAF\_BACSU P45903 BACILLUS SUBTILIS 1423 -11531526 7000688293 yqaf hypothetical protein yqaf (cl:phage phi-105 immunity repressor protein) (db:pir2.dat) E69944 E69944 Bacillus subtilis 1423 -11531526 215968 yqaf (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:20895) (re:21125) (di:direct) BACJH642 D84432 g1303724 Bacillus subtilis 1423 -11531526 216758 orf8 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which islocated between spoivcb and spoiiiic.) (nt:similarity to phi-105 cro-like protein) (le:2651) (re:2881) (di:direct) BACSKIN D32216 g1217834 Bacillus subtilis 1423 -11531526 7500952331 yqaf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:98305) (re:98535) (di:complement) BSUB0014 Z99117 g2635079 Bacillus subtilis 1423 -11531526 6500727668 hypothetical protein:hypothetical transcriptional regulator in spoiiiic-cwla intergenic region:orf8 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaF yqaF Bacillus subtilis 1423 -11531526

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501806666	5368	27524	264	87

Description

5000688926 hypothetical protein:hypothetical transcriptional regulator in spoiiic-cwla intergenic region:orf7 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaE yqaE Bacillus subtilis 1423 -11531527 115799 yqaE (de:region (orf7)) (db:swissprot) YQAE\_BACSU P45902 BACILLUS SUBTILIS 1423 -11531527 7000688292 yqaE transcription regulator phage-related homolog yqaE (cl:probable transcription repressor yowr) (db:pir2.dat) D69944 D69944 Bacillus subtilis 1423 -11531527 215967 yqaE (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:20368) (re:20718) (di:complement) BACJH642 D84432 g1303723 Bacillus subtilis 1423 -11531527 216757 orf7 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiic.) (nt:similarity to phi-105 immunity repressor) (le:2124) (re:2474) (di:co... BACSKIN D32216 g1217833 Bacillus subtilis 1423 -11531527 7500952326 yqaE (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to transcriptional regulator) (le:98712) (re:99062) (di:direct) BSUB0014 Z99117 g2635080 Bacillus subtilis 1423 -11531527 6500727669 hypothetical protein:hypothetical transcriptional regulator in spoiiic-cwla intergenic region:orf7 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaE yqaE Bacillus subtilis 1423 -11531527

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806667	5369	27525	450	150

Description

5000689628 hypothetical protein:hypothetical 6.8 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yqaD yqaD Bacillus subtilis 1423 -11531528  
115798 yqaD (de:hypothetical 6.8 kd protein in spoiiic-cwla intergenic region) (db:swissprot) YQAD\_BACSU P45901 BACILLUS SUBTILIS 1423 -11531528  
7000688291 yqaD hypothetical protein yqaD (db:pir2.dat) C69944 C69944 Bacillus subtilis 1423 -11531528 215966 yqaD (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:19934) (re:20101) (di:direct) BACJH642 D84432 g1303722 Bacillus subtilis 1423 -11531528  
216756 orf9 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which islocated between spoivcb and spoiiic.) (le:1690) (re:1857) (di:direct) BACSKIN D32216 g1217832 Bacillus subtilis 1423 -11531528  
7500952325 yqaD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:99329) (re:99496) (di:complement) BSUB0014 Z99117 g2635081 Bacillus subtilis 1423 -11531528 6500727670 hypothetical protein:hypothetical 6.8 kd protein in spoiiic-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaD yqaD Bacillus subtilis 1423 -11531528

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806672	5370	27526	576	191

Description

5000689627 hypothetical protein:hypothetical 20.7 kd protein in spoiii-cwla intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaC yqaC Bacillus subtilis 1423 -11531529 115797 yqaC (de:precursor) (db:swissprot) YQAC\_BACSU P45900 BACILLUS SUBTILIS 1423 -11531529 7000688290 yqaC hypothetical protein yqaC (db:pir2.dat) B69944 B69944 Bacillus subtilis 1423 -11531529 215965 yqaC (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:19042) (re:19578) (di:direct) BACJH642 D84432 g1303721 Bacillus subtilis 1423 -11531529 216755 orf6 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiiic.) (le:798) (re:1334) (di:direct) BACSKIN D32216 g1217831 Bacillus subtilis 1423 -11531529 7500952324 yqaC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (le:99852) (re:100388) (di:complement) BSUB0014 Z99117 g2635082 Bacillus subtilis 1423 -11531529 6500727671 hypothetical protein:hypothetical 20.7 kd protein in spoiii-cwla intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaC yqaC Bacillus subtilis 1423 -11531529

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806705	5371	27527	1347	448

Description

5000689626 hypothetical protein:hypothetical 20.6 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaB yqaB Bacillus subtilis 1423 -11531530  
 115796 yqab (de:hypothetical 20.6 kd protein in spoiii-cwla intergenic region) (db:swissprot) YQAB\_BACSU P45899 BACILLUS SUBTILIS 1423 -11531530  
 7000688289 yqab phage-related protein homolog yqab (db:pir2.dat) A69944 A69944 Bacillus subtilis 1423 -11531530 215964 yqab (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:18255) (re:18773) (di:complement) BACJH642 D84432 g1303720 Bacillus subtilis 1423 -11531530  
 216754 orf45 (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which is located between spoivcb and spoiii-cwla) (le:11) (re:529) (di:complement) BACSKIN D32216 g1217830 Bacillus subtilis 1423 -11531530  
 7500952319 yqab (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to phage-related protein) (le:100657) (re:101175) (di:direct) BSUB0014 Z99117 g2635083 Bacillus subtilis 1423 -11531530 6500727672 hypothetical protein:hypothetical 20.6 kd protein in spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqaB yqaB Bacillus subtilis 1423 -11531530

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806720	5372	27528	909	303

Description

5000689403 hypothetical protein:hypothetical 6.4 kd protein in bltr-spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkS yrkS Bacillus subtilis 1423 -11531531  
 116181 yrks (de:hypothetical 6.4 kd protein in bltr-spoiii-cwla intergenic region) (db:swissprot) YRKS\_BACSU P54446 BACILLUS SUBTILIS 1423 -11531531  
 7000688570 yrks hypothetical protein yrks (db:pir2.dat) A69978 A69978 Bacillus subtilis 1423 -11531531 215962 yrks (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:17468) (re:17632) (di:direct) BACJH642 D84432 g1303718 Bacillus subtilis 1423 -11531531  
 7500952689 yrks (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (le:101798) (re:101962) (di:complement) BSUB0014 Z99117 g2635085 Bacillus subtilis 1423 -11531531 6500727673 hypothetical protein:hypothetical 6.4 kd protein in bltr-spoiii-cwla intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkS yrkS Bacillus subtilis 1423 -11531531

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806737	5373	27529	717	238

Description

5000689402 hypothetical protein:hypothetical 16.5 kd protein in bltr-spoiiiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yrkR yrkR Bacillus subtilis 1423 -11531532  
116180 yrkr (de:hypothetical 16.5 kd protein in bltr-spoiiiic intergenic region) (db:swissprot) YRKR\_BACSU P54445 BACILLUS SUBTILIS 1423 -11531532  
7000688569 yrkr conserved hypothetical protein yrkr (cl:escherichia coli yjba protein) (db:pir2.dat) H69977 H69977 Bacillus subtilis 1423 -11531532  
215961 yrkr (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:16504) (re:16923) (di:direct) BACJH642 D84432 g1303717  
Bacillus subtilis 1423 -11531532 7500952688 yrkr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:102507) (re:102926) (di:complement) BSUB0014 Z99117 g2635086 Bacillus subtilis 1423 -11531532 6500727674 hypothetical protein:hypothetical 16.5 kd protein in bltr-spoiiiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkR yrkR Bacillus subtilis 1423 -11531532

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806745	5374	27530	384	128

Description

GTC ORF with score 102 to: (db:genpept-pln2) (de:emerella nidulans sterigmatocystin biosynthetic gene cluster:(stca), (stcb), (stcc), (stce), (aflr), (stcf), (stci), (stcj), (stck), (stcl), (stco), (stcq), (stcs), (stct), (stcu), (stcv) and(stcw) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806747	5375	27531	360	119

Description

GTC ORF with score 101 to: (db:genpept-pln2) (de:emerella nidulans sterigmatocystin biosynthetic gene cluster:(stca), (stcb), (stcc), (stce), (aflr), (stcf), (stci), (stcj), (stck), (stcl), (stco), (stcq), (stcs), (stct), (stcu), (stcv) and(stcw) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806755	5376	27532	192	63

Description

5000689401 hypothetical protein:hypothetical 49.7 kd protein in bltr-spoiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkQ yrkQ Bacillus subtilis 1423 -11531533 116179 yrkq (de:hypothetical 49.7 kd protein in bltr-spoiic intergenic region) (db:swissprot) YRKQ\_BACSU P54444 BACILLUS SUBTILIS 1423 -11531533 7000688568 yrkq two-component sensor histidine kinase homolog yrkq (db:pir2.dat) G69977 G69977 Bacillus subtilis 1423 -11531533 215960 yrkq (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:15163) (re:16461) (di:direct) BACJH642 D84432 g1303716 Bacillus subtilis 1423 -11531533 7500952687 yrkq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to two-component sensor histidine kinase) (le:102969) (re:104267) (di:complement) BSUB0014 Z99117 g2635087 Bacillus subtilis 1423 -11531533 6500727675 hypothetical protein:hypothetical 49.7 kd protein in bltr-spoiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkQ yrkQ Bacillus subtilis 1423 -11531533

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806758	5377	27533	438	145

Description

5000689400 hypothetical protein:hypothetical 26.8 kd sensory transduction protein in bltr-spoiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkP yrkP Bacillus subtilis 1423 -11531534 116178 yrkp (de:intergenic region) (db:swissprot) YRKP\_BACSU P54443 BACILLUS SUBTILIS 1423 -11531534 7000688567 yrkp two-component response regulator yrkq homolog yrkp) (cl:ompr protein:response regulator homology) (db:pir2.dat) F69977 F69977 Bacillus subtilis 1423 -11531534 215959 yrkp (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:14481) (re:15176) (di:direct) BACJH642 D84432 g1303715 Bacillus subtilis 1423 -11531534 7500952686 yrkp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to two-component response regulator (yrkq)) (le:104254) (re:104949) (di:complement) BSUB0014 Z99117 g2635088 Bacillus subtilis 1423 -11531534 6500727676 hypothetical protein:hypothetical 26.8 kd sensory transduction protein in bltr-spoiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkP yrkP Bacillus subtilis 1423 -11531534

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806775	5378	27534	204	68

Description

5000689399 hypothetical protein:hypothetical 46.4 kd protein in bltr-spoiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkO yrkO Bacillus subtilis 1423 -11531535  
 116177 yrko (de:hypothetical 46.4 kd protein in bltr-spoiic intergenic region) (db:swissprot) YRKO\_BACSU P54442 BACILLUS SUBTILIS 1423 -11531535  
 7000688566 yrko conserved hypothetical protein yrko (db:pir2.dat) E69977  
 E69977 Bacillus subtilis 1423 -11531535 215958 yrko (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:12996) (re:14213)  
 (di:complement) BACJH642 D84432 g1303714 Bacillus subtilis 1423 -11531535  
 7500952685 yrko (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:105217) (re:106434) (di:direct) BSUB0014 Z99117  
 g2635089 Bacillus subtilis 1423 -11531535 6500727677 hypothetical protein:hypothetical 46.4 kd protein in bltr-spoiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkO yrkO Bacillus subtilis 1423 -11531535

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806783	5379	27535	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806804	5380	27536	441	147

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806820	5381	27537	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806828	5382	27538	1680	559

Description

5000689398 hypothetical protein: hypothetical 21.3 kd protein in bltr-spoiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkN yrkN Bacillus subtilis 1423 -11531536  
 116176 yrkN (de: hypothetical 21.3 kd protein in bltr-spoiic intergenic region) (db:swissprot) YRKN\_BACSU P54441 BACILLUS SUBTILIS 1423 -11531536  
 7000688565 yrkN hypothetical protein yrkN (db:pir2.dat) D69977 D69977 Bacillus subtilis 1423 -11531536 215957 yrkN (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:11927) (re:12484) (di:complement) BACJH642 D84432 g1303713 Bacillus subtilis 1423 -11531536  
 7500952684 yrkN (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (le:106946) (re:107503) (di:direct) BSUB0014 Z99117 g2635090 Bacillus subtilis 1423 -11531536 6500727678 hypothetical protein: hypothetical 21.3 kd protein in bltr-spoiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkN yrkN Bacillus subtilis 1423 -11531536

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806844	5383	27539	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806845	5384	27540	243	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501806861	5385	27541	756	251

Description

5000689397 hypothetical protein:hypothetical 4.0 kd protein in bltr-spoiiiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkm yrkm Bacillus subtilis 1423 -11531537 116175 yrkm (de:hypothetical 4.0 kd protein in bltr-spoiiiic intergenic region) (db:swissprot) YRKM\_BACSU P54440 BACILLUS SUBTILIS 1423 -11531537 7000688564 yrkm hypothetical protein yrkm (db:pir2.dat) C69977 C69977 Bacillus subtilis 1423 -11531537 215956 yrkm (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:11741) (re:11848) (di:complement) BACJH642 D84432 g1303712 Bacillus subtilis 1423 -11531537 7500952683 yrkm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:107582) (re:107689) (di:direct) BSUB0014 Z99117 g2635091 Bacillus subtilis 1423 -11531537 6500727679 hypothetical protein:hypothetical 4.0 kd protein in bltr-spoiiiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkm yrkm Bacillus subtilis 1423 -11531537

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501806862	5386	27542	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806877	5387	27543	711	236

Description

5000689396 hypothetical protein:hypothetical nad:ph oxidoreductase in bltr-spoiiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkL yrkL Bacillus subtilis 1423 -11531538 116174 yrkL (ec:1.6.99.-) (de:putative nad(p)h oxidoreductase yrkL,) (db:swissprot) YRKL\_BACSU P54439 BACILLUS SUBTILIS 1423 -11531538 7000688563 yrkL nad p h oxidoreductase homolog yrkL (cl:probable nad(p)h oxidoreductase yabf) (db:pir2.dat) B69977 Bacillus subtilis 1423 -11531538 215955 yrkL (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:10912) (re:11436) (di:direct) BACJH642 D84432 g1303711 Bacillus subtilis 1423 -11531538 7500952682 yrkL (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to nad(p)h oxidoreductase) (le:107994) (re:108518) (di:complement) BSUB0014 Z99117 g2635092 Bacillus subtilis 1423 -11531538 6500727680 hypothetical protein:hypothetical nad:ph oxidoreductase in bltr-spoiiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkL yrkL Bacillus subtilis 1423 -11531538

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806882	5388	27544	600	200

Description

5000689395 hypothetical protein:hypothetical 17.8 kd protein in bltr-spoiiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkK yrkK Bacillus subtilis 1423 -11531539 116173 yrkK (de:hypothetical 17.8 kd protein in bltr-spoiiic intergenic region) (db:swissprot) YRKK\_BACSU P54438 BACILLUS SUBTILIS 1423 -11531539 7000688562 yrkK hypothetical protein yrkK (db:pir2.dat) A69977 A69977 Bacillus subtilis 1423 -11531539 215954 yrkK (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:10192) (re:10668) (di:direct) BACJH642 D84432 g1303710 Bacillus subtilis 1423 -11531539 7500952681 yrkK (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:108762) (re:109238) (di:complement) BSUB0014 Z99117 g2635093 Bacillus subtilis 1423 -11531539 6500727681 hypothetical protein:hypothetical 17.8 kd protein in bltr-spoiiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkK yrkK Bacillus subtilis 1423 -11531539



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806885	5389	27545	750	249

Description

5000689394 hypothetical protein:hypothetical 27.6 kd protein in bltr-spoiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkJ yrkJ Bacillus subtilis 1423 -11531540 116172 yrkJ (de:hypothetical 27.6 kd protein in bltr-spoiic intergenic region) (db:swissprot) YRKJ\_BACSU P54437 BACILLUS SUBTILIS 1423 -11531540 7000688561 yrkJ hypothetical protein yrkJ (db:pir2.dat) H69976 H69976 Bacillus subtilis 1423 -11531540 215953 yrkJ (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:8824) (re:9609) (di:direct) BACJH642 D84432 g1303709 Bacillus subtilis 1423 -11531540 7500952680 yrkJ (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:109821) (re:110606) (di:complement) BSUB0014 Z99117 g2635094 Bacillus subtilis 1423 -11531540 6500727682 hypothetical protein:hypothetical 27.6 kd protein in bltr-spoiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkJ yrkJ Bacillus subtilis 1423 -11531540

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806897	5390	27546	231	76

Description

5000689393 hypothetical protein:hypothetical 8.2 kd protein in bltr-spoiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkI yrkI Bacillus subtilis 1423 -11531541 116171 yrkI (de:hypothetical 8.2 kd protein in bltr-spoiic intergenic region) (db:swissprot) YRKI\_BACSU P54436 BACILLUS SUBTILIS 1423 -11531541 7000688560 yrkI conserved hypothetical protein yrkI (cl:conserved hypothetical protein hi0721) (db:pir2.dat) G69976 G69976 Bacillus subtilis 1423 -11531541 215952 yrkI (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:8536) (re:8763) (di:direct) BACJH642 D84432 g1303708 Bacillus subtilis 1423 -11531541 7500952679 yrkI (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:110667) (re:110894) (di:complement) BSUB0014 Z99117 g2635095 Bacillus subtilis 1423 -11531541 6500727683 hypothetical protein:hypothetical 8.2 kd protein in bltr-spoiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkI yrkI Bacillus subtilis 1423 -11531541

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806903	5391	27547	498	165

Description

5000689392 hypothetical protein:hypothetical 32.9 kd protein in bltr-spoiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkH yrkH Bacillus subtilis 1423 -11531542  
116170 yrkH (de:hypothetical 32.9 kd protein in bltr-spoiic intergenic region) (db:swissprot) YRKH\_BACSU P54435 BACILLUS SUBTILIS 1423 -11531542  
7000688559 yrkH conserved hypothetical protein yrkH (db:pir2.dat) F69976 F69976 Bacillus subtilis 1423 -11531542 215951 yrkH (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:7615) (re:8502) (di:direct) BACJH642 D84432 g1303707 Bacillus subtilis 1423 -11531542 7500952678 yrkH (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:110928) (re:111815) (di:complement) BSUB0014 Z99117 g2635096 Bacillus subtilis 1423 -11531542 6500727684 hypothetical protein:hypothetical 32.9 kd protein in bltr-spoiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkH yrkH Bacillus subtilis 1423 -11531542

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806920	5392	27548	288	95

Description

5000689391 hypothetical protein:hypothetical 4.2 kd protein in bltr-spoiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkG yrkG Bacillus subtilis 1423 -11531543  
116169 yrkG (de:hypothetical 4.2 kd protein in bltr-spoiic intergenic region) (db:swissprot) YRKG\_BACSU P54434 BACILLUS SUBTILIS 1423 -11531543  
7000688558 yrkG hypothetical protein yrkG (db:pir2.dat) E69976 E69976 Bacillus subtilis 1423 -11531543 215950 yrkG (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:7376) (re:7486) (di:direct) BACJH642 D84432 g1303706 Bacillus subtilis 1423 -11531543 7500952677 yrkG (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:111944) (re:112054) (di:complement) BSUB0014 Z99117 g2635097 Bacillus subtilis 1423 -11531543  
6500727685 hypothetical protein:hypothetical 4.2 kd protein in bltr-spoiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkG yrkG Bacillus subtilis 1423 -11531543

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501806928	5393	27549	432	144

Description

GTC ORF with score 176 to: (sr:mus musculus (strain:129) es cells dna, clone\_lib:p1) (db:genpept-rod) (de:mus musculus supl15h gene, exon 6,7 and complete cds.) (nt:compaired with cricetulus griseus sl15 mrna;) (le:ab014468:401:ab014469:406) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501806936	5394	27550	999	333

Description

5000689390 hypothetical protein:hypothetical 20.7 kd protein in bltr-spoiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkF yrkF Bacillus subtilis 1423 -11531544 116168 yrkf (de:hypothetical 20.7 kd protein in bltr-spoiic intergenic region) (db:swissprot) YRKF\_BACSU P54433 BACILLUS SUBTILIS 1423 -11531544 7000688557 yrkf conserved hypothetical protein yrkf (db:pir2.dat) D69976 D69976 Bacillus subtilis 1423 -11531544 215949 yrkf (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:6477) (re:7034) (di:direct) BACJH642 D84432 g1303705 Bacillus subtilis 1423 -11531544 7500952676 yrkf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins from b. subtilis) (le:112396) (re:112953) (di:complement) BSUB0014 Z99117 g2635098 Bacillus subtilis 1423 -11531544 6500727686 hypothetical protein:hypothetical 20.7 kd protein in bltr-spoiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkF yrkF Bacillus subtilis 1423 -11531544

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806942	5395	27551	618	205

Description

5000689389 hypothetical protein:hypothetical 17.8 kd protein in bltr-spoiiiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkE yrkE Bacillus subtilis 1423 -11531545 116167 yrke (de:hypothetical 17.8 kd protein in bltr-spoiiiic intergenic region) (db:swissprot) YRKE\_BACSU P54432 BACILLUS SUBTILIS 1423 -11531545 7000688556 yrke hypothetical protein yrke (db:pir2.dat) C69976 C69976 Bacillus subtilis 1423 -11531545 215948 yrke (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:5809) (re:6291) (di:direct) BACJH642 D84432 g1303704 Bacillus subtilis 1423 -11531545 7500952675 yrke (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:113139) (re:113621) (di:complement) BSUB0014 Z99117 g2635099 Bacillus subtilis 1423 -11531545 6500727687 hypothetical protein:hypothetical 17.8 kd protein in bltr-spoiiiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkE yrkE Bacillus subtilis 1423 -11531545

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806963	5396	27552	795	264

Description

5000689388 hypothetical protein:hypothetical 7.0 kd protein in bltr-spoiiiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkD yrkD Bacillus subtilis 1423 -11531546 116166 yrkd (de:hypothetical 7.0 kd protein in bltr-spoiiiic intergenic region) (db:swissprot) YRKD\_BACSU P54431 BACILLUS SUBTILIS 1423 -11531546 7000688555 yrkd hypothetical protein yrkd (db:pir2.dat) B69976 B69976 Bacillus subtilis 1423 -11531546 215947 yrkd (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:5473) (re:5664) (di:direct) BACJH642 D84432 g1303703 Bacillus subtilis 1423 -11531546 7500952674 yrkd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:113768) (re:113959) (di:complement) BSUB0014 Z99117 g2635100 Bacillus subtilis 1423 -11531546 6500727688 hypothetical protein:hypothetical 7.0 kd protein in bltr-spoiiiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkD yrkD Bacillus subtilis 1423 -11531546

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806968	5397	27553	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806974	5398	27554	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501806977	5399	27555	627	209

Description

5000689387 hypothetical protein: hypothetical 21.3 kd protein in bltr-spoiiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkC yrkC Bacillus subtilis 1423 -11531547 116165 yrkC (de: hypothetical 21.3 kd protein in bltr-spoiiic intergenic region) (db:swissprot) YRKC\_BACSU P54430 BACILLUS SUBTILIS 1423 -11531547 7000688554 yrkC hypothetical protein yrkC (db:pir2.dat) A69976 A69976 Bacillus subtilis 1423 -11531547 215946 yrkC (sr: bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de: bacillus subtilis dna, 283 kb region containing skin element.) (le:4120) (re:4680) (di:direct) BACJH642 D84432 g1303702 Bacillus subtilis 1423 -11531547 7500952673 yrkC (fn:unknown) (db:genpept-bct1) (de: bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (le:114752) (re:115312) (di:complement) BSUB0014 Z99117 g2635101 Bacillus subtilis 1423 -11531547 6500727689 hypothetical protein: hypothetical 21.3 kd protein in bltr-spoiiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkC yrkC Bacillus subtilis 1423 -11531547

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807011	5400	27556	1239	412

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807018	5401	27557	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807032	5402	27558	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807033	5403	27559	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807034	5404	27560	372	123

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807040	5405	27561	1143	380

Description

5000689386 hypothetical protein:hypothetical 5.6 kd protein in bltr-spoiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yrkB yrkB Bacillus subtilis 1423 -11531548  
116164 yrkb (de:hypothetical 5.6 kd protein in bltr-spoiic intergenic region) (db:swissprot) YRKB\_BACSU P54429 BACILLUS SUBTILIS 1423 -11531548  
7000688553 yrkb hypothetical protein yrkb (db:pir2.dat) H69975 H69975  
Bacillus subtilis 1423 -11531548 215945 yrkb (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:3748) (re:3894) (di:direct)  
BACJH642 D84432 g1303701 Bacillus subtilis 1423 -11531548 7500952672 yrkb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:115538) (re:115684) (di:complement) BSUB0014 Z99117 g2635102 Bacillus subtilis 1423 -11531548  
6500727690 hypothetical protein:hypothetical 5.6 kd protein in bltr-spoiic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yrkB yrkB Bacillus subtilis 1423 -11531548

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807042	5406	27562	291	96

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807048	5407	27563	411	136

Description

6500727691 hypothetical protein:similar to hemolysin-like (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrkA yrkA Bacillus subtilis 1423 -11531549 7500952668 yrka (de:hypothetical 49.0 kd protein in bltd-trka intergenic region) (db:swissprot) YRKA\_BACSU P54428 BACILLUS SUBTILIS 1423 -11531549 7000693090 yrka hemolysin-like homolog yrka (cl:hypothetical protein hi0107) (db:pir2.dat) G69975 G69975 Bacillus subtilis 1423 -11531549 1500692688 yrka hypothetical protein yrka (db:genpept-bct1) (de:bacillus subtilis aminoglycoside 6-adenylyltransferase (aadk) gene,partial cds, and yrda (yrda), yrdb (yrdb), hypothetical proteinyrdc (yrdc), yrdd (yrdd), hypothetical cytochrome p450 protein yrde(yrde), ribonuclease inhibitor (y... BSU93876 U93876 g1934660 Bacillus subtilis 1423 -11531549 7500952671 yrka (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hemolysin-like) (le:118778) (re:120082) (di:complement) BSUB0014 Z99117 g2635106 Bacillus subtilis 1423 -11531549

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807058	5408	27564	411	136

Description

6500727692 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrdR yrdR Bacillus subtilis 1423 -11531550 7000693859 yrdR hypothetical protein yrdR (db:pir2.dat) G69973 G69973 Bacillus subtilis 1423 -11531550 1500692687 yrdR hypothetical protein yrdR (db:genpept-bct1) (de:bacillus subtilis aminoglycoside 6-adenylyltransferase (aadk) gene,partial cds, and yrda (yrda), yrdb (yrdb), hypothetical proteinyrdc (yrdc), yrdd (yrdd), hypothetical cytochrome p450 protein yrde(yrde), ribonuclease inhibitor (y... BSU93876 U93876 g1934659 Bacillus subtilis 1423 -11531550 7500964669 yrdR (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:120506) (re:121471) (di:complement) BSUB0014 Z99117 g2635107 Bacillus subtilis 1423 -11531550

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807071	5409	27565	978	325

Description

6500727693 hypothetical protein:similar to transcriptional regulator:lysr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrdQ yrdQ Bacillus subtilis 1423 -11531551 7000694758 yrdq transcription regulator lysr family homolog yrdq (cl:pseudomonas putida regulatory protein catr) (db:pir2.dat) F69973 F69973 Bacillus subtilis 1423 -11531551 220154 (db:genpept-bct1) (de:bacillus subtilis czcd (czcd) gene, partial cds, trka (trka) gene,complete cds.) (nt:orfr) (le:2135) (re:3001) (di:complement) BSU62055 U62055 g1772644 Bacillus subtilis 1423 -11531551 1500689780 yrdq lysr family transcription regulator yrdq (db:genpept-bct1) (de:bacillus subtilis aminoglycoside 6-adenylyltransferase (aadk) gene,partial cds, and yrda (yrda), yrdb (yrdb), hypothetical proteinyrdc (yrdc), yrdd (yrdd), hypothetical cytochrome p450 protein yrde(yrde), ribonuclease inhibitor (y... BSU93876 U93876 g1934658 Bacillus subtilis 1423 -11531551 7500965328 yrdq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to transcriptional regulator (lysr family)) (le:121597) (re:122463) (di:direct) BSUB0014 Z99117 g2635108 Bacillus subtilis 1423 -11531551

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807085	5410	27566	891	297

Description

6500727694 yrdp:trka hypothetical protein:potassium uptake (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) trkA trkA Bacillus subtilis 1423 -11531552 7000694440 trka potassium uptake trka (db:pir2.dat) E69725 E69725 Bacillus subtilis 1423 -11531552 1500692686 yrdp hypothetical protein yrdp (db:genpept-bct1) (de:bacillus subtilis aminoglycoside 6-adenylyltransferase (aadk) gene,partial cds, and yrda (yrda), yrdb (yrdb), hypothetical proteinyrdc (yrdc), yrdd (yrdd), hypothetical cytochrome p450 protein yrde(yrde), ribonuclease inhibitor (y... BSU93876 U93876 g1934657 Bacillus subtilis 1423 -11531552 7500965095 trka (fn:potassium uptake) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yrdp) (le:122586) (re:123623) (di:complement) BSUB0014 Z99117 g2635109 Bacillus subtilis 1423 -11531552

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807088	5411	27567	282	93

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807102	5412	27568	501	166

Description

6500727695 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrdN yrdN Bacillus subtilis 1423 -11531553  
7500952641 yrdn (de:hypothetical protein in czcd-gltr intergenic region (orf129)) (db:swissprot) YRDN\_BACSU P94502 BACILLUS SUBTILIS 1423 -11531553  
7000693858 yrdn hypothetical protein yrdn (cl:hypothetical protein yrdn) (db:pir2.dat) E69973 E69973 Bacillus subtilis 1423 -11531553 220199 orf129 orf129 (fn:putative target of gltr) (db:genpept-bct1) (de:bacillus subtilis brnq (brnq), orf105 (orf105), lysr-typetranscription regulator gltr (gltr) and orf129 (orf129) genes,complete cds.) (nt:putative 15k protein) (le:3076) (re:3465) (di:direct) BSU79494 U79494 g1710376 Bacillus subtilis 1423 -11531553 1500689782 yrdn yrdn (db:genpept-bct1) (de:bacillus subtilis aminoglycoside 6-adenylyltransferase (aadk) gene,partial cds, and yrda (yrda), yrdb (yrdb), hypothetical proteinyrdc (yrdc), yrdd (yrdd), hypothetical cytochrome p450 protein yrde(yrde), ribonuclease inhibitor (y... BSU93876 U93876 g1934655 Bacillus subtilis 1423 -11531553 7500952643 yrdn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:124933) (re:125322) (di:complement) BSUB0014 Z99117 g2635111 Bacillus subtilis 1423 -11531553 295589 orf129 orf129 (fn:putative target of gltr) (db:genpept-bct1) (de:bacillus subtilis brnq (brnq), orf105 (orf105), lysr-typetranscription regulator gltr (gltr) and orf129 (orf129) genes,complete cds.) (nt:putative 15k protein) (le:3076) (re:3465) (di:direct) BSU79494 U79494 g1710376 Bacillus subtilis 1423 -11531553

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807114	5413	27569	321	106

Description

6500727696 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrdK yrdK Bacillus subtilis 1423 -11531554  
7500952638 yrdk (de:hypothetical 12.3 kd protein in gltr-brnq intergenic region (orf105)) (db:swissprot) YRDK\_BACSU P94500 BACILLUS SUBTILIS 1423 -11531554 7000693857 yrdk hypothetical protein yrdk (db:pir2.dat) D69973 D69973 Bacillus subtilis 1423 -11531554 220197 orf105 orf105 (db:genpept-bct1) (de:bacillus subtilis brnq (brnq), orf105 (orf105), lysr-typetranscription regulator gltr (gltr) and orf129 (orf129) genes,complete cds.) (nt:putative 12k protein) (le:1377) (re:1694) (di:direct) BSU79494 U79494 g1710374 Bacillus subtilis 1423 -11531554 1500689781 yrdk yrdk (db:genpept-bct1) (de:bacillus subtilis aminoglycoside 6-adenylyltransferase (aadk) gene,partial cds, and yrda (yrda), yrdb (yrdb), hypothetical proteinyrdc (yrdc), yrdd (yrdd), hypothetical cytochrome p450 protein yrde(yrde), ribonuclease inhibitor (y... BSU93876 U93876 g1934653 Bacillus subtilis 1423 -11531554 7500952640 yrdk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:126704) (re:127021) (di:complement) BSUB0014 Z99117 g2635113 Bacillus subtilis 1423 -11531554 295587 orf105 orf105 (db:genpept-bct1) (de:bacillus subtilis brnq (brnq), orf105 (orf105), lysr-typetranscription regulator gltr (gltr) and orf129 (orf129) genes,complete cds.) (nt:putative 12k protein) (le:1377) (re:1694) (di:direct) BSU79494 U79494 g1710374 Bacillus subtilis 1423 -11531554

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807118	5414	27570	282	93

Description

6500727697 hypothetical protein:similar to ribonuclease inhibitor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrdF yrdF Bacillus subtilis 1423 -11531555 7000694516 yrdF ribonuclease inhibitor homolog yrdF (cl:bacillus ribonuclease inhibitor) (db:pir2.dat) C69973 C69973 Bacillus subtilis 1423 -11531555 500685413 hypothetical barstar-like protein (db:genpept-bct1) (de:bacillus subtilis cypa, azlb, azlc and azld genes orf49 and orf91.) (nt:orf91) (le:2696) (re:2971) (di:direct) BSCYPAZL Y11043 g1926279 Bacillus subtilis 1423 -11531555 1500689773 yrdF ribonuclease inhibitor (db:genpept-bct1) (de:bacillus subtilis aminoglycoside 6-adenylyltransferase (aadk) gene,partial cds, and yrda (yrda), yrdb (yrdb), hypothetical proteinyrdc (yrdc), yrdd (yrdd), hypothetical cytochrome p450 protein yrde(yrde), ribonuclease inhibitor (y... BSU93876 U93876 g1934648 Bacillus subtilis 1423 -11531555 7500954537 yrdF (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to ribonuclease inhibitor) (le:130379) (re:130654) (di:complement) BSUB0014 Z99117 g2635118 Bacillus subtilis 1423 -11531555

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807126	5415	27571	939	312

Description

GTC ORF with score 410 to: (db:genpept-bct1) (de:haloferax volcanii plasmid phv3 aminotransferase gene, partial cds, dehydrogenase and hydantoinase genes, complete cds, and oligopeptide abc transporter gene, partial cds.) (nt:expressed during exponential...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807131	5416	27572	660	219

Description

6500727698 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrdD yrdD Bacillus subtilis 1423 -11531556 7000693856 yrdd hypothetical protein yrdd (db:pir2.dat) B69973 B69973 Bacillus subtilis 1423 -11531556 500685411 hypothetical protein (db:genpept-bct1) (de:b.subtilis cypa, azlb, azlc and azld genes orf49 and orf91.) (nt:orf49) (le:650) (re:799) (di:direct) BSCYPAZL Y11043 g1926277 Bacillus subtilis 1423 -11531556 1500689771 yrdd yrdd (db:genpept-bct1) (de:bacillus subtilis aminoglycoside 6-adenylyltransferase (aadk) gene, partial cds, and yrda (yrda), yrdb (yrdb), hypothetical proteinyrdc (yrdc), yrdd (yrdd), hypothetical cytochrome p450 protein yrde (yrde), ribonuclease inhibitor (y... BSU93876 U93876 g1934646 Bacillus subtilis 1423 -11531556 7500964668 yrdd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (le:132551) (re:132700) (di:complement) BSUB0014 Z99117 g2635120 Bacillus subtilis 1423 -11531556

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807135	5417	27573	339	113

Description

6500727699 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrdC yrdC Bacillus subtilis 1423 -11531557 7000693855 yrdC hypothetical protein yrdC (cl:hypothetical protein yddq) (db:pir2.dat) A69973 A69973 Bacillus subtilis 1423 -11531557 1500692682 yrdC hypothetical protein yrdC (db:genpept-bct1) (de:bacillus subtilis aminoglycoside 6-adenylyltransferase (aadk) gene, partial cds, and yrda (yrda), yrdb (yrdb), hypothetical proteinyrdC (yrdc), yrdd (yrdd), hypothetical cytochrome p450 protein yrde (yrde), ribonuclease inhibitor (y... BSU93876 U93876 g1934645 Bacillus subtilis 1423 -11531557 7500955949 yrdC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (le:132799) (re:133362) (di:complement) BSUB0014 Z99117 g2635121 Bacillus subtilis 1423 -11531557

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807140	5418	27574	516	171

Description

6500727700 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrdB yrdB Bacillus subtilis 1423 -11531558  
7502851721 yrdB (de:hypothetical 13.9 kd protein in cypa-aadk intergenic region) (db:swissprot) YRDB\_BACSU 007080 BACILLUS SUBTILIS 1423 -11531558  
7000693854 yrdB hypothetical protein yrdB (db:pir2.dat) H69972 H69972 Bacillus subtilis 1423 -11531558 1500692681 yrdB yrdB (db:genpept-bct1) (de:bacillus subtilis aminoglycoside 6-adenylyltransferase (aadk) gene,partial cds, and yrda (yrda), yrdB (yrdB), hypothetical proteinyrdc (yrdc), yrdd (yrdd), hypothetical cytochrome p450 protein yrde(yrde), ribonuclease inhibitor (y... BSU93876 U93876 g1934644 Bacillus subtilis 1423 -11531558 7500964667 yrdB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:133591) (re:133962) (di:complement) BSUB0014 Z99117 g2635122 Bacillus subtilis 1423 -11531558

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807148	5419	27575	258	86

Description

6500727701 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrdA yrdA Bacillus subtilis 1423 -11531559  
7502851722 yrdA (de:hypothetical 18.9 kd protein in cypa-aadk intergenic region) (db:swissprot) YRDA\_BACSU 007079 BACILLUS SUBTILIS 1423 -11531559  
7000693853 yrdA hypothetical protein yrdA (db:pir2.dat) G69972 G69972 Bacillus subtilis 1423 -11531559 1500692680 yrdA yrdA (db:genpept-bct1) (de:bacillus subtilis aminoglycoside 6-adenylyltransferase (aadk) gene,partial cds, and yrda (yrda), yrdB (yrdB), hypothetical proteinyrdc (yrdc), yrdd (yrdd), hypothetical cytochrome p450 protein yrde(yrde), ribonuclease inhibitor (y... BSU93876 U93876 g1934643 Bacillus subtilis 1423 -11531559 7500964666 yrdA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:134772) (re:135275) (di:complement) BSUB0014 Z99117 g2635123 Bacillus subtilis 1423 -11531559

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807149	5420	27576	1764	587

Description

6500727702 hypothetical protein:similar to 2-nitropropane dioxygenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrpB yrpB Bacillus subtilis 1423 -11531560 7000692038 yrpB 2-nitropropane dioxygenase homolog yrpB (db:pir2.dat) B69978 B69978 Bacillus subtilis 1423 -11531560 1500692677 yrpB 2-nitropropane dioxygenase (db:genpept-bct1) (de:bacillus subtilis alcohol dehydrogenase (adhb) gene, partial cds,hypothetical spore coat protein (yraf), hypothetical spore coatprotein (yrag), yrah (yrah), yrai (yrai), yraj (yraj), yrak (yrak), yral (yral), chitosanase precursor ... BSU93875 U93875 g1934639 Bacillus subtilis 1423 -11531560 7500963290 yrpB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to 2-nitropropane dioxygenase) (le:136734) (re:137777) (di:direct) BSUB0014 Z99117 g2635125 Bacillus subtilis 1423 -11531560

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807164	5421	27577	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807172	5422	27578	321	106

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807173	5423	27579	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807178	5424	27580	351	116

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807184	5425	27581	189	62

Description

6500727703 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrpD yrpD Bacillus subtilis 1423 -11531561 7502851723 yrpD (de:hypothetical 24.9 kd protein in aadk-sigz intergenic region) (db:swissprot) YRPD\_BACSU 005411 BACILLUS SUBTILIS 1423 -11531561 7000692726 yrpD conserved hypothetical protein yrpD (db:pir2.dat) D69978 D69978 Bacillus subtilis 1423 -11531561 1500692675 yrpD yrpD (db:genpept-bct1) (de:bacillus subtilis alcohol dehydrogenase (adhb) gene, partial cds,hypothetical spore coat protein (yraf), hypothetical spore coatprotein (yrag), yrah (yrah), yrai (yrai), yraj (yraj), yrak (yrak),yral (yral), chitosanase precursor ... BSU93875 U93875 g1934637 Bacillus subtilis 1423 -11531561 7500963810 yrpD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins from b. subtilis) (le:139305) (re:140012) (di:direct) BSUB0014 Z99117 g2635127 Bacillus subtilis 1423 -11531561

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807200	5426	27582	1302	433

Description

6500727704 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrpE yrpE Bacillus subtilis 1423 -11531562 7502851724 yrpe (de:hypothetical 28.9 kd protein in aadk-sigz intergenic region) (db:swissprot) YRPE\_BACSU 005410 BACILLUS SUBTILIS 1423 -11531562 7000692727 yrpe conserved hypothetical protein yrpe (cl:hypothetical protein yrpe) (db:pir2.dat) E69978 E69978 Bacillus subtilis 1423 -11531562 1500692674 yrpe yrpe (db:genpept-bct1) (de:bacillus subtilis alcohol dehydrogenase (adhb) gene, partial cds,hypothetical spore coat protein (yraf), hypothetical spore coatprotein (yrag), yrah (yrah), yrai (yrai), yraj (yraj), yrak (yrak),yral (yral), chitosanase precursor ... BSU93875 U93875 g1934636 Bacillus subtilis 1423 -11531562 7500955901 yrpe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:141176) (re:141931) (di:complement) BSUB0014 Z99117 g2635128 Bacillus subtilis 1423 -11531562

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807210	5427	27583	726	241

Description

6500727705 hypothetical protein:similar to sugar-phosphate dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrpG yrpG Bacillus subtilis 1423 -11531563 7000694652 yrpG sugar-phosphate dehydrogenase homolog yrpG (cl:conserved hypothetical protein ypl088w) (db:pir2.dat) F69978 F69978 Bacillus subtilis 1423 -11531563 1500692672 yrpG yrpG (db:genpept-bct1) (de:bacillus subtilis alcohol dehydrogenase (adhb) gene, partial cds,hypothetical spore coat protein (yraf), hypothetical spore coatprotein (yrag), yrah (yrah), yrai (yrai), yraj (yraj), yrak (yrak), yral (yral), chitosanase precursor ... BSU93875 U93875 g1934634 Bacillus subtilis 1423 -11531563 7500965236 yrpG (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to sugar-phosphate dehydrogenase) (le:142758) (re:143708) (di:direct) BSUB0014 Z99117 g2635130 Bacillus subtilis 1423 -11531563

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807212	5428	27584	351	117

Description

6500727706 hypothetical protein:similar to citrate transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yraO yraO Bacillus subtilis 1423 -11531564 7000692376 yraO citrate transporter homolog yraO (db:pir2.dat) G69971 G69971 Bacillus subtilis 1423 -11531564 1500692671 yraO yraO (db:genpept-bct1) (de:bacillus subtilis alcohol dehydrogenase (adhb) gene, partial cds,hypothetical spore coat protein (yraf), hypothetical spore coatprotein (yrag), yrah (yrah), yrai (yrai), yraj (yraj), yrak (yrak), yral (yral), chitosanase precursor ... BSU93875 U93875 g1934633 Bacillus subtilis 1423 -11531564 7500963539 yraO (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to citrate transporter) (le:143982) (re:145298) (di:complement) BSUB0014 Z99117 g2635131 Bacillus subtilis 1423 -11531564

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807216	5429	27585	1251	416

Description

6500727707 hypothetical protein:similar to transcriptional regulator:lysr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yraN yraN Bacillus subtilis 1423 -11531565 7000694757 yran transcription regulator lysr family homolog yran (db:pir2.dat) F69971 F69971 Bacillus subtilis 1423 -11531565 1500692669 yran transcriptional regulator (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on the chromosome.) (nt:lysr family) (le:21849) (re:22718) (di:direct) BS233DEG X92868 g2108283 Bacillus subtilis 1423 -11531565 1500692670 yran lysr-family transcription regulator (db:genpept-bct1) (de:bacillus subtilis alcohol dehydrogenase (adhb) gene, partial cds,hypothetical spore coat protein (yraf), hypothetical spore coatprotein (yrag), yrah (yrah), yrai (yrai), yraj (yraj), yrak (yrak), yral (yral), chitosanase precursor ... BSU93875 U93875 g1934632 Bacillus subtilis 1423 -11531565 7500965327 yran (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to transcriptional regulator (lysr family)) (le:145413) (re:146282) (di:complement) BSUB0014 Z99117 g2635132 Bacillus subtilis 1423 -11531565

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807220	5430	27586	228	75

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807228	5431	27587	288	95

Description

6500727708 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yram yram Bacillus subtilis 1423 -11531566 7000688521 yram (de:hypothetical 39.5 kd protein in sigz-csn intergenic region) (db:swissprot) YRAM\_BACSU 007931 BACILLUS SUBTILIS 1423 -11531566 7000688522 yram conserved hypothetical protein yram (db:pir2.dat) E69971 E69971 Bacillus subtilis 1423 -11531566 1500692667 yram unknown (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on thechromosome.) (nt:putative) (le:20601) (re:21704) (di:complement) BS233DEG X92868 g2108282 Bacillus subtilis 1423 -11531566 1500692668 yram yram (db:genpept-bct1) (de:bacillus subtilis alcohol dehydrogenase (adhb) gene, partial cds,hypothetical spore coat protein (yraf), hypothetical spore coatprotein (yrag), yrah (yrah), yrai (yrai), yraj (yraj), yrak (yrak), yral (yral), chitosanase precursor ... BSU93875 U93875 g1934631 Bacillus subtilis 1423 -11531566 7500952599 yram (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:146427) (re:147530) (di:direct) BSUB0014 Z99117 g2635133 Bacillus subtilis 1423 -11531566

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807233	5432	27588	708	235

Description

GTC ORF with score 311 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1608.) (nt:unnamed protein product) (le:<1) (re:738) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807239	5433	27589	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807254	5434	27590	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807259	5435	27591	933	310

Description

6500727709 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yral yral Bacillus subtilis 1423 -11531567 7000692722 yral conserved hypothetical protein yral (db:pir2.dat) D69971 D69971 Bacillus subtilis 1423 -11531567 1500692663 yral unknown (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on thechromosome.) (nt:putative) (le:18789) (re:19052) (di:complement) BS233DEG X92868 g2108280 Bacillus subtilis 1423 -11531567 1500692664 yral yral (db:genpept-bct1) (de:bacillus subtilis alcohol dehydrogenase (adhb) gene, partial cds,hypothetical spore coat protein (yraf), hypothetical spore coatprotein (yrag), yrah (yrah), yrai (yrai), yraj (yraj), yrak (yrak),yral (yral), chitosanase precursor ... BSU93875 U93875 g1934629 Bacillus subtilis 1423 -11531567 7500963806 yral (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins from b. subtilis) (le:149079) (re:149342) (di:direct) BSUB0014 Z99117 g2635135 Bacillus subtilis 1423 -11531567

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807265	5436	27592	960	319

Description

6500727710 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrak yrak Bacillus subtilis 1423 -11531568 7000692721 yrak conserved hypothetical protein yrak (db:pir2.dat) C69971 C69971 Bacillus subtilis 1423 -11531568 1500692661 yrak unknown (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on thechromosome.) (nt:putative) (le:17963) (re:18652) (di:complement) BS233DEG X92868 g2108279 Bacillus subtilis 1423 -11531568 1500692662 yrak yrak (db:genpept-bct1) (de:bacillus subtilis alcohol dehydrogenase (adhb) gene, partial cds,hypothetical spore coat protein (yraf), hypothetical spore coatprotein (yrag), yrah (yrah), yrai (yrai), yraj (yraj), yrak (yrak),yral (yral), chitosanase precursor ... BSU93875 U93875 g1934628 Bacillus subtilis 1423 -11531568 7500963805 yrak (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins from b. subtilis) (le:149479) (re:150168) (di:direct) BSUB0014 Z99117 g2635136 Bacillus subtilis 1423 -11531568

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807276	5437	27593	237	78
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807288	5438	27594	1473	490
<u>Description</u>				

6500727711 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yraj yraj Bacillus subtilis 1423 -11531569 7502851725 yraj (de:hypothetical 13.1 kd protein in csu-adhb intergenic region) (db:swissprot) YRAJ\_BACSU O07934 BACILLUS SUBTILIS 1423 -11531569 7000692720 yraj conserved hypothetical protein yraj (db:pir2.dat) B69971 B69971 Bacillus subtilis 1423 -11531569 1500692659 yraj unknown (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on the chromosome.) (nt:putative) (le:17068) (re:17430) (di:direct) BS233DEG X92868 g2108278 Bacillus subtilis 1423 -11531569 1500692660 yraj yraj (db:genpept-bct1) (de:bacillus subtilis alcohol dehydrogenase (adhb) gene, partial cds, hypothetical spore coat protein (yraf), hypothetical spore coat protein (yrag), yrah (yrah), yrai (yrai), yraj (yraj), yrak (yrak), yral (yral), chitosanase precursor ... BSU93875 U93875 g1934627 Bacillus subtilis 1423 -11531569 7500963804 yraj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to hypothetical proteins from b. subtilis) (le:150701) (re:151063) (di:complement) BSUB0014 Z99117 g2635137 Bacillus subtilis 1423 -11531569

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807297	5439	27595	966	322

Description

6500727712 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrai yrai Bacillus subtilis 1423 -11531570 7502851726 yrai (de:hypothetical 15.6 kd protein in csu-adhb intergenic region) (db:swissprot) YRAI\_BACSU 007909 BACILLUS SUBTILIS 1423 -11531570 7000692719 yrai conserved hypothetical protein yrai (db:pir2.dat) A69971 A69971 Bacillus subtilis 1423 -11531570 1500692657 yrai unknown (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on the chromosome.) (nt:putative) (le:16587) (re:17021) (di:direct) BS233DEG X92868 g2108277 Bacillus subtilis 1423 -11531570 1500692658 yrai yrai (db:genpept-bct1) (de:bacillus subtilis alcohol dehydrogenase (adh) gene, partial cds, hypothetical spore coat protein (yraf), hypothetical spore coat protein (yrag), yrah (yrah), yrai (yrai), yraj (yraj), yrak (yrak), yral (yral), chitosanase precursor ... BSU93875 U93875 g1934626 Bacillus subtilis 1423 -11531570 7500963803 yrai (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to hypothetical proteins from b. subtilis) (le:151110) (re:151544) (di:complement) BSUB0014 Z99117 g2635138 Bacillus subtilis 1423 -11531570

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807298	5440	27596	336	111

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807300	5441	27597	486	161

Description

6500727713 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrah yrah Bacillus subtilis 1423 -11531571 7000692718 yrah conserved hypothetical protein yrah (db:pir2.dat) H69970 H69970 Bacillus subtilis 1423 -11531571 1500692655 yrah unknown (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on the chromosome.) (nt:putative) (le:15760) (re:16146) (di:direct) BS233DEG X92868 g2108276 Bacillus subtilis 1423 -11531571 1500692656 yrah yrah (db:genpept-bct1) (de:bacillus subtilis alcohol dehydrogenase (adhb) gene, partial cds, hypothetical spore coat protein (yraf), hypothetical spore coat protein (yrag), yrah (yrah), yrai (yrai), yraj (yraj), yrak (yrak), yral (yral), chitosanase precursor ... BSU93875 U93875 g1934625 Bacillus subtilis 1423 -11531571 7500963802 yrah (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.) (nt:similar to hypothetical proteins) (le:151985) (re:152371) (di:complement) BSUB0014 Z99117 g2635139 Bacillus subtilis 1423 -11531571

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807301	5442	27598	321	106

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807303	5443	27599	453	151

Description

GTC ORF with score 109 to: (fn:er membrane protein; amino acid permease) (sr:saccharomyces cerevisiae (strain s288c) (library: ycp50 (from ros) (db:genpept-pln1) (de:saccharomyces cerevisiae secretory component gene, complete cds.) (nt:chromosome iv; ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807316	5444	27600	987	328

Description

GTC ORF with score 1613 to: (sr:aspergillus fumigatus (library: cbs 144.89) (clone: fp4) myceliu) (db:genpept-pln1) (de:aspergillus fumigatus 88 kda secreted dipetidyl peptidase gene, complete cds.) (nt:putative) (le:326:461:571:860:1922) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807317	5445	27601	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807319	5446	27602	330	109

Description

GTC ORF with score 410 to: (sr:aspergillus fumigatus (library: cbs 144.89) (clone: fp4) myceliu) (db:genpept-pln1) (de:aspergillus fumigatus 88 kda secreted dipetidyl peptidase gene,complete cds.) (nt:putative) (le:326:461:571:860:1922) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807337	5447	27603	1005	334

Description

6500727714 hypothetical protein:similar to spore coat protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrag yrag Bacillus subtilis 1423 -11531572 7000694615 yrag spore coat protein homolog yrag (db:pir2.dat) G69970 G69970 Bacillus subtilis 1423 -11531572 1500692653 yrag spore coat protein (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on thechromosome.) (le:15266) (re:15511) (di:complement) BS233DEG X92868 g2108275 Bacillus subtilis 1423 -11531572 1500692654 yrag hypothetical spore coat protein (db:genpept-bct1) (de:bacillus subtilis alcohol dehydrogenase (adhb) gene, partial cds,hypothetical spore coat protein (yraf), hypothetical spore coatprotein (yrag), yrah (yrah), yrai (yrai), yraj (yraj), yrak (yrak),yral (yral), chitosanase precursor ... BSU93875 U93875 g1934624 Bacillus subtilis 1423 -11531572 7500965210 yrag (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to spore coat protein) (le:152620) (re:152865) (di:direct) BSUB0014 Z99117 g2635140 Bacillus subtilis 1423 -11531572

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807354	5448	27604	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807370	5449	27605	201	66

Description

6500727715 hypothetical protein:similar to spore coat protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yraf yraf Bacillus subtilis 1423 -11531573 7000694614 yraf spore coat protein homolog yraf (db:pir2.dat) F69970 F69970 Bacillus subtilis 1423 -11531573 1500692651 yraf spore coat protein f (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on thechromosome.) (le:14880) (re:15248) (di:complement) BS233DEG X92868 g2108274 Bacillus subtilis 1423 -11531573 1500692652 yraf hypothetical spore coat protein (db:genpept-bct1) (de:bacillus subtilis alcohol dehydrogenase (adhb) gene, partial cds,hypothetical spore coat protein (yraf), hypothetical spore coatprotein (yrag), yrah (yrah), yrai (yrai), yraj (yraj), yrak (yrak),yral (yral), chitosanase precursor ... BSU93875 U93875 g1934623 Bacillus subtilis 1423 -11531573 7500965209 yraf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to spore coat protein) (le:152883) (re:153251) (di:direct) BSUB0014 Z99117 g2635141 Bacillus subtilis 1423 -11531573

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807375	5450	27606	582	194

Description

6500727716 hypothetical protein:similar to spore coat protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yraE yraE Bacillus subtilis 1423 -11531574 7000694613 yrae spore coat protein homolog yrae (db:pir2.dat) E69970 E69970 Bacillus subtilis 1423 -11531574 1500695696 yrae spore coat protein f (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on thechromosome.) (le:13509) (re:13706) (di:complement) BS233DEG X92868 g2108272 Bacillus subtilis 1423 -11531574 7500965208 yrae (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to spore coat protein) (le:154425) (re:154622) (di:direct) BSUB0014 Z99117 g2635143 Bacillus subtilis 1423 -11531574

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807380	5451	27607	558	186

Description

6500727717 hypothetical protein:similar to spore coat protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yraD yraD Bacillus subtilis 1423 -11531575 7000694612 yrad spore coat protein homolog yrad (db:pir2.dat) D69970 D69970 Bacillus subtilis 1423 -11531575 1500695695 yrad spore coat protein f (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on thechromosome.) (le:13194) (re:13493) (di:complement) BS233DEG X92868 g2108271 Bacillus subtilis 1423 -11531575 7500965207 yrad (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to spore coat protein) (le:154638) (re:154937) (di:direct) BSUB0014 Z99117 g2635144 Bacillus subtilis 1423 -11531575

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807390	5452	27608	531	176

Description

6500727718 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrac yrac Bacillus subtilis 1423 -11531576 7000693852 yrac hypothetical protein yrac (db:pir2.dat) C69970 C69970 Bacillus subtilis 1423 -11531576 1500695694 yrac unknown (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on thechromosome.) (nt:putative) (le:12912) (re:13187) (di:complement) BS233DEG X92868 g2108270 Bacillus subtilis 1423 -11531576 7500964665 yrac (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:154944) (re:155219) (di:direct) BSUB0014 Z99117 g2635145 Bacillus subtilis 1423 -11531576

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807395	5453	27609	195	65

Description

GTC ORF with score 110 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807420	5454	27610	1311	437

Description

6500727719 hypothetical protein:similar to transcriptional regulator:merr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yraB yraB Bacillus subtilis 1423 -11531577 7000694777 yrab transcription regulator merr family homolog yrab (db:pir2.dat) B69970 B69970 Bacillus subtilis 1423 -11531577 1500695693 yrab mercuric resistance operon regulatory protein (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on thechromosome.) (le:12510) (re:12932) (di:direct) BS233DEG X92868 g2108269 Bacillus subtilis 1423 -11531577 7500965340 yrab (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to transcriptional regulator (merr family)) (le:155199) (re:155621) (di:complement) BSUB0014 Z99117 g2635146 Bacillus subtilis 1423 -11531577

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807427	5455	27611	495	164

Description

6500727720 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yraA yraA Bacillus subtilis 1423 -11531578 7500952589 yraa (de:hypothetical 16.8 kd protein in adha-sacc intergenic region) (db:swissprot) YRAA\_BACSU 006006 BACILLUS SUBTILIS 1423 -11531578 7000692717 yraa conserved hypothetical protein yraa (cl:archaeoglobus intracellular proteinase i) (db:pir2.dat) A69970 A69970 Bacillus subtilis 1423 -11531578 1500695691 yraa (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on thechromosome.) (le:10358) (re:10822) (di:complement) BS233DEG X92868 g2108267 Bacillus subtilis 1423 -11531578 7500952592 yraa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:157309) (re:157773) (di:direct) BSUB0014 Z99117 g2635148 Bacillus subtilis 1423 -11531578

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807428	5456	27612	612	204

Description

6500727721 hypothetical protein:similar to dihydrodipicolinate reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrhP yrhP Bacillus subtilis 1423 -11531579 7500952663 yrhp (de:hypothetical 23.4 kd protein in aapa-sigv intergenic region) (db:swissprot) YRHP\_BACSU 005406 BACILLUS SUBTILIS 1423 -11531579 7000692918 yrhp dihydrodipicolinate reductase homolog yrhp (cl:hypothetical protein b1798) (db:pir2.dat) F69975 F69975 Bacillus subtilis 1423 -11531579 7500952665 yrhp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to dihydrodipicolinate reductase) (le:167862) (re:168494) (di:complement) BSUB0014 Z99117 g2635156 Bacillus subtilis 1423 -11531579

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807435	5457	27613	384	127

Description

6500727722 hypothetical protein:similar to cyclodextrin metabolism (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrhO yrhO Bacillus subtilis 1423 -11531580 7000692883 yrho cyclodextrin metabolism homolog yrho (db:pir2.dat) E69975 E69975 Bacillus subtilis 1423 -11531580 1500692648 yrho yrho (db:genpept-bct1) (de:bacillus subtilis cysteine synthase (yrha), cystathioninegamma-lyase (yrhb), yrhc (yrhc), yrhd (yrhd), formate dehydrogenasechain a (yrhe), yrhf (yrhf), formate dehydrogenase (yrhg), yrhh(yrhh), regulatory protein (yrhi), cytochro... BSU93874 U93874 g1934619 Bacillus subtilis 1423 -11531580 7500963913 yrho (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to cyclodextrin metabolism) (le:168647) (re:169474) (di:direct) BSUB0014 Z99117 g2635157 Bacillus subtilis 1423 -11531580

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807439	5458	27614	819	273

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807460	5459	27615	1047	348

Description

6500727723 hypothetical protein:similar to anti-sigma factor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrhM yrhM Bacillus subtilis 1423 -11531581 7000692212 yrhM anti-sigma factor homolog yrhM (db:pir2.dat) D69975 D69975 Bacillus subtilis 1423 -11531581 1500692646 yrhM putative anti-sigv factor (db:genpept-bct1) (de:bacillus subtilis cysteine synthase (yrha), cystathioninegamma-lyase (yrhb), yrhC (yrhc), yrhD (yrhd), formate dehydrogenasechain a (yrhe), yrhF (yrhf), formate dehydrogenase (yrhg), yrhH(yrhh), regulatory protein (yrhi), cytochro... BSU93874 U93874 g1934617 Bacillus subtilis 1423 -11531581 7500963418 yrhM (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to anti-sigma factor) (le:170170) (re:171027) (di:direct) BSUB0014 Z99117 g2635159 Bacillus subtilis 1423 -11531581

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807462	5460	27616	486	161

Description

GTC ORF with score 112 to: (db:genpept-bct2) (de:streptomyces hygroscopicus putative pteridine-dependentdioxygenase, pks modules 1,2,3 and 4, and putative regulatoryprotein genes, complete cds and putative hydroxylase gene, partialcds.) (nt:orf1; ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807465	5461	27617	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807471	5462	27618	336	111

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807482	5463	27619	282	93

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807486	5464	27620	639	212

Description

6500727724 hypothetical protein:similar to acyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrhL yrhL Bacillus subtilis 1423 -11531582 7000692154 yrhL acyltransferase homolog yrhL (db:pir2.dat) C69975 C69975 Bacillus subtilis 1423 -11531582 1500692645 yrhL hypothetical protein yrhL (db:genpept-bct1) (de:bacillus subtilis cysteine synthase (yrha), cystathioninegamma-lyase (yrhb), yrhC (yrhc), yrhD (yrhd), formate dehydrogenasechain a (yrhe), yrhF (yrhf), formate dehydrogenase (yrhg), yrhH(yrhh), regulatory protein (yrhi), cytochro... BSU93874 U93874 g1934616 Bacillus subtilis 1423 -11531582 7500963381 yrhL (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to acyltransferase) (le:171138) (re:173042) (di:direct) BSUB0014 Z99117 g2635160 Bacillus subtilis 1423 -11531582

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807489	5465	27621	234	77

Description

6500727725 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrhK yrhK Bacillus subtilis 1423 -11531583 7502851727 yrhK (de:hypothetical 11.6 kd protein in sigv-grea intergenic region) (db:swissprot) YRHK\_BACSU O05401 BACILLUS SUBTILIS 1423 -11531583 7000693862 yrhK hypothetical protein yrhK (db:pir2.dat) B69975 B69975 Bacillus subtilis 1423 -11531583 1500692644 yrhK yrhK (db:genpept-bct1) (de:bacillus subtilis cysteine synthase (yrha), cystathioninegamma-lyase (yrhb), yrhC (yrhc), yrhD (yrhd), formate dehydrogenasechain a (yrhe), yrhF (yrhf), formate dehydrogenase (yrhg), yrhH(yrhh), regulatory protein (yrhi), cytochro... BSU93874 U93874 g1934615 Bacillus subtilis 1423 -11531583 7500964672 yrhK (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:173176) (re:173466) (di:direct) BSUB0014 Z99117 g2635161 Bacillus subtilis 1423 -11531583

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807491	5466	27622	267	88

Description

6500727726 hypothetical protein:similar to cytochrome p450 /  
 nadph-cytochrome p450 reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
 (db:gtc-bacillus subtilis) yrhJ yrhJ Bacillus subtilis 1423 -11531584  
 7000692900 yrhj cytochrome p450 / nadph-cytochrome p450 r homolog yrhj  
 (cl:p450 bifunctional enzyme cyp102:flavodoxin  
 homology:nadph--ferrihemoprotein reductase homology) (db:pir2.dat) A69975  
 A69975 Bacillus subtilis 1423 -11531584 1500692643 yrhj cytochrome p450 102  
 (db:genpept-bct1) (de:bacillus subtilis cysteine synthase (yrha),  
 cystathioninegamma-lyase (yrhb), yrhc (yrhc), yrhj (yrhj), formate  
 dehydrogenasechain a (yrhe), yrhf (yrhf), formate dehydrogenase (yrhg),  
 yrhj (yrhj), regulatory protein (yrhi), cytochrome... BSU93874 U93874 g1934614  
 Bacillus subtilis 1423 -11531584 7500953862 yrhj (fn:unknown)  
 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21):  
 from 2599451to 2812870.) (nt:similar to cytochrome p450 / nadph-cytochrome  
 p450) (le:173710) (re:176874) (di:complement) BSUB0014 Z99117 g2635162  
 Bacillus subtilis 1423 -11531584

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807501	5467	27623	411	136

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807507	5468	27624	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807512	5469	27625	597	198

Description

6500727727 hypothetical protein:similar to transcriptional regulator:tetr/acrr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrhI yrhI Bacillus subtilis 1423 -11531585 7000694785 yrhI probable transcription regulator yrhI (cl:bacillus subtilis probable transcription regulator yrhI) (db:pir2.dat) H69974 H69974 Bacillus subtilis 1423 -11531585 1500692642 yrhI regulatory protein (db:genpept-bct1) (de:bacillus subtilis cysteine synthase (yrha), cystathioninegamma-lyase (yrhb), yrhC (yrhc), yrhD (yrhd), formate dehydrogenasechain a (yrhe), yrhf (yrhf), formate dehydrogenase (yrhg), yrhH(yrhh), regulatory protein (yrhi), cytochro... BSU93874 U93874 g1934613 Bacillus subtilis 1423 -11531585 7500965347 yrhI (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to transcriptional regulator (tetr/acrr) (le:176890) (re:177474) (di:complement) BSUB0014 Z99117 g2635163 Bacillus subtilis 1423 -11531585

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807515	5470	27626	477	159

Description

6500727728 hypothetical protein:similar to methyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrhH yrhH Bacillus subtilis 1423 -11531586 7000694218 yrhH methyltransferase homolog yrhH (cl:bioc homology) (db:pir2.dat) G69974 G69974 Bacillus subtilis 1423 -11531586 1500692641 yrhH yrhH (db:genpept-bct1) (de:bacillus subtilis cysteine synthase (yrha), cystathioninegamma-lyase (yrhb), yrhC (yrhc), yrhD (yrhd), formate dehydrogenasechain a (yrhe), yrhf (yrhf), formate dehydrogenase (yrhg), yrhH(yrhh), regulatory protein (yrhi), cytochro... BSU93874 U93874 g1934612 Bacillus subtilis 1423 -11531586 7500964943 yrhH (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to methyltransferase) (le:177697) (re:178239) (di:complement) BSUB0014 Z99117 g2635164 Bacillus subtilis 1423 -11531586

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807519	5471	27627	291	97

Description

6500727729 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrzI yrzI Bacillus subtilis 1423 -11531587  
7000693877 yrzi hypothetical protein yrzi (db:pir2.dat) H69982 H69982 Bacillus subtilis 1423 -11531587 7500964687 yrzi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:178743) (re:178892) (di:complement) BSUB0014 Z99117 g2635165 Bacillus subtilis 1423 -11531587

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807526	5472	27628	333	110

Description

GTC ORF with score 176 to: (or:Mus musculus) (sr:house mouse) (db:genpept-rod) (de:mus musculus sh3-containing protein sh3p7 mrna, complete cds.similar to human drebrin.) (nt:sh3-containing protein; similar to human drebrin) (le:31) (re:1332) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807533	5473	27629	855	284

Description

6500727730 hypothetical protein:similar to formate dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrhG yrhG Bacillus subtilis 1423 -11531588 7500952659 yrhg (de:hypothetical 28.5 kd protein in sigv-grea intergenic region) (db:swissprot) YRHG\_BACSU 005399 BACILLUS SUBTILIS 1423 -11531588 7000693003 yrhg formate dehydrogenase homolog yrhg (cl:formate dehydrogenase foch) (db:pir2.dat) F69974 F69974 Bacillus subtilis 1423 -11531588 1500692640 yrhg formate dehydrogenase (db:genpept-bct1) (de:bacillus subtilis cysteine synthase (yrha), cystathioninegamma-lyase (yrhb), yrhc (yrhc), yrh d (yrhd), formate dehydrogenasechain a (yrhe), yrhf (yrhf), formate dehydrogenase (yrhg), yrh h (yrhh), regulatory protein (yrhi), cytochro... BSU93874 U93874 g1934611 Bacillus subtilis 1423 -11531588 7500952662 yrhg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14' of 21): from 2599451to 2812870.) (nt:similar to formate dehydrogenase) (le:179282) (re:180082) (di:complement) BSUB0014 Z99117 g2635166 Bacillus subtilis 1423 -11531588

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807542	5474	27630	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807553	5475	27631	201	66

Description

6500727731 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrhF yrhF Bacillus subtilis 1423 -11531589  
7502851728 yrhf (de:hypothetical 14.0 kd protein in sigv-grea intergenic region) (db:swissprot) YRHF\_BACSU 005398 BACILLUS SUBTILIS 1423 -11531589  
7000693861 yrhf hypothetical protein yrhf (db:pir2.dat) E69974 E69974 Bacillus subtilis 1423 -11531589 1500692639 yrhf yrhf (db:genpept-bct1) (de:bacillus subtilis cysteine synthase (yrha), cystathioninegamma-lyase (yrhb), yrhc (yrhc), yrh d (yrhd), formate dehydrogenasechain a (yrhe), yrhf (yrhf), formate dehydrogenase (yrhg), yrh h(yrhh), regulatory protein (yrhi), cytochro... BSU93874 U93874 g1934610 Bacillus subtilis 1423 -11531589  
7500964671 yrhf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:180345) (re:180713) (di:complement) BSUB0014 Z99117 g2635167 Bacillus subtilis 1423 -11531589

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807571	5476	27632	324	107

Description

6500727732 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrhD yrhD Bacillus subtilis 1423 -11531590 7502851729 yrh d (de:hypothetical 17.5 kd protein in sigv-grea intergenic region) (db:swissprot) YRHD\_BACSU 005396 BACILLUS SUBTILIS 1423 -11531590  
7000692725 yrh d conserved hypothetical protein yrh d (db:pir2.dat) C69974 C69974 Bacillus subtilis 1423 -11531590 1500692637 yrh d yrh d (db:genpept-bct1) (de:bacillus subtilis cysteine synthase (yrha), cystathioninegamma-lyase (yrhb), yrh c (yrhc), yrh d (yrhd), formate dehydrogenasechain a (yrhe), yrh f (yrhf), formate dehydrogenase (yrhg), yrh h(yrhh), regulatory protein (yrhi), cytochro... BSU93874 U93874 g1934608 Bacillus subtilis 1423 -11531590 7500963809 yrh d (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins from b. subtilis) (le:183990) (re:184472) (di:direct) BSUB0014 Z99117 g2635169 Bacillus subtilis 1423 -11531590



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807583	5477	27633	321	107

Description

6500727733 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrhC yrhC Bacillus subtilis 1423 -11531591  
7502851730 yrhC (de:hypothetical 8.6 kd protein in sigv-grea intergenic region) (db:swissprot) YRHC\_BACSU O05395 BACILLUS SUBTILIS 1423 -11531591  
7000693860 yrhC hypothetical protein yrhC (db:pir2.dat) B69974 B69974 Bacillus subtilis 1423 -11531591 1500692636 yrhC yrhC (db:genpept-bct1) (de:bacillus subtilis cysteine synthase (yrhA), cystathioninegamma-lyase (yrhB), yrhC (yrhC), yrhD (yrhD), formate dehydrogenasechain a (yrhE), yrhF (yrhF), formate dehydrogenase (yrhG), yrhH(yrhH), regulatory protein (yrhI), cytochro... BSU93874 U93874 g1934607 Bacillus subtilis 1423 -11531591  
7500964670 yrhC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:184508) (re:184738) (di:complement) BSUB0014 Z99117 g2635170 Bacillus subtilis 1423 -11531591

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807594	5478	27634	576	191

Description

6500727734 hypothetical protein:similar to cystathionine gamma-synthase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrhB yrhB Bacillus subtilis 1423 -11531592 7000692886 yrhB cystathionine gamma-synthase homolog yrhB (cl:o-succinylhomoserine (thiol)-lyase) (db:pir2.dat) A69974 A69974 Bacillus subtilis 1423 -11531592 1500692635 yrhB cystathionine gamma-lyase (db:genpept-bct1) (de:bacillus subtilis cysteine synthase (yrhA), cystathioninegamma-lyase (yrhB), yrhC (yrhC), yrhD (yrhD), formate dehydrogenasechain a (yrhE), yrhF (yrhF), formate dehydrogenase (yrhG), yrhH(yrhH), regulatory protein (yrhI), cytochro... BSU93874 U93874 g1934606 Bacillus subtilis 1423 -11531592 7500963916 yrhB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to cystathionine gamma-synthase) (le:184821) (re:185960) (di:complement) BSUB0014 Z99117 g2635171 Bacillus subtilis 1423 -11531592

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807595	5479	27635	321	106

Description

6500727735 hypothetical protein:similar to cysteine synthase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrhA yrhA Bacillus subtilis 1423 -11531593 7000692888 yrha cysteine synthase homolog yrha (cl:threonine dehydratase) (db:pir2.dat) H69973 H69973 Bacillus subtilis 1423 -11531593 1500692634 yrha cysteine synthase (db:genpept-bct1) (de:bacillus subtilis cysteine synthase (yrha), cystathioninegamma-lyase (yrhb), yrhc (yrhc), yrhd (yrhd), formate dehydrogenasechain a (yrhe), yrhf (yrhf), formate dehydrogenase (yrhg), yrhh(yrhh), regulatory protein (yrhi), cytochro... BSU93874 U93874 g1934605 Bacillus subtilis 1423 -11531593 7500963918 yrha (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to cysteine synthase) (le:185962) (re:186885) (di:complement) BSUB0014 Z99117 g2635172 Bacillus subtilis 1423 -11531593

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807601	5480	27636	1509	503

Description

6500727736 hypothetical protein:similar to purine nucleoside phosphorylase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrrU yrrU Bacillus subtilis 1423 -11531594 7500887915 pfs (ec:3.2.2.16:3.2.2.9) (de:nucleosidase, (mta/sah nucleosidase) (p46)) (db:swissprot) PFS\_BACSU 032028 BACILLUS SUBTILIS 1423 -11531594 7000694473 yrru purine nucleoside phosphorylase homolog yrru (cl:escherichia coli pfs protein) (db:pir2.dat) D69980 D69980 Bacillus subtilis 1423 -11531594 7500887917 yrru (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to purine nucleoside phosphorylase) (le:186950) (re:187645) (di:complement) BSUB0014 Z99117 g2635173 Bacillus subtilis 1423 -11531594

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807609	5481	27637	933	310

Description

6500727737 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrrT yrrT Bacillus subtilis 1423 -11531595 7000693865 yrrt hypothetical protein yrrt (db:pir2.dat) C69980 C69980 Bacillus subtilis 1423 -11531595 7500964675 yrrt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:187666) (re:188307) (di:complement) BSUB0014 Z99117 g2635174 Bacillus subtilis 1423 -11531595

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807616	5482	27638	1239	412

Description

6500727738 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrzA yrzA Bacillus subtilis 1423 -11531596  
7000693870 yrza hypothetical protein yrza (db:pir2.dat) H69981 H69981  
Bacillus subtilis 1423 -11531596 7500964680 yrza (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21):  
from 2599451to 2812870.) (le:188500) (re:188703) (di:direct) BSUB0014 Z99117  
g2635175 Bacillus subtilis 1423 -11531596

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807626	5483	27639	477	158

Description

6500727739 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrrS yrrS Bacillus subtilis 1423 -11531597  
7000693864 yrrs hypothetical protein yrrs (db:pir2.dat) B69980 B69980  
Bacillus subtilis 1423 -11531597 7500964674 yrrs (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21):  
from 2599451to 2812870.) (le:188740) (re:189441) (di:complement) BSUB0014  
Z99117 g2635176 Bacillus subtilis 1423 -11531597

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807627	5484	27640	321	106

Description

6500727740 hypothetical protein:similar to penicillin-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrrR yrrR Bacillus subtilis 1423 -11531598 7000694355 yrrr penicillin-binding protein homolog yrrr (db:pir2.dat) A69980 A69980 Bacillus subtilis 1423 -11531598 7500965045 yrrr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to penicillin-binding protein) (le:189506) (re:191260) (di:complement) BSUB0014 Z99117 g2635177 Bacillus subtilis 1423 -11531598

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807634	5485	27641	597	198

Description

6500727741 hypothetical protein:similar to protease (gtcfc:10.11)  
(keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrrO yrrO Bacillus  
subtilis 1423 -11531599 7000694462 yrrO proteinase homolog yrrO  
(db:pir2.dat) H69979 H69979 Bacillus subtilis 1423 -11531599 7500965112  
yrrO (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome  
(section 14 of 21): from 2599451to 2812870.) (nt:similar to protease)  
(le:192680) (re:193948) (di:complement) BSUB0014 Z99117 g2635180 Bacillus  
subtilis 1423 -11531599

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807644	5486	27642	390	129

Description

6500727742 hypothetical protein:similar to protease (gtcfc:10.11)  
(keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrrN yrrN Bacillus  
subtilis 1423 -11531600 7000694461 yrrN proteinase homolog yrrN  
(db:pir2.dat) G69979 G69979 Bacillus subtilis 1423 -11531600 7500965111  
yrrN (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome  
(section 14 of 21): from 2599451to 2812870.) (nt:similar to protease)  
(le:193967) (re:194896) (di:complement) BSUB0014 Z99117 g2635181 Bacillus  
subtilis 1423 -11531600

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807645	5487	27643	801	266

Description

6500727743 hypothetical protein:similar to caffeoyl-coa o-methyltransferase  
(gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrrM  
yrrM Bacillus subtilis 1423 -11531601 7000692301 yrrM caffeoyl-coa  
o-methyltransferase homolog yrrM (db:pir2.dat) F69979 F69979 Bacillus  
subtilis 1423 -11531601 7500963470 yrrM (fn:unknown) (db:genpept-bct1)  
(de:bacillus subtilis complete genome (section 14 of 21): from 2599451to  
2812870.) (nt:similar to caffeoyl-coa o-methyltransferase) (le:194902)  
(re:195555) (di:complement) BSUB0014 Z99117 g2635182 Bacillus subtilis 1423  
-11531601

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807661	5488	27644	402	134

Description

6500727744 hypothetical protein:similar to folate metabolism (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrrL yrrL Bacillus subtilis 1423 -11531602 7000692996 yrrl folate metabolism homolog yrrl (db:pir2.dat) E69979 E69979 Bacillus subtilis 1423 -11531602 6000691235 yrrl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to folate metabolism) (le:195707) (re:196789) (di:complement) BSUB0014 Z99117 g2635183 Bacillus subtilis 1423 -11531602 7500963989 yrrl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to folate metabolism) (le:27) (re:1109) (di:complement) BSUB0015 Z99118 g2635201 Bacillus subtilis 1423 -11531602

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807664	5489	27645	561	186

Description

6500727745 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrzB yrzB Bacillus subtilis 1423 -11531603 7000693871 yrzB hypothetical protein yrzB (db:pir2.dat) A69982 A69982 Bacillus subtilis 1423 -11531603 6000691237 yrzB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:196920) (re:197201) (di:complement) BSUB0014 Z99117 g2635184 Bacillus subtilis 1423 -11531603 7500964681 yrzB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:1240) (re:1521) (di:complement) BSUB0015 Z99118 g2635202 Bacillus subtilis 1423 -11531603

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807670	5490	27646	252	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807678	5491	27647	912	303

Description

6500727746 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrrK yrrK Bacillus subtilis 1423 -11531604 7000692731 yrrk conserved hypothetical protein yrrk (cl:haemophilus influenzae conserved hypothetical protein hi0305) (db:pir2.dat) D69979 D69979 Bacillus subtilis 1423 -11531604 6000691239 yrrk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:197219) (re:197635) (di:complement) BSUB0014 Z99117 g2635185 Bacillus subtilis 1423 -11531604 7500963813 yrrk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:1539) (re:1955) (di:complement) BSUB0015 Z99118 g2635203 Bacillus subtilis 1423 -11531604

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807679	5492	27648	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807681	5493	27649	579	192

Description

6500727747 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrrI yrrI Bacillus subtilis 1423 -11531605 7000692730 yrrI conserved hypothetical protein yrrI (db:pir2.dat) C69979 C69979 Bacillus subtilis 1423 -11531605 6000691243 yrrI (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:200961) (re:202022) (di:complement) BSUB0014 Z99117 g2635187 Bacillus subtilis 1423 -11531605 7500963812 yrrI (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:5281) (re:6342) (di:complement) BSUB0015 Z99118 g2635205 Bacillus subtilis 1423 -11531605

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807687	5494	27650	369	122

Description

6500727748 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrrD yrrD Bacillus subtilis 1423 -11531606  
 7000693863 yrrd hypothetical protein yrrd (db:pir2.dat) B69979 B69979  
 Bacillus subtilis 1423 -11531606 6000691245 yrrd (fn:unknown)  
 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21):  
 from 2599451to 2812870.) (le:205524) (re:206048) (di:complement) BSUB0014  
 Z99117 g2635192 Bacillus subtilis 1423 -11531606 7500964673 yrrd  
 (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome  
 (section 15 of 21): from 2795131to 3013540.) (le:9844) (re:10368)  
 (di:complement) BSUB0015 Z99118 g2635210 Bacillus subtilis 1423 -11531606

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807690	5495	27651	555	184

Description

GTC ORF with score 141 to: (sr:thale cress) (db:genpept) (de:arabidopsis  
 thaliana dna chromosome 4, essa i ap2 contig fragmentno. 2.) (nt:strong  
 similarity to beta vulgaris putative sugar) (le:79935:80357)  
 (re:80034:81738) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807693	5496	27652	525	174

Description

6500727749 hypothetical protein:similar to conjugation transfer protein  
 (gtcfc:14.1) (ec:3.1.11.5) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus  
 subtilis) yrrC yrrC Bacillus subtilis 1423 -11531607 7000692382 yrrc  
 conjugation transfer protein homolog yrrc (db:pir2.dat) A69979 A69979  
 Bacillus subtilis 1423 -11531607 6000691247 yrrc (fn:unknown)  
 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21):  
 from 2599451to 2812870.) (nt:similar to conjugation transfer protein)  
 (le:206106) (re:208502) (di:complement) BSUB0014 Z99117 g2635193 Bacillus  
 subtilis 1423 -11531607 7500963543 yrrc (fn:unknown) (db:genpept-bct1)  
 (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to  
 3013540.) (nt:similar to conjugation transfer protein) (le:10426) (re:12822)  
 (di:complement) BSUB0015 Z99118 g2635211 Bacillus subtilis 1423 -11531607

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807694	5497	27653	288	95

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807695	5498	27654	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807708	5499	27655	249	82

Description

6500727750 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrrB yrrB Bacillus subtilis 1423 -11531608 7000692729 yrrb conserved hypothetical protein yrrb (cl:tetratricopeptide repeat homology) (db:pir2.dat) H69978 H69978 Bacillus subtilis 1423 -11531608 6000691249 yrrb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:208527) (re:209147) (di:complement) BSUB0014 Z99117 g2635194 Bacillus subtilis 1423 -11531608 7500963811 yrrb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:12847) (re:13467) (di:complement) BSUB0015 Z99118 g2635212 Bacillus subtilis 1423 -11531608

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807712	5500	27656	693	230

Description

6500727751 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrrA yrrA Bacillus subtilis 1423 -11531609 7000692728 yrra probable atpase yrra (cl:probable membrane protein ydl033c) (db:pir2.dat) G69978 G69978 Bacillus subtilis 1423 -11531609 6000691251 yrra (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:209233) (re:210171) (di:complement) BSUB0014 Z99117 g2635195 Bacillus subtilis 1423 -11531609 7500955325 yrra (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:13553) (re:14491) (di:complement) BSUB0015 Z99118 g2635213 Bacillus subtilis 1423 -11531609

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807717	5501	27657	213	70

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807721	5502	27658	198	65

Description

6500727752 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrvP yrvP Bacillus subtilis 1423 -11531610  
 7000693869 yrvp hypothetical protein yrvp (db:pir2.dat) F69981 F69981 Bacillus subtilis 1423 -11531610 6000691253 yrvp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:210288) (re:210503) (di:direct) BSUB0014 Z99117 g2635196 Bacillus subtilis 1423 -11531610 7500964679 yrvp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:14608) (re:14823) (di:direct) BSUB0015 Z99118 g2635214 Bacillus subtilis 1423 -11531610

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807723	5503	27659	681	227

Description

GTC ORF with score 159 to: (sr:escherichia coli(strain:k12) dna, clone:kohara clone #167) (db:genpept) (de:escherichia coli genomic dna. (13.7 - 14.1 min).) (nt:orf\_id:o167#10; similar to pir accession number) (le:11523) (re:12431) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807727	5504	27660	417	138

Description

6500727753 hypothetical protein:similar to nifs protein homolog (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrvO yrvO Bacillus subtilis 1423 -11531611 7000694318 yrvO nifs protein homolog homolog yrvO (cl:nitrogen fixation protein nifs) (db:pir2.dat) E69981 E69981 Bacillus subtilis 1423 -11531611 6000691255 yrvO (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to nifs protein homolog) (le:210475) (re:211515) (di:complement) BSUB0014 Z99117 g2635197 Bacillus subtilis 1423 -11531611 7500965017 yrvO (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to nifs protein homolog) (le:14795) (re:15835) (di:complement) BSUB0015 Z99118 g2635215 Bacillus subtilis 1423 -11531611

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807733	5505	27661	1545	515

#### Description

6500727754 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrzC yrzC Bacillus subtilis 1423 -11531612 7000692735 yrzC conserved hypothetical protein yrzC (cl:hypothetical protein b2531) (db:pir2.dat) B69982 B69982 Bacillus subtilis 1423 -11531612 6000691257 yrzC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:211617) (re:211952) (di:complement) BSUB0014 Z99117 g2635198 Bacillus subtilis 1423 -11531612 7500963817 yrzC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:15937) (re:16272) (di:complement) BSUB0015 Z99118 g2635216 Bacillus subtilis 1423 -11531612

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807740	5506	27662	1176	391

#### Description

6500727755 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrvN yrvN Bacillus subtilis 1423 -11531613 7000692734 yrvN conserved hypothetical protein yrvN (cl:haemophilus influenzae conserved hypothetical protein hi1590) (db:pir2.dat) D69981 D69981 Bacillus subtilis 1423 -11531613 6000691259 yrvN (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:212152) (re:213417) (di:direct) BSUB0014 Z99117 g2635199 Bacillus subtilis 1423 -11531613 7500963816 yrvN (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:16472) (re:17737) (di:direct) BSUB0015 Z99118 g2635217 Bacillus subtilis 1423 -11531613

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807744	5507	27663	429	142

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807758	5508	27664	255	84

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807764	5509	27665	426	141

Description

GTC ORF with score 104 to: (db:genpept-bct2) (de:pseudomonas aeruginosa wzz (rol) (wzz (rol)) gene, partial cds,wbpa (wbpb), wbpb (wbpb), wbp (wbpc), wbpd (wbpd), wbpe (wbpe),wzy (rfc) (wzy (rfc)), wzx (wzx), hish (hish), hisf (hisf), wbp (wbpg), wbph...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807772	5510	27666	492	163

Description

6500727756 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrvM yrvM Bacillus subtilis 1423 -11531614 7000692733 yrvM conserved hypothetical protein yrvM (db:pir2.dat) C69981 C69981 Bacillus subtilis 1423 -11531614 7500963815 yrvM (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:17779) (re:18264) (di:complement) BSUB0015 Z99118 g2635218 Bacillus subtilis 1423 -11531614

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807774	5511	27667	699	232

Description

GTC ORF with score 725 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c14f11.) (nt:similar to aspartate aminotransferase; coded for by) (le:33773:34079:34846) (re:34028:34627:35285) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807786	5512	27668	1608	536

Description

GTC ORF with score 147 to: (sr:drosophila melanogaster (strain oregon r) (library: embl4; embl13) (db:genpept-inv) (de:drosophila melanogaster frequenin gene, complete cds, introns incoding region excluded.) (le:535) (re:1098) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807791	5513	27669	354	117

Description

6500727757 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrzK yrzK Bacillus subtilis 1423 -11531615  
7000693878 yrzK hypothetical protein yrzK (db:pir2.dat) A69983 A69983 Bacillus subtilis 1423 -11531615 7500964688 yrzK (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:22326) (re:22496) (di:complement) BSUB0015 Z99118 g2635221 Bacillus subtilis 1423 -11531615

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807793	5514	27670	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807798	5515	27671	348	115

Description

6500727758 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrvI yrvI Bacillus subtilis 1423 -11531616 7000692732 yrvI conserved hypothetical protein yrvI (cl:conserved hypothetical protein hi0670) (db:pir2.dat) A69981 A69981 Bacillus subtilis 1423 -11531616 7500963814 yrvI (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:24212) (re:24571) (di:complement) BSUB0015 Z99118 g2635223 Bacillus subtilis 1423 -11531616

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807809	5516	27672	1227	409

Description

6500727759 hypothetical protein:similar to single-strand dna-specific exonuclease (gtcfc:14.1) (ec:3.1.-.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrvE yrvE Bacillus subtilis 1423 -11531617 7000694589 yrvE single-strand dna-specific exonuclease homolog yrvE (db:pir2.dat) H69980 H69980 Bacillus subtilis 1423 -11531617 7500965188 yrvE (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to single-strand dna-specific exonuclease) (le:27554) (re:29914) (di:complement) BSUB0015 Z99118 g2635226 Bacillus subtilis 1423 -11531617

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807812	5517	27673	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807820	5518	27674	621	206

Description

6500727760 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yrvD yrvD Bacillus subtilis 1423 -11531618  
7000693868 yrvd hypothetical protein yrvd (db:pir2.dat) G69980 G69980  
Bacillus subtilis 1423 -11531618 7500964678 yrvd (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21):  
from 2795131to 3013540.) (le:29981) (re:30304) (di:complement) BSUB0015  
Z99118 g2635227 Bacillus subtilis 1423 -11531618

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807823	5519	27675	222	74

Description

6500727761 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yrvC yrvC Bacillus subtilis 1423 -11531619  
7000693867 yrvC hypothetical protein yrvC (db:pir2.dat) F69980 F69980  
Bacillus subtilis 1423 -11531619 7500964677 yrvC (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21):  
from 2795131to 3013540.) (le:30380) (re:30877) (di:complement) BSUB0015  
Z99118 g2635228 Bacillus subtilis 1423 -11531619

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807826	5520	27676	336	111

Description

6500727762 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yrvB yrvB Bacillus subtilis 1423 -11531620  
7000693866 yrvb hypothetical protein yrvb (db:pir2.dat) E69980 E69980  
Bacillus subtilis 1423 -11531620 7500964676 yrvb (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21):  
from 2795131to 3013540.) (le:32876) (re:33244) (di:complement) BSUB0015  
Z99118 g2635230 Bacillus subtilis 1423 -11531620

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807838	5521	27677	711	237

Description

6500727763 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrzD yrzD Bacillus subtilis 1423 -11531621  
 7000693872 yrzD hypothetical protein yrzD (db:pir2.dat) C69982 C69982 Bacillus subtilis 1423 -11531621 7500964682 yrzD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:33283) (re:33579) (di:complement) BSUB0015 Z99118 g2635231 Bacillus subtilis 1423 -11531621

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807841	5522	27678	654	217

Description

6500727764 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrbG yrbG Bacillus subtilis 1423 -11531622 7000692724 yrbg probable membrane protein yrbg (cl:probable membrane protein ycap) (db:pir2.dat) F69972 F69972 Bacillus subtilis 1423 -11531622 7500963808 yrbg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins from b. subtilis) (le:35255) (re:35911) (di:complement) BSUB0015 Z99118 g2635233 Bacillus subtilis 1423 -11531622

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807847	5523	27679	528	175

Description

GTC ORF with score 363 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k06a5.) (nt:similar to acyl-coa dehydrogenase; coded for by c.) (le:6497:6873:7067) (re:6817:7018:7607) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807863	5524	27680	276	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807864	5525	27681	555	184

Description

6500727765 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrzE yrzE Bacillus subtilis 1423 -11531623  
7000693873 yrze hypothetical protein yrze (db:pir2.dat) D69982 D69982 Bacillus subtilis 1423 -11531623 7500964683 yrze (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:36046) (re:36498) (di:direct) BSUB0015 Z99118 g2635234 Bacillus subtilis 1423 -11531623

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807865	5526	27682	738	245

Description

6500727766 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrbF yrbF Bacillus subtilis 1423 -11531624 7000692723 yrbf conserved hypothetical protein yrbf (cl:yajc protein) (db:pir2.dat) E69972 E69972 Bacillus subtilis 1423 -11531624 7500963807 yrbf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:36555) (re:36824) (di:complement) BSUB0015 Z99118 g2635235 Bacillus subtilis 1423 -11531624

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807869	5527	27683	804	268

Description

6500727767 hypothetical protein:forespore regulator of the sigma-k checkpoint (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) bofC bofC Bacillus subtilis 1423 -11531625 7000692997 bofC forespore regulator of the sigma-k checkpoint bofC (db:pir2.dat) A69596 A69596 Bacillus subtilis 1423 -11531625 1500693771 bofC (db:genpept-bct1) (de:b.subtilis bofC, orf1, csbx, and orf4 genes.) (nt:sigma f/sigma g transcribed gene) (le:1698) (re:2210) (di:direct) BSBOFCGEN X93081 g1941918 Bacillus subtilis 1423 -11531625 7500963990 bofC (fn:forespore regulator of the sigma-k checkpoint) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:41040) (re:41552) (di:complement) BSUB0015 Z99118 g2635240 Bacillus subtilis 1423 -11531625

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807881	5528	27684	264	87

Description

6500727768 hypothetical protein:similar to opine catabolism (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrbE yrbE Bacillus subtilis 1423 -11531626 7000694342 yrbe opine catabolism homolog yrbe (cl:streptomyces griseus stri protein) (db:pir2.dat) D69972 D69972 Bacillus subtilis 1423 -11531626 7500965032 yrbe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to opine catabolism) (le:42978) (re:44003) (di:complement) BSUB0015 Z99118 g2635242 Bacillus subtilis 1423 -11531626

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807884	5529	27685	528	175

Description

6500727769 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrzF yrzF Bacillus subtilis 1423 -11531627 7000693874 yrzf hypothetical protein yrzf (db:pir2.dat) E69982 E69982 Bacillus subtilis 1423 -11531627 7500964684 yrzf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:44241) (re:44633) (di:direct) BSUB0015 Z99118 g2635243 Bacillus subtilis 1423 -11531627

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807885	5530	27686	1491	496

Description

6500727770 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrzG yrzG Bacillus subtilis 1423 -11531628 7000693875 yrzg hypothetical protein yrzg (db:pir2.dat) F69982 F69982 Bacillus subtilis 1423 -11531628 7500964685 yrzg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:44666) (re:44887) (di:direct) BSUB0015 Z99118 g2635244 Bacillus subtilis 1423 -11531628

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807892	5531	27687	183	60

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807895	5532	27688	1542	513

Description

6500727771 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrzH yrzH Bacillus subtilis 1423 -11531629  
 7000693876 yrzH hypothetical protein yrzH (db:pir2.dat) G69982 G69982 Bacillus subtilis 1423 -11531629 7500964686 yrzH (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:45299) (re:45430) (di:direct) BSUB0015 Z99118 g2635245 Bacillus subtilis 1423 -11531629

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807901	5533	27689	300	99

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807919	5534	27690	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807935	5535	27691	1002	333

Description

6500727772 hypothetical protein:similar to sodium/proton-dependent alanine carrier protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrbD yrbD Bacillus subtilis 1423 -11531630 7000694596 yrbD sodium/proton-dependent alanine carrier pr homolog yrbD (cl:sodium-dependent d-alanine/glycine transport protein) (db:pir2.dat) C69972 C69972 Bacillus subtilis 1423 -11531630 7500955465 yrbD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to sodium/proton-dependent alanine carrier) (le:45741) (re:47195) (di:direct) BSUB0015 Z99118 g2635246 Bacillus subtilis 1423 -11531630

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807938	5536	27692	447	148

Description

6500727773 hypothetical protein:similar to spore coat protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrbC yrbC Bacillus subtilis 1423 -11531631 7000694618 yrbC spore coat protein homolog yrbC (cl:hypothetical protein mg332) (db:pir2.dat) B69972 B69972 Bacillus subtilis 1423 -11531631 7500965213 yrbC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to spore coat protein) (le:47236) (re:47958) (di:complement) BSUB0015 Z99118 g2635247 Bacillus subtilis 1423 -11531631

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807941	5537	27693	633	210

Description

6500727774 hypothetical protein:similar to spore coat protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrbB yrbB Bacillus subtilis 1423 -11531632 7000694617 yrbB spore coat protein homolog yrbB (db:pir2.dat) A69972 A69972 Bacillus subtilis 1423 -11531632 7500965212 yrbB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to spore coat protein) (le:48061) (re:48579) (di:complement) BSUB0015 Z99118 g2635248 Bacillus subtilis 1423 -11531632

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807948	5538	27694	1014	337

Description

6500727775 hypothetical protein:similar to spore coat protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrbA yrbA Bacillus subtilis 1423 -11531633 7000694616 yrbA spore coat protein homolog yrbA (db:pir2.dat) H69971 H69971 Bacillus subtilis 1423 -11531633 7500965211 yrbA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to spore coat protein) (le:48805) (re:49968) (di:complement) BSUB0015 Z99118 g2635249 Bacillus subtilis 1423 -11531633

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807950	5539	27695	354	118

Description

5000689687 hypothetical protein: hypothetical 19.7 kd protein in phea-nifs intergeinc region: orf1 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrxA yrxA Bacillus subtilis 1423 -11531634 116245 yrxa (de: hypothetical 19.7 kd protein in phea-nifs intergeinc region (orf1)) (db:swissprot) YRXA\_BACSU P39667 BACILLUS SUBTILIS 1423 -11531634 7000688571 yrxa hypothetical protein yrxa:orf1 immediately 5 of nifs (db:pir2.dat) A47071 A47071 Bacillus subtilis 1423 -11531634 7500952697 yrxa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:54846) (re:55382) (di:direct) BSUB0015 Z99118 g2635254 Bacillus subtilis 1423 -11531634 170393 yrxa hypothetical protein yrxa:orf1 immediately 5 of nifs (db:pir) A47071 A47071 Bacillus subtilis 1423 -11531634 6500727776 hypothetical protein: hypothetical 19.7 kd protein in phea-nifs intergeinc region: orf1 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrxA yrxA Bacillus subtilis 1423 -11531634

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807958	5540	27696	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807966	5541	27697	621	206

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807973	5542	27698	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807974	5543	27699	612	203

Description

5000689690 hypothetical protein:hypothetical 12.3 kd protein in rplu-rpma intergenic region:orf x (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysbB ysbB Bacillus subtilis 1423 -11531635 7500952731 ysbB (de:hypothetical 12.3 kd protein in rplu-rpma intergenic region (orf x)) (db:swissprot) YSB\_BACSU P26942 BACILLUS SUBTILIS 1423 -11531635 7000688606 ysbB conserved hypothetical protein ysbB (db:pir2.dat) S18440 S18440 Bacillus subtilis 1423 -11531635 6500727777 (db:genpept-bct1) (de:b.subtilis spoivfa, spoivfb, l20, orfx and l24 genes.) (nt:orf x) (le:2270) (re:2608) (di:direct) BSSPOIVFO X59528 g40174 Bacillus subtilis 1423 -11531635 219649 ysbB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:59308) (re:59646) (di:complement) BSUB0015 Z99118 g2635260 Bacillus subtilis 1423 -11531635 116360 ysbB (de:hypothetical 12.3 kd protein in rplu-rpma intergenic region (orf x)) (db:swissprot) YSB\_BACSU P26942 BACILLUS SUBTILIS 1423 -11531635 170262 ysbB conserved hypothetical protein ysbB (db:pir) S18440 S18440 Bacillus subtilis 1423 -11531635

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501807977	5544	27700	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807987	5545	27701	468	155

Description

5000689693 hypothetical protein:hypothetical 40.6 kd protein in spovid 3region:orf2 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysxE ysxE Bacillus subtilis 1423 -11531636 116365 ysx (de:hypothetical 40.6 kd protein in spovid 3'region (orf2)) (db:swissprot) YSX\_E\_BACSU P37964 BACILLUS SUBTILIS 1423 -11531636 7000688609 ysx hypothetical protein ysx:orf2 3 of spovid (db:pir2.dat) C47083 C47083 Bacillus subtilis 1423 -11531636 7500952733 orf2 unknown (sr:bacillus subtilis (strain w168) library made from vegetative cell) (db:genpept-bct1) (de:bacillus subtilis sporulation protein (spovid) gene, complete cds.) (le:2056) (re:3081) (di:direct) BAC\_SPOVID L07792 g143662 Bacillus subtilis 1423 -11531636 216898 ysx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:73934) (re:74959) (di:complement) BSUB0015 Z99118 g2635275 Bacillus subtilis 1423 -11531636 170395 ysx hypothetical protein ysx:orf2 3 of spovid (db:pir) C47083 C47083 Bacillus subtilis 1423 -11531636 6500727778 hypothetical protein:hypothetical 40.6 kd protein in spovid 3region:orf2 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysxE ysxE Bacillus subtilis 1423 -11531636

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501807994	5546	27702	303	100

Description

6500727779 hypothetical protein:hypothetical 21.7 kd protein in lon-hema intergenic region:orfy (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxD yxD Bacillus subtilis 1423 -11531637 116364 yxD (de:hypothetical 21.7 kd protein in lon-hema intergenic region (orfy)) (db:swissprot) YXD\_BACSU P40736 BACILLUS SUBTILIS 1423 -11531637 7000688608 yxD hypothetical protein yxD (db:pir2.dat) D69987 D69987 Bacillus subtilis 1423 -11531637 220356 yxD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:83267) (re:83830) (di:direct) BSUB0015 Z99118 g2635283 Bacillus subtilis 1423 -11531637 304229 yxD hypothetical protein (db:genpept-bct1) (de:bacillus subtilis genomic sequence 89009bp.) (nt:unknown function; putative) (le:86077) (re:86640) (di:complement) BSZ75208 Z75208 g1770080 Bacillus subtilis 1423 -11531637

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808007	5547	27703	555	184

Description

5000689691 hypothetical protein:hypothetical gtp-binding protein in lona-hema intergenic region:orfx (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxC yxC Bacillus subtilis 1423 -11531638 7500952732 yxC (de:orfx) (db:swissprot) YXC\_BACSU P38424 BACILLUS SUBTILIS 1423 -11531638 7000688607 yxC conserved hypothetical protein yxC (cl:bacillus subtilis conserved hypothetical protein yxC:translation elongation factor tu homology) (db:pir2.dat) I40422 I40422 Bacillus subtilis 1423 -11531638 304228 (db:genpept-bct1) (de:b.subtilis lon gene for protease la.) (nt:orfx) (le:2669) (re:3256) (di:direct) BSLONLA X76424 g496558 Bacillus subtilis 1423 -11531638 219378 yxC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:83852) (re:84439) (di:complement) BSUB0015 Z99118 g2635284 Bacillus subtilis 1423 -11531638 6500727780 yxC hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:unknown function; putative) (le:85468) (re:86055) (di:direct) BSZ75208 Z75208 g1770079 Bacillus subtilis 1423 -11531638 116362 yxC (de:orfx) (db:swissprot) YXC\_BACSU P38424 BACILLUS SUBTILIS 1423 -11531638 170258 yxC conserved hypothetical protein yxC (db:pir) I40422 I40422 Bacillus subtilis 1423 -11531638 220355 yxC hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:unknown function; putative) (le:85468) (re:86055) (di:direct) BSZ75208 Z75208 g1770079 Bacillus subtilis 1423 -11531638

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808021	5548	27704	951	316

Description

6500727781 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysoA ysoA Bacillus subtilis 1423 -11531639 7000693890 ysoA hypothetical protein ysoA (db:pir2.dat) H69986 H69986 Bacillus subtilis 1423 -11531639 220349 ysoA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:91788) (re:92720) (di:complement) BSUB0015 Z99118 g2635289 Bacillus subtilis 1423 -11531639 304222 ysoA hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:unknown function; putative) (le:77187) (re:78119) (di:direct) BSZ75208 Z75208 g1770073 Bacillus subtilis 1423 -11531639

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808022	5549	27705	426	141

Description

6500727782 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysnD ysnD Bacillus subtilis 1423 -11531640  
7000693888 ysnD hypothetical protein ysnD (db:pir2.dat) E69986 E69986 Bacillus subtilis 1423 -11531640 220341 ysnD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:101757) (re:102092) (di:direct) BSUB0015 Z99118 g2635297 Bacillus subtilis 1423 -11531640 304214 ysnD hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:unknown function; putative) (le:67815) (re:68150) (di:complement) BSZ75208 Z75208 g1770065 Bacillus subtilis 1423 -11531640

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808036	5550	27706	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808039	5551	27707	231	77

Description

6500727783 hypothetical protein:similar to acetyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysnE ysnE Bacillus subtilis 1423 -11531641 7000692145 ysnE acetyltransferase homolog ysnE (db:pir2.dat) F69986 F69986 Bacillus subtilis 1423 -11531641 220340 ysnE (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to acetyltransferase) (le:102261) (re:102716) (di:direct) BSUB0015 Z99118 g2635298 Bacillus subtilis 1423 -11531641 304213 ysnE hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to acetyltransferase within the trpgdc) (le:67191) (re:67646) (di:complement) BSZ75208 Z75208 g1770064 Bacillus subtilis 1423 -11531641

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808042	5552	27708	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808053	5553	27709	195	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808054	5554	27710	336	111

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808067	5555	27711	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808073	5556	27712	294	97

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808079	5557	27713	519	172

Description

6500727784 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysnF ysnF Bacillus subtilis 1423 -11531642  
7000693889 ysnf hypothetical protein ysnf (db:pir2.dat) G69986 G69986  
Bacillus subtilis 1423 -11531642 220338 ysnf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:103337) (re:103759) (di:direct) BSUB0015 Z99118 g2635299  
Bacillus subtilis 1423 -11531642 304211 ysnf hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:unknown function; putative) (le:66148) (re:66570) (di:complement) BSZ75208 Z75208  
g1770062 Bacillus subtilis 1423 -11531642



ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501808081	5558	27714	192	63

Description

6500727785 hypothetical protein:hypothetical 19.2 kd protein in rph-ilvb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysnB ysnB Bacillus subtilis 1423 -11531643 4000709975 ysnb (de:hypothetical 19.2 kd protein in rph-ilvb intergenic region) (db:swissprot) YSNB\_BACSU P94559 BACILLUS SUBTILIS 1423 -11531643 7000688605 ysnb conserved hypothetical protein ysnb (cl:conserved hypothetical protein mg207:phosphoesterase core homology) (db:pir2.dat) D69986 D69986 Bacillus subtilis 1423 -11531643 220337 ysnb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:103990) (re:104505) (di:complement) BSUB0015 Z99118 g2635300 Bacillus subtilis 1423 -11531643 304210 ysnb hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to hi0260 of haemophilus influenzae;) (le:65402) (re:65917) (di:direct) BSZ75208 Z75208 g1770061 Bacillus subtilis 1423 -11531643

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501808087	5559	27715	423	140

Description

6500727786 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysnA ysnA Bacillus subtilis 1423 -11531644 7000692741 ysnA conserved hypothetical protein ysnA (cl:methanococcus jannaschii conserved hypothetical protein mj0226) (db:pir2.dat) C69986 C69986 Bacillus subtilis 1423 -11531644 220336 ysnA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:104515) (re:105111) (di:complement) BSUB0015 Z99118 g2635301 Bacillus subtilis 1423 -11531644 304209 ysnA hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to orf0197 of escherichia coli; unknown) (le:64796) (re:65392) (di:direct) BSZ75208 Z75208 g1770060 Bacillus subtilis 1423 -11531644

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808096	5560	27716	747	248

Description

6500727787 hypothetical protein:similar to transcriptional regulator:marr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysmB ysmB Bacillus subtilis 1423 -11531645 7000694771 ysmB transcription regulator marr family homolog ysmB (cl:regulatory protein mpra) (db:pir2.dat) B69986 B69986 Bacillus subtilis 1423 -11531645 304204 ysmB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to transcriptional regulator (marr family)) (le:108014) (re:108454) (di:complement) BSUB0015 Z99118 g2635305 Bacillus subtilis 1423 -11531645 304205 ysmB hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to marr type transcriptional regulators;) (le:61453) (re:61893) (di:direct) BSZ75208 Z75208 g1770054 Bacillus subtilis 1423 -11531645 220331 ysmB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to transcriptional regulator (marr family)) (le:108014) (re:108454) (di:complement) BSUB0015 Z99118 g2635305 Bacillus subtilis 1423 -11531645 220332 ysmB hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to marr type transcriptional regulators;) (le:61453) (re:61893) (di:direct) BSZ75208 Z75208 g1770054 Bacillus subtilis 1423 -11531645

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808112	5561	27717	261	86

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808118	5562	27718	1602	533
<u>Description</u>				
5000689689 hypothetical protein:hypothetical 17.1 kd protein in sdhb-gere intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysmA ysmA Bacillus subtilis 1423 -11531646 116331 ysmA (de:hypothetical 17.1 kd protein in sdhb-gere intergenic region) (db:swissprot) YSMA_BACSU P11469 BACILLUS SUBTILIS 1423 -11531646 7000688604 ysmA hypothetical protein ysmA (db:pir2.dat) B27893 B27893 Bacillus subtilis 1423 -11531646 7500952721 (sr:b.subtilis (strain 168) dna) (db:genpept-bct1) (de:b.subtilis succinate dehydrogenase (sdhc) gene, partial cds, andgermination protein (gere) gene, complete cds.) (nt:open reading frame 2 (orf2)) (le:490) (re:933) (di:direct) BACGERE M17642 g142968 Bacillus subtilis 1423 -11531646 215657 ysmA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:109038) (re:109481) (di:complement) BSUB0015 Z99118 g2635307 Bacillus subtilis 1423 -11531646 5500684825 ysmA hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:unknown function; putative) (le:60426) (re:60869) (di:direct) BSZ75208 Z75208 g2575781 Bacillus subtilis 1423 -11531646 170044 ysmA hypothetical protein ysmA (db:pir) B27893 B27893 Bacillus subtilis 1423 -11531646 6500727788 hypothetical protein:hypothetical 17.1 kd protein in sdhb-gere intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysmA ysmA Bacillus subtilis 1423 -11531646				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808120	5563	27719	426	141

#### Description

5000689688 hypothetical protein:hypothetical 17.3 kd protein in lysc 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yslB yslB Bacillus subtilis 1423 -11531647 116325 yslb (de:hypothetical 17.3 kd protein in lysc 3'region) (db:swissprot) YSLB\_BACSU P42955 BACILLUS SUBTILIS 1423 -11531647 7000688603 yslb hypothetical protein yslb (db:pir2.dat) H69985 H69985 Bacillus subtilis 1423 -11531647 215196 (sr:bacillus subtilis (strain 168) (tissue library: atcc 6633) dna) (db:genpept-bct1) (de:bacillus subtilis thioredoxin (trx), uvrB and aspartokinase iigenes, complete cds.) (nt:orf; putative) (le:3872) (re:4318) (di:complement) BACAPKII J03294 g1129090 Bacillus subtilis 1423 -11531647 220325 yslb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:113003) (re:113449) (di:direct) BSUB0015 Z99118 g2635311 Bacillus subtilis 1423 -11531647 304198 yslb hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:unknown function; putative) (le:56458) (re:56904) (di:complement) BSZ75208 Z75208 g1770049 Bacillus subtilis 1423 -11531647 6500727789 hypothetical protein:hypothetical 17.3 kd protein in lysc 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yslB yslB Bacillus subtilis 1423 -11531647

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808121	5564	27720	558	185

#### Description

6500727790 hypothetical protein:similar to 3-hydroxybutyryl-coa dehydratase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysiB ysiB Bacillus subtilis 1423 -11531648 7000692043 ysiB 3-hydroxybutyryl-coa dehydratase homolog ysiB (cl:naphthoate synthase:enoyl-coa hydratase homology) (db:pir2.dat) G69985 G69985 Bacillus subtilis 1423 -11531648 220316 ysiB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to 3-hydroxybutyryl-coa dehydratase) (le:121138) (re:121914) (di:complement) BSUB0015 Z99118 g2635319 Bacillus subtilis 1423 -11531648 304189 ysiB hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology with crotonase from clostridium) (le:47993) (re:48769) (di:direct) BSZ75208 Z75208 g1770040 Bacillus subtilis 1423 -11531648

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808129	5565	27721	687	229

Description

6500727791 hypothetical protein:similar to transcriptional regulator:tetr/acrr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysiA ysiA Bacillus subtilis 1423 -11531649 7000694786 ysiA transcription regulator tetr/acrr family homolog ysiA (db:pir2.dat) F69985 F69985 Bacillus subtilis 1423 -11531649 220315 ysiA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to transcriptional regulator (tetr/acrr) (le:121929) (re:122513) (di:complement) BSUB0015 Z99118 g2635320 Bacillus subtilis 1423 -11531649 304188 ysiA hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology with regulatory proteins of the hth-tetr) (le:47394) (re:47978) (di:direct) BSZ75208 Z75208 g1770039 Bacillus subtilis 1423 -11531649

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808140	5566	27722	570	189

Description

GTC ORF with score 106 to: (sr:fruit fly) (db:genpept-inv) (de:drosophila melanogaster centrosomal and chromosomal factor (ccf)mRNA, complete cds and 5' genomic segment.) (nt:required for mitotic chromosome condensation;) (le:1479) (re:3131) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808147	5567	27723	981	326

Description

6500727792 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yshE yshE Bacillus subtilis 1423 -11531650 7000693887 yshe hypothetical protein yshe (db:pir2.dat) E69985 E69985 Bacillus subtilis 1423 -11531650 220313 yshe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:124489) (re:124893) (di:complement) BSUB0015 Z99118 g2635322 Bacillus subtilis 1423 -11531650 304186 yshe hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:unknown function;putative) (le:45014) (re:45418) (di:direct) BSZ75208 Z75208 g1770037 Bacillus subtilis 1423 -11531650

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808154	5568	27724	834	277

Description

6500727793 hypothetical protein:similar to dna mismatch repair protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yshD yshD Bacillus subtilis 1423 -11531651 7502851731 muts2 (de:muts2 protein) (db:swissprot) MUS2\_BACSU P94545 BACILLUS SUBTILIS 1423 -11531651 7000692934 yshd dna mismatch repair protein homolog yshd (db:pir2.dat) D69985 D69985 Bacillus subtilis 1423 -11531651 220312 yshd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to dna mismatch repair protein) (le:124908) (re:127265) (di:complement) BSUB0015 Z99118 g2635323 Bacillus subtilis 1423 -11531651 304185 yshd hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:shows homology to muts of thermus aquaticus;) (le:42642) (re:44999) (di:direct) BSZ75208 Z75208 g1770036 Bacillus subtilis 1423 -11531651

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808155	5569	27725	510	169

Description

6500727794 hypothetical protein:similar to dna polymerase beta (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yshC yshC Bacillus subtilis 1423 -11531652 7000692935 yshc dna polymerase beta homolog yshc (db:pir2.dat) C69985 C69985 Bacillus subtilis 1423 -11531652 220311 yshc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to dna polymerase beta) (le:127286) (re:128998) (di:complement) BSUB0015 Z99118 g2635324 Bacillus subtilis 1423 -11531652 304184 yshc hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:unknown function;putative) (le:40909) (re:42621) (di:direct) BSZ75208 Z75208 g1770035 Bacillus subtilis 1423 -11531652

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808158	5570	27726	384	127

Description

6500727795 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yshB yshB Bacillus subtilis 1423 -11531653 7000693886 yshb hypothetical protein yshb (db:pir2.dat) B69985 B69985 Bacillus subtilis 1423 -11531653 220310 yshb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:129072) (re:129605) (di:complement) BSUB0015 Z99118 g2635325 Bacillus subtilis 1423 -11531653 304183 yshb hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:unknown function; putative) (le:40302) (re:40835) (di:direct) BSZ75208 Z75208 g1770034 Bacillus subtilis 1423 -11531653

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808181	5571	27727	876	291
<u>Description</u>				
6500727796 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yshA yshA Bacillus subtilis 1423 -11531654				
7000693885 ysha hypothetical protein ysha (db:pir2.dat) A69985 A69985 Bacillus subtilis 1423 -11531654 220309 ysha (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:129612) (re:129869) (di:complement) BSUB0015 Z99118 g2635326 Bacillus subtilis 1423 -11531654 304182 ysha hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:unknown function; putative) (le:40038) (re:40295) (di:direct) BSZ75208 Z75208 g1770033 Bacillus subtilis 1423 -11531654				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808184	5572	27728	249	82
<u>Description</u>				
6500727797 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysgB ysgB Bacillus subtilis 1423 -11531655 7000692740 ysgb conserved hypothetical protein ysgb (db:pir2.dat) H69984 H69984 Bacillus subtilis 1423 -11531655 220308 ysgb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:130003) (re:130944) (di:direct) BSUB0015 Z99118 g2635327 Bacillus subtilis 1423 -11531655 304181 ysgb hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:unknown function; putative) (le:38963) (re:39904) (di:complement) BSZ75208 Z75208 g1770032 Bacillus subtilis 1423 -11531655				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808194	5573	27729	846	281
<u>Description</u>				
6500727798 hypothetical protein:similar to rrna methylase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysgA ysgA Bacillus subtilis 1423 -11531656 7000694568 ysga rrna methylase homolog ysga (db:pir2.dat) G69984 G69984 Bacillus subtilis 1423 -11531656 220305 ysga (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to rrna methylase) (le:134799) (re:135545) (di:complement) BSUB0015 Z99118 g2635330 Bacillus subtilis 1423 -11531656 304178 ysga hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to spou-type rrna methyltransferases;) (le:34362) (re:35108) (di:direct) BSZ75208 Z75208 g1770029 Bacillus subtilis 1423 -11531656				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808212	5574	27730	273	90

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808220	5575	27731	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808224	5576	27732	315	104

Description

6500727799 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysfa ysfa Bacillus subtilis 1423 -11531657  
7000693883 ysfa hypothetical protein ysfa (db:pir2.dat) B69984 B69984 Bacillus subtilis 1423 -11531657 220304 ysfa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:135664) (re:135879) (di:direct) BSUB0015 Z99118 g2635331 Bacillus subtilis 1423 -11531657 304177 ysfa hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:unknown function; putative) (le:34028) (re:34243) (di:complement) BSZ75208 Z75208 g1770028 Bacillus subtilis 1423 -11531657

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808226	5577	27733	1212	404

Description

6500727800 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysfB ysfB Bacillus subtilis 1423 -11531658 7000692739 ysfB conserved hypothetical protein ysfB (db:pir2.dat) C69984 C69984 Bacillus subtilis 1423 -11531658 220303 ysfB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:135948) (re:137054) (di:direct) BSUB0015 Z99118 g2635332 Bacillus subtilis 1423 -11531658 304176 ysfB hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to yaeg from escherichia coli; unknown) (le:32853) (re:33959) (di:complement) BSZ75208 Z75208 g1770027 Bacillus subtilis 1423 -11531658



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808244	5578	27734	222	73

Description

6500727801 hypothetical protein:similar to glycolate oxidase subunit (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysfc ysfc Bacillus subtilis 1423 -11531659 7000693068 ysfc glycolate oxidase subunit homolog ysfc (cl:glycolate oxidase chain glcd) (db:pir2.dat) D69984 D69984 Bacillus subtilis 1423 -11531659 220302 ysfc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to glycolate oxidase subunit) (le:137157) (re:138569) (di:direct) BSUB0015 Z99118 g2635333 Bacillus subtilis 1423 -11531659 304175 ysfc hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to glcd of escherichia coli; unknown) (le:31338) (re:32750) (di:complement) BSZ75208 Z75208 g1770026 Bacillus subtilis 1423 -11531659

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808252	5579	27735	669	222

Description

GTC ORF with score 434 to: (fn:mitochondrial anion transporter) (sr:baker's yeast) (db:genpept-pln1) (de:saccharomyces cerevisiae dicarboxylate transport protein gene,nuclear gene encoding mitochondrial protein, complete cds.) (le:1) (re:897) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808260	5580	27736	810	270

Description

6500727802 hypothetical protein:similar to glycolate oxidase subunit (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysfd ysfd Bacillus subtilis 1423 -11531660 7000693069 ysfd glycolate oxidase subunit homolog ysfd (cl:synechocystis (s)-2-hydroxy-acid oxidase) (db:pir2.dat) E69984 E69984 Bacillus subtilis 1423 -11531660 220301 ysfd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to glycolate oxidase subunit) (le:138566) (re:139900) (di:direct) BSUB0015 Z99118 g2635334 Bacillus subtilis 1423 -11531660 304174 ysfd hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to glcf of escherichia coli; unknown) (le:30007) (re:31341) (di:complement) BSZ75208 Z75208 g1770025 Bacillus subtilis 1423 -11531660

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808263	5581	27737	474	158

Description

6500727803 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysfE ysfE Bacillus subtilis 1423 -11531661  
 7000693884 ysfe hypothetical protein ysfe (db:pir2.dat) F69984 F69984 Bacillus subtilis 1423 -11531661 220300 ysfe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:139939) (re:140181) (di:complement) BSUB0015 Z99118 g2635335 Bacillus subtilis 1423 -11531661 304173 ysfe hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:unknown function; putative) (le:29726) (re:29968) (di:direct) BSZ75208 Z75208 g1770024 Bacillus subtilis 1423 -11531661

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808281	5582	27738	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808284	5583	27739	450	149

Description

6500727804 yseb:aram hypothetical protein:l-arabinose operon (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) araM araM Bacillus subtilis 1423 -11531662 7502851732 aram (de:arabinose operon protein aram) (db:swissprot) ARAM\_BACSU P94527 BACILLUS SUBTILIS 1423 -11531662  
 7000694142 aram l-arabinose operon aram (db:pir2.dat) H69587 H69587 Bacillus subtilis 1423 -11531662 220294 aram (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: yseb; l-arabinose operon) (le:146978) (re:148162) (di:complement) BSUB0015 Z99118 g2635341 Bacillus subtilis 1423 -11531662 304167 yseb hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:unknown function;putative) (le:21745) (re:22929) (di:direct) BSZ75208 Z75208 g1770018 Bacillus subtilis 1423 -11531662

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808296	5584	27740	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808301	5585	27741	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808321	5586	27742	432	143

Description

GTC ORF with score 141 to: (sr:homo sapiens (tissue library: primary b cell) cdna to mrna) (db:genpept-pri1) (de:human splicing factor sc35 mrna, complete cds.) (nt:the aas encoded by bases 200-218 and 315-341 bind) (le:156) (re:821) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808327	5587	27743	192	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808332	5588	27744	189	62

Description

6500727805 ysea:aral hypothetical protein:l-arabinose operon (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) aral aral Bacillus subtilis 1423 -11531663 7000694141 aral l-arabinose operon aral (cl:nagd protein) (db:pir2.dat) G69587 G69587 Bacillus subtilis 1423 -11531663 220293 aral (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: ysea; l-arabinose operon) (le:148159) (re:148977) (di:complement) BSUB0015 Z99118 g2635342 Bacillus subtilis 1423 -11531663 304166 ysea hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to yzdg of bacillus subtilis; unknown) (le:20930) (re:21748) (di:direct) BSZ75208 Z75208 g1770017 Bacillus subtilis 1423 -11531663

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808333	5589	27745	675	224

Description

6500727806 hypothetical protein:similar to endo-1:4-beta-glucanase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysdC ysdC Bacillus subtilis 1423 -11531664 7000692959 ysdC endo-1:4-beta-glucanase homolog ysdC (cl:thermophilic aminopeptidase i alpha chain) (db:pir2.dat) A69984 A69984 Bacillus subtilis 1423 -11531664 220288 ysdC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to endo-1,4-beta-glucanase) (le:154199) (re:155284) (di:complement) BSUB0015 Z99118 g2635347 Bacillus subtilis 1423 -11531664 304161 ysdC hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to cela of clostridium thermocellum and) (le:14623) (re:15708) (di:direct) BSZ75208 Z75208 g1770012 Bacillus subtilis 1423 -11531664

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808336	5590	27746	486	161

Description

6500727807 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysdB ysdB Bacillus subtilis 1423 -11531665 7000693882 ysdB hypothetical protein ysdB (db:pir2.dat) H69983 H69983 Bacillus subtilis 1423 -11531665 220287 ysdB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:155468) (re:155860) (di:direct) BSUB0015 Z99118 g2635348 Bacillus subtilis 1423 -11531665 304160 ysdB hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:unknown function; putative) (le:14047) (re:14439) (di:complement) BSZ75208 Z75208 g1770011 Bacillus subtilis 1423 -11531665

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808363	5591	27747	624	208

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808364	5592	27748	1326	441

Description

6500727808 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysdA ysdA Bacillus subtilis 1423 -11531666  
7000693881 ysdA hypothetical protein ysdA (db:pir2.dat) G69983 G69983  
Bacillus subtilis 1423 -11531666 220286 ysdA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:155876) (re:156145) (di:complement) BSUB0015 Z99118 g2635349  
Bacillus subtilis 1423 -11531666 304159 ysdA hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:unknown function; putative) (le:13762) (re:14031) (di:direct) BSZ75208 Z75208  
g1770010 Bacillus subtilis 1423 -11531666

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808374	5593	27749	426	141

Description

6500727809 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysca ysca Bacillus subtilis 1423 -11531667  
7000693879 ysca hypothetical protein ysca (db:pir2.dat) E69983 E69983  
Bacillus subtilis 1423 -11531667 220282 ysca (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:157499) (re:157723) (di:direct) BSUB0015 Z99118 g2635353  
Bacillus subtilis 1423 -11531667 304155 ysca hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:unknown function; putative) (le:12184) (re:12408) (di:complement) BSZ75208 Z75208  
g1770006 Bacillus subtilis 1423 -11531667

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808384	5594	27750	1350	450

Description

6500727810 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yscB yscB Bacillus subtilis 1423 -11531668  
7000693880 yscB hypothetical protein yscB (db:pir2.dat) F69983 F69983  
Bacillus subtilis 1423 -11531668 220281 yscB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:157773) (re:158405) (di:direct) BSUB0015 Z99118 g2635354  
Bacillus subtilis 1423 -11531668 304154 yscB hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:unknown function; putative) (le:11502) (re:12134) (di:complement) BSZ75208 Z75208  
g1770005 Bacillus subtilis 1423 -11531668

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808404	5595	27751	1449	482

Description

6500727811 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysbB ysbB Bacillus subtilis 1423 -11531669 7000692738 ysbB conserved hypothetical protein ysbB (cl:yohk protein) (db:pir2.dat) D69983 D69983 Bacillus subtilis 1423 -11531669 220280 ysbB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:158437) (re:159132) (di:complement) BSUB0015 Z99118 g2635355 Bacillus subtilis 1423 -11531669 304153 ysbB hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to ywbg of bacillus subtilis; putative) (le:10775) (re:11470) (di:direct) BSZ75208 Z75208 gl770004 Bacillus subtilis 1423 -11531669

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808419	5596	27752	819	272

Description

6500727812 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysbA ysbA Bacillus subtilis 1423 -11531670 7000692737 ysbA conserved hypothetical protein ysbA (cl:conserved hypothetical protein hi1297) (db:pir2.dat) C69983 C69983 Bacillus subtilis 1423 -11531670 220279 ysbA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins from b. subtilis) (le:159154) (re:159594) (di:complement) BSUB0015 Z99118 g2635356 Bacillus subtilis 1423 -11531670 304152 ysbA hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to ywbh of bacillus subtilis; putative) (le:10313) (re:10753) (di:direct) BSZ75208 Z75208 gl770003 Bacillus subtilis 1423 -11531670

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808426	5597	27753	417	139

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808427	5598	27754	831	276

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808429	5599	27755	366	121

Description

6500727813 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ysaA ysaA Bacillus subtilis 1423 -11531671 7000692736 ysaA conserved hypothetical protein ysaA (db:pir2.dat) B69983 B69983 Bacillus subtilis 1423 -11531671 220276 ysaA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:162379) (re:163161) (di:direct) BSUB0015 Z99118 g2635359 Bacillus subtilis 1423 -11531671 304149 ysaA hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to escherichia coli yjgg; putative) (le:6746) (re:7528) (di:complement) BSZ75208 Z75208 g1770000 Bacillus subtilis 1423 -11531671

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808432	5600	27756	1749	583

Description

5000689695 hypothetical protein:hypothetical 33.3 kd protein in dnai-thrs intergenic region:orf-281 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytxC ytxC Bacillus subtilis 1423 -11531672 219161 ytxC (de:hypothetical 33.3 kd protein in dnai-thrs intergenic region (orf-281)) (db:swissprot) YTXC\_BACSU P06569 BACILLUS SUBTILIS 1423 -11531672 7000688616 ytxC hypothetical protein ytxC (db:pir2.dat) D24720 D24720 Bacillus subtilis 1423 -11531672 4000707471 ytxC ytxC (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:216692) (re:217537) (di:direct) AF008220 AF008220 g2293283 Bacillus subtilis 1423 -11531672 304147 (db:genpept-bct1) (de:bacillus subtilis dnab gene for initiation of chromosomal replication.) (nt:orf 281 (aa 1-281)) (le:3532) (re:4377) (di:direct) BSDNAB X04963 g39883 Bacillus subtilis 1423 -11531672 220274 ytxC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:165530) (re:166375) (di:complement) BSUB0015 Z99118 g2635361 Bacillus subtilis 1423 -11531672 6500727814 ytxC hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:unknown function; putative) (le:3532) (re:4377) (di:direct) BSZ75208 Z75208 g1769998 Bacillus subtilis 1423 -11531672 116454 ytxC (de:hypothetical 33.3 kd protein in dnai-thrs intergenic region (orf-281)) (db:swissprot) YTXC\_BACSU P06569 BACILLUS SUBTILIS 1423 -11531672 170400 ytxC hypothetical protein ytxC (db:pir) D24720 D24720 Bacillus subtilis 1423 -11531672

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808441	5601	27757	192	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808451	5602	27758	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808454	5603	27759	273	90

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808461	5604	27760	465	154

Description

GTC ORF with score 219 to: (sr:lithospermum erythrorhizon dedifferentiated cells cell\_line:m1) (db:genpept-pln1) (de:lithospermum erythrorhizon mrna for lec14b protein, complete cds.) (nt:single copy gene in the lithospermum genome) (le:153) (re:1574) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808480	5605	27761	354	117

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808515	5606	27762	438	145

Description

5000689694 hypothetical protein:hypothetical 23.3 kd protein in dnai-thrs intergenic region:orf-213 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytxB ytxB Bacillus subtilis 1423 -11531673 219160 ytxb (de:hypothetical 23.3 kd protein in dnai-thrs intergenic region (orf-213)) (db:swissprot) YTXB\_BACSU P06568 BACILLUS SUBTILIS 1423 -11531673 7000688615 ytxb conserved hypothetical protein ytxb (db:pir2.dat) C24720 C24720 Bacillus subtilis 1423 -11531673 4000707470 ytxb ytxb (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:215972) (re:216613) (di:direct) AF008220 AF008220 g2293282 Bacillus subtilis 1423 -11531673 304146 (db:genpept-bct1) (de:bacillus subtilis dnab gene for initiation of chromosomal replication.) (nt:orf 213 (aa 1-213)) (le:2812) (re:3453) (di:direct) BSDNAB X04963 g39882 Bacillus subtilis 1423 -11531673 220273 ytxb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:166454) (re:167095) (di:complement) BSUB0015 Z99118 g2635362 Bacillus subtilis 1423 -11531673 6500727815 ytxb hypothetical protein (db:genpept-bct1) (de:bacillus subtilis genomic sequence 89009bp.) (nt:unknown function; putative) (le:2812) (re:3453) (di:direct) BSZ75208 Z75208 g1769997 Bacillus subtilis 1423 -11531673 116453 ytxb (de:hypothetical 23.3 kd protein in dnai-thrs intergenic region (orf-213)) (db:swissprot) YTXB\_BACSU P06568 BACILLUS SUBTILIS 1423 -11531673 170399 ytxb conserved hypothetical protein ytxb (db:pir) C24720 C24720 Bacillus subtilis 1423 -11531673

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808522	5607	27763	918	306

Description

6500727816 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytcG ytcG Bacillus subtilis 1423 -11531674 7000693897 ytcg hypothetical protein ytcg:hypothetical protein x dnab 5 region (cl:conserved hypothetical protein hi0943) (db:pir2.dat) D69989 D69989 Bacillus subtilis 1423 -11531674 4000714273 ytcg ytcg (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to hypothetical protein hi0943 from h.) (le:212984) (re:213442) (di:direct) AF008220 AF008220 g2293279 Bacillus subtilis 1423 -11531674 7500964695 ytcg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:169625) (re:170083) (di:complement) BSUB0015 Z99118 g2635365 Bacillus subtilis 1423 -11531674

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808523	5608	27764	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808530	5609	27765	639	212

Description

6500727817 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytcF ytcF Bacillus subtilis 1423 -11531675  
 7000693896 ytcF hypothetical protein ytcF (cl:conserved hypothetical protein mj0315) (db:pir2.dat) C69989 C69989 Bacillus subtilis 1423 -11531675  
 4000714272 ytcF ytcF (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:212324) (re:212710) (di:direct) AF008220 AF008220 g2293278 Bacillus subtilis 1423 -11531675 7500964694 ytcF (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:170357) (re:170743) (di:complement) BSUB0015 Z99118 g2635366 Bacillus subtilis 1423 -11531675

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808531	5610	27766	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808547	5611	27767	570	189

Description

6500727818 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytcD ytcD Bacillus subtilis 1423 -11531676  
 7000693895 ytcD hypothetical protein ytcD (cl:conserved hypothetical protein mth1285) (db:pir2.dat) B69989 B69989 Bacillus subtilis 1423 -11531676 4000714270 ytcD ytcD (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity with hypothetical protein yckh from b.) (le:210483) (re:210863) (di:direct) AF008220 AF008220 g2293276 Bacillus subtilis 1423 -11531676 7500964693 ytcD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:172204) (re:172584) (di:complement) BSUB0015 Z99118 g2635368 Bacillus subtilis 1423 -11531676

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808556	5612	27768	240	79

Description

6500727819 hypothetical protein:similar to antibiotic resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytbD ytbD Bacillus subtilis 1423 -11531677 7000692216 ytbD chloramphenicol resistance protein homolog ytbD (cl:streptomyces lividans chloramphenicol resistance protein) (db:pir2.dat) C69988 C69988 Bacillus subtilis 1423 -11531677 4000714269 ytbD ytbD (db:genpept-bct1) (de:bacillus subtilis rrnB-dnab genomic region.) (nt:similar to e. coli araj precursor) (le:209109) (re:210299) (di:complement) AF008220 AF008220 g2293329 Bacillus subtilis 1423 -11531677 7500963422 ytbD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to antibiotic resistance protein) (le:172768) (re:173958) (di:direct) BSUB0015 Z99118 g2635369 Bacillus subtilis 1423 -11531677

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808559	5613	27769	399	132

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808562	5614	27770	363	120

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808574	5615	27771	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808577	5616	27772	462	153

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808586	5617	27773	552	183

#### Description

6500727820 hypothetical protein:similar to plant metabolite dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytbE ytbE Bacillus subtilis 1423 -11531678 7000694427 ytbE plant metabolite dehydrogenase homolog ytbE (cl:aldehyde reductase) (db:pir2.dat) D69988 D69988 Bacillus subtilis 1423 -11531678 4000714268 ytbE putative morphine dehydrogenase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:208243) (re:209085) (di:complement) AF008220 AF008220 g2293328 Bacillus subtilis 1423 -11531678 7500953793 ytbE (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to plant metabolite dehydrogenase) (le:173982) (re:174824) (di:direct) BSUB0015 Z99118 g2635370 Bacillus subtilis 1423 -11531678

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808603	5618	27774	279	93

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808607	5619	27775	843	280

#### Description

6500727821 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytag ytag Bacillus subtilis 1423 -11531679 7500952742 ytag (de:hypothetical 22.0 kd protein in gapb-mutm intergenic region) (db:swissprot) YTAG\_BACSU 034932 BACILLUS SUBTILIS 1423 -11531679 7000692742 ytag conserved hypothetical protein ytag (cl:conserved hypothetical protein ydr196c) (db:pir2.dat) A69988 A69988 Bacillus subtilis 1423 -11531679 4000714267 ytag ytag (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to hypothetical protein hi0890 from h.) (le:207608) (re:208201) (di:direct) AF008220 AF008220 g2293275 Bacillus subtilis 1423 -11531679 7500952745 ytag (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:174866) (re:175459) (di:complement) BSUB0015 Z99118 g2635371 Bacillus subtilis 1423 -11531679

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808612	5620	27776	204	67

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808617	5621	27777	270	89

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808623	5622	27778	582	194

Description

6500727822 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytaF ytaF Bacillus subtilis 1423 -11531680  
7000693892 ytaF hypothetical protein ytaF (db:pir2.dat) H69987 H69987 Bacillus subtilis 1423 -11531680 4000714266 ytaF ytaF (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:206967) (re:207446) (di:direct) AF008220 AF008220 g2293274 Bacillus subtilis 1423 -11531680  
7500964690 ytaF (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:175621) (re:176100) (di:complement) BSUB0015 Z99118 g2635372 Bacillus subtilis 1423 -11531680

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808628	5623	27779	1053	350

Description

6500727823 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytwI ytwI Bacillus subtilis 1423 -11531681 7000692766 ytwI conserved hypothetical protein ytwI (cl:hypothetical protein ytwI) (db:pir2.dat) F70002 F70002 Bacillus subtilis 1423 -11531681 4000714261 ytwI ytwI (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to hypothetical protein hi1074 from h.) (le:196057) (re:196521) (di:direct) AF008220 AF008220 g2293266 Bacillus subtilis 1423 -11531681  
7500955924 ytwI (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:186546) (re:187010) (di:complement) BSUB0015 Z99118 g2635380 Bacillus subtilis 1423 -11531681

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808632	5624	27780	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808635	5625	27781	315	104

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808648	5626	27782	285	94

Description

6500727824 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytvI ytvI Bacillus subtilis 1423 -11531682 7000692763 ytvI conserved hypothetical protein ytvI (db:pir2.dat) C70002 C70002 Bacillus subtilis 1423 -11531682 4000714260 ytvI ytvI (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to hypothetical protein hi0237 from h.) (le:194845) (re:195960) (di:complement) AF008220 AF008220 g2293327 Bacillus subtilis 1423 -11531682 7500963837 ytvI (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:187107) (re:188222) (di:direct) BSUB0015 Z99118 g2635381 Bacillus subtilis 1423 -11531682

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808650	5627	27783	654	217

Description

6500727825 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytzA ytzA Bacillus subtilis 1423 -11531683 7000692767 ytzA conserved hypothetical protein ytzA (db:pir2.dat) C70004 C70004 Bacillus subtilis 1423 -11531683 7500963840 ytzA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:188255) (re:188638) (di:complement) BSUB0015 Z99118 g2635382 Bacillus subtilis 1423 -11531683

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808653	5628	27784	222	73

Description

6500727826 hypothetical protein:similar to acetyl-coa carboxylase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yttI yttI Bacillus subtilis 1423 -11531684 7000692141 ytti acetyl-coa carboxylase homolog ytti (cl:acetyl-coa carboxylase, carboxyltransferase beta chain) (db:pir2.dat) G70001 G70001 Bacillus subtilis 1423 -11531684 4000714256 ytti acetyl-coa carboxylase subunit (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:189643) (re:190431) (di:direct) AF008220 AF008220 g2293262 Bacillus subtilis 1423 -11531684 7500954529 ytti (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to acetyl-coa carboxylase) (le:192636) (re:193424) (di:complement) BSUB0015 Z99118 g2635386 Bacillus subtilis 1423 -11531684

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808656	5629	27785	219	72

Description

6500727827 hypothetical protein:similar to malate dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytsJ ytsJ Bacillus subtilis 1423 -11531685 7000694185 ytsj malate dehydrogenase homolog ytsj (cl:malate dehydrogenase (oxaloacetate-decarboxylating)) (db:pir2.dat) C70001 C70001 Bacillus subtilis 1423 -11531685 4000714255 ytsj ytsj (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to malate dehydrogenase (nadp+) from) (le:187992) (re:189224) (di:direct) AF008220 AF008220 g2293261 Bacillus subtilis 1423 -11531685 7500953803 ytsj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to malate dehydrogenase) (le:193843) (re:195075) (di:complement) BSUB0015 Z99118 g2635387 Bacillus subtilis 1423 -11531685

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808686	5630	27786	426	141

Description

6500727828 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytrI ytrI Bacillus subtilis 1423 -11531686 7000693928 ytri hypothetical protein ytri (db:pir2.dat) E70000 E70000 Bacillus subtilis 1423 -11531686 4000714253 ytri ytri (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:183527) (re:184030) (di:complement) AF008220 AF008220 g2293326 Bacillus subtilis 1423 -11531686 7500964726 ytri (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:199037) (re:199540) (di:direct) BSUB0015 Z99118 g2635389 Bacillus subtilis 1423 -11531686

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808692	5631	27787	957	318

Description

6500727829 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytgI ytgI Bacillus subtilis 1423 -11531687 7000692760 ytgI conserved hypothetical protein ytgI (db:pir2.dat) F69999 F69999 Bacillus subtilis 1423 -11531687 4000714252 ytgI ytgI (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to mgpa protein from m.genitalium) (le:182275) (re:183216) (di:direct) AF008220 AF008220 g2293259 Bacillus subtilis 1423 -11531687 7500963834 ytgI (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:199851) (re:200792) (di:complement) BSUB0015 Z99118 g2635390 Bacillus subtilis 1423 -11531687

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808696	5632	27788	459	152

Description

6500727830 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytpI ytpI Bacillus subtilis 1423 -11531688 7000693924 ytpI hypothetical protein ytpI (db:pir2.dat) F69998 F69998 Bacillus subtilis 1423 -11531688 4000714251 ytpI ytpI (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:181842) (re:182144) (di:complement) AF008220 AF008220 g2293325 Bacillus subtilis 1423 -11531688 7500964722 ytpI (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:200923) (re:201225) (di:direct) BSUB0015 Z99118 g2635391 Bacillus subtilis 1423 -11531688

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808705	5633	27789	405	134

Description

6500727831 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytoI ytoI Bacillus subtilis 1423 -11531689 7000693921 ytoI hypothetical protein ytoi (db:pir2.dat) A69998 A69998 Bacillus subtilis 1423 -11531689 4000714250 ytoi ytoi (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity with hypothetical protein 3 from) (le:180504) (re:181823) (di:direct) AF008220 AF008220 g2293258 Bacillus subtilis 1423 -11531689 7500964719 ytoi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:201244) (re:202563) (di:complement) BSUB0015 Z99118 g2635392 Bacillus subtilis 1423 -11531689



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808710	5634	27790	321	106

Description

6500727832 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytnM ytnM Bacillus subtilis 1423 -11531690  
7000693919 ytnm hypothetical protein ytnm (db:pir2.dat) F69997 F69997 Bacillus subtilis 1423 -11531690 4000714249 ytnm ytnm (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to a hypothetical protein) (le:179426) (re:180328) (di:direct) AF008220 AF008220 g2293257 Bacillus subtilis 1423 -11531690 6000689075 ytnm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:202739) (re:203641) (di:complement) BSUB0015 Z99118 g2635393 Bacillus subtilis 1423 -11531690 7500964717 ytnm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:99) (re:1001) (di:complement) BSUB0016 Z99119 g2635412 Bacillus subtilis 1423 -11531690

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808711	5635	27791	297	98

Description

6500727833 hypothetical protein:similar to nitrilotriacetate monooxygenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytnJ ytnJ Bacillus subtilis 1423 -11531691 7000694326 ytnj nitrilotriacetate monooxygenase homolog ytnj (cl:nitrilotriacetate monooxygenase) (db:pir2.dat) E69997 E69997 Bacillus subtilis 1423 -11531691 4000714246 ytnj ytnj (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to nitrilotriacetate monooxygenase) (le:176072) (re:177400) (di:direct) AF008220 AF008220 g2293254 Bacillus subtilis 1423 -11531691 6000689071 ytnj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to nitrilotriacetate monooxygenase) (le:205667) (re:206995) (di:complement) BSUB0015 Z99118 g2635396 Bacillus subtilis 1423 -11531691 7500953934 ytnj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to nitrilotriacetate monooxygenase) (le:3027) (re:4355) (di:complement) BSUB0016 Z99119 g2635415 Bacillus subtilis 1423 -11531691

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808713	5636	27792	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808732	5637	27793	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808745	5638	27794	2184	727

Description

6500727834 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytnI ytnI Bacillus subtilis 1423 -11531692  
7000693918 ytni hypothetical protein ytni (db:pir2.dat) D69997 D69997  
Bacillus subtilis 1423 -11531692 4000714245 ytni glutaredoxin  
(db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.)  
(le:175794) (re:176075) (di:direct) AF008220 AF008220 g2293253 Bacillus  
subtilis 1423 -11531692 6000689069 ytni (fn:unknown) (db:genpept-bct1)  
(de:bacillus subtilis complete genome (section 15 of 21): from 2795131to  
3013540.) (le:206992) (re:207273) (di:complement) BSUB0015 Z99118 g2635397  
Bacillus subtilis 1423 -11531692 7500964716 ytni (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21):  
from 2997771to 3213410.) (le:4352) (re:4633) (di:complement) BSUB0016 Z99119  
g2635416 Bacillus subtilis 1423 -11531692

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808752	5639	27795	1452	483

Description

6500727835 hypothetical protein:similar to hypothetical proteins  
(gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytmO  
ytmo Bacillus subtilis 1423 -11531693 7000692756 ytmO conserved  
hypothetical protein ytmO (cl:ynbw protein) (db:pir2.dat) H69996 H69996  
Bacillus subtilis 1423 -11531693 4000714244 ytmO ytmO (db:genpept-bct1)  
(de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to  
luciferase from xenorhabdus lumenes) (le:174775) (re:175779) (di:direct)  
AF008220 AF008220 g2293252 Bacillus subtilis 1423 -11531693 6000689067 ytmO  
(fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome  
(section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical  
proteins) (le:207288) (re:208292) (di:complement) BSUB0015 Z99118 g2635398  
Bacillus subtilis 1423 -11531693 7500963831 ytmO (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21):  
from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:4648)  
(re:5652) (di:complement) BSUB0016 Z99119 g2635417 Bacillus subtilis 1423  
-11531693

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808754	5640	27796	285	94

#### Description

6500727836 hypothetical protein:similar to amino acid abc transporter:permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytmM ytmM Bacillus subtilis 1423 -11531694 7000692193 ytmM amino acid abc transporter permease homolog ytmM (cl:histidine permease protein m) (db:pir2.dat) G69996 G69996 Bacillus subtilis 1423 -11531694 4000714242 ytmM transporter (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:173295) (re:174002) (di:direct) AF008220 AF008220 g2293250 Bacillus subtilis 1423 -11531694 6000689063 ytmM (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to amino acid abc transporter (permease)) (le:209065) (re:209772) (di:complement) BSUB0015 Z99118 g2635400 Bacillus subtilis 1423 -11531694 7500963402 ytmM (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to amino acid abc transporter (permease)) (le:6425) (re:7132) (di:complement) BSUB0016 Z99119 g2635419 Bacillus subtilis 1423 -11531694

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808764	5641	27797	354	117

#### Description

6500727837 hypothetical protein:similar to amino acid abc transporter:permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytmL ytmL Bacillus subtilis 1423 -11531695 7000692192 ytmL amino acid abc transporter permease homolog ytmL (cl:histidine permease protein m) (db:pir2.dat) F69996 F69996 Bacillus subtilis 1423 -11531695 4000714241 ytmL amino acid transporter (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:172546) (re:173265) (di:direct) AF008220 AF008220 g2293249 Bacillus subtilis 1423 -11531695 6000689061 ytmL (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to amino acid abc transporter (permease)) (le:209802) (re:210521) (di:complement) BSUB0015 Z99118 g2635401 Bacillus subtilis 1423 -11531695 7500963401 ytmL (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to amino acid abc transporter (permease)) (le:7162) (re:7881) (di:complement) BSUB0016 Z99119 g2635420 Bacillus subtilis 1423 -11531695

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808766	5642	27798	204	67

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808773	5643	27799	261	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808774	5644	27800	1050	350

Description

GTC ORF with score 144 to: (fn:required for cytokinesis) (sr:human) (db:genpept-pri2) (de:homo sapiens protein regulating cytokinesis 1 (prcl) mrna, completedcds.) (nt:mitotic spindle-associated cdk substrate) (le:79) (re:1941) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808779	5645	27801	531	176

Description

GTC ORF with score 311 to: (sr:baker"s yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome iv cosmid 9481, 9509, 9926,9461, and lambda 3641.) (nt:involved in spore wall maturation; ydr402c;) (le:34974) (re:36443) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808784	5646	27802	825	274

Description

6500727838 hypothetical protein:similar to amino acid abc transporter:binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytmK ytmK Bacillus subtilis 1423 -11531696 7000692190 ytmk amino acid abc transporter binding protei homolog ytmk (db:pir2.dat) E69996 E69996 Bacillus subtilis 1423 -11531696 4000714240 ytmk putative lysine-binding protein (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:171712) (re:172524) (di:direct) AF008220 AF008220 g2293248 Bacillus subtilis 1423 -11531696 6000689059 ytmk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to amino acid abc transporter (binding) (le:210543) (re:211355) (di:complement) BSUB0015 Z99118 g2635402 Bacillus subtilis 1423 -11531696 7500963400 ytmk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to amino acid abc transporter (binding) (le:7903) (re:8715) (di:complement) BSUB0016 Z99119 g2635421 Bacillus subtilis 1423 -11531696

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808800	5647	27803	1275	424

Description

GTC ORF with score 595 to: (db:genpept-pln2) (de:emericaella nidulans negative-acting regulatory protein (qutr) gene, complete cds; and unknown gene.) (nt:repressor protein; coding region predicted from dna) (le:3826) (re:6531) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808824	5648	27804	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808826	5649	27805	300	99

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808841	5650	27806	342	113

Description

6500727839 hypothetical protein:similar to amino acid abc transporter:binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytmJ ytmJ Bacillus subtilis 1423 -11531697 7000692189 ytmj amino acid abc transporter binding protei homolog ytmj (db:pir2.dat) D69996 D69996 Bacillus subtilis 1423 -11531697 4000714239 ytmj putative glutamine-binding protein (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:170889) (re:171698) (di:direct) AF008220 AF008220 g2293247 Bacillus subtilis 1423 -11531697 6000689057 ytmj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to amino acid abc transporter (binding) (le:211369) (re:212178) (di:complement) BSUB0015 Z99118 g2635403 Bacillus subtilis 1423 -11531697 7500963399 ytmj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to amino acid abc transporter (binding) (le:8729) (re:9538) (di:complement) BSUB0016 Z99119 g2635422 Bacillus subtilis 1423 -11531697

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808843	5651	27807	1179	393

Description

6500727840 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytmI ytmI Bacillus subtilis 1423 -11531698 7000692755 ytmI conserved hypothetical protein ytmI (db:pir2.dat) C69996 C69996 Bacillus subtilis 1423 -11531698 4000714238 ytmI ytmI (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to a hypothetical 19 kd protein from b.) (le:170339) (re:170875) (di:direct) AF008220 AF008220 g2293246 Bacillus subtilis 1423 -11531698 6000689055 ytmI (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins from b. subtilis) (le:212192) (re:212728) (di:complement) BSUB0015 Z99118 g2635404 Bacillus subtilis 1423 -11531698 7500963830 ytmI (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins from b. subtilis) (le:9552) (re:10088) (di:complement) BSUB0016 Z99119 g2635423 Bacillus subtilis 1423 -11531698

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808845	5652	27808	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808855	5653	27809	351	116

Description

6500727841 hypothetical protein:similar to transcriptional regulator:lysr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytli ytli Bacillus subtilis 1423 -11531699 7000694759 ytli transcription regulator lysr family homolog ytli (db:pir2.dat) E69995 E69995 Bacillus subtilis 1423 -11531699 4000714237 ytli lysr family transcription regulator (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:169260) (re:170186) (di:complement) AF008220 AF008220 g2293324 Bacillus subtilis 1423 -11531699 6000689053 ytli (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to transcriptional regulator (lysr family)) (le:212881) (re:213807) (di:direct) BSUB0015 Z99118 g2635405 Bacillus subtilis 1423 -11531699 7500965329 ytli (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to transcriptional regulator (lysr family)) (le:10241) (re:11167) (di:direct) BSUB0016 Z99119 g2635424 Bacillus subtilis 1423 -11531699

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808858	5654	27810	588	195

Description

6500727842 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytkL ytkL Bacillus subtilis 1423 -11531700 7000692754 ytkL conserved hypothetical protein ytkL (db:pir2.dat) G69994 G69994 Bacillus subtilis 1423 -11531700 4000714236 ytkL ytkL (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to 3-ketoacyl-acp reductase from e.) (le:168527) (re:168829) (di:direct) AF008220 AF008220 g2293245 Bacillus subtilis 1423 -11531700 6000689051 ytkL (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to hypothetical proteins) (le:214238) (re:214540) (di:complement) BSUB0015 Z99118 g2635406 Bacillus subtilis 1423 -11531700 7500963829 ytkL (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:11598) (re:11900) (di:complement) BSUB0016 Z99119 g2635425 Bacillus subtilis 1423 -11531700

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808861	5655	27811	267	88

Description

6500727843 hypothetical protein:similar to 3-oxoacyl-acyl-carrier protein reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytkK ytkK Bacillus subtilis 1423 -11531701 7000692054 ytkK 3-oxoacyl-acyl-carrier protein reductase homolog ytkK (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) F69994 F69994 Bacillus subtilis 1423 -11531701 4000714235 ytkK 3-ketoacyl-acp reductase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:167697) (re:168464) (di:direct) AF008220 AF008220 g2293244 Bacillus subtilis 1423 -11531701 6000689049 ytkK (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to 3-oxoacyl-acyl-carrier protein) (le:214603) (re:215370) (di:complement) BSUB0015 Z99118 g2635407 Bacillus subtilis 1423 -11531701 7500963299 ytkK (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to 3-oxoacyl-acyl-carrier protein) (le:11963) (re:12730) (di:complement) BSUB0016 Z99119 g2635426 Bacillus subtilis 1423 -11531701

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808864	5656	27812	750	249

Description

6500727844 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytzD ytzD Bacillus subtilis 1423 -11531702  
7000693937 ytzd hypothetical protein ytzd (db:pir2.dat) F70004 F70004 Bacillus subtilis 1423 -11531702 6000691340 ytzd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:215497) (re:215733) (di:complement) BSUB0015 Z99118 g2635408 Bacillus subtilis 1423 -11531702 7500964735 ytzd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:12857) (re:13093) (di:complement) BSUB0016 Z99119 g2635427 Bacillus subtilis 1423 -11531702

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808870	5657	27813	426	141

Description

6500727845 ythi:ytzk hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytxK ytxK Bacillus subtilis 1423 -11531703 7502851733 ytxk (de:hypothetical 37.4 kd protein in acka-sspa intergenic region) (db:swissprot) YTXK\_BACSU P37876 BACILLUS SUBTILIS 1423 -11531703 7000693933 ytxk hypothetical protein ytxk:hypothetical protein acka 5 region (db:pir2.dat) G70003 G70003 Bacillus subtilis 1423 -11531703 4000714231 ytxk ytxk (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to modification metilase acci) (le:161490) (re:162479) (di:direct) AF008220 AF008220 g2293239 Bacillus subtilis 1423 -11531703 7500964731 ytxk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: ythi) (le:17948) (re:18937) (di:complement) BSUB0016 Z99119 g2635432 Bacillus subtilis 1423 -11531703

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808881	5658	27814	585	195

Description

6500727846 hypothetical protein:similar to thiol peroxidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytgI ytgI Bacillus subtilis 1423 -11531704 7000694676 ytgI thiol peroxidase homolog ytgi (cl:thiol peroxidase) (db:pir2.dat) F69992 F69992 Bacillus subtilis 1423 -11531704 4000714230 ytgi ytgi (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to tagd protein from v.cholerae) (le:160926) (re:161429) (di:direct) AF008220 AF008220 g2293238 Bacillus subtilis 1423 -11531704 7500965261 ytgi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to thiol peroxidase) (le:18998) (re:19501) (di:complement) BSUB0016 Z99119 g2635433 Bacillus subtilis 1423 -11531704



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808889	5659	27815	930	309

Description

6500727847 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytfJ ytfJ Bacillus subtilis 1423 -11531705  
7000693903 ytfj hypothetical protein ytfj (db:pir2.dat) H69991 H69991 Bacillus subtilis 1423 -11531705 4000714229 ytfj ytfj (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:160361) (re:160816) (di:direct) AF008220 AF008220 g2293237 Bacillus subtilis 1423 -11531705  
7500964701 ytfj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:19611) (re:20066) (di:complement) BSUB0016 Z99119 g2635434 Bacillus subtilis 1423 -11531705

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808892	5660	27816	348	115

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808897	5661	27817	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808905	5662	27818	279	92

Description

6500727848 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytfI ytfI Bacillus subtilis 1423 -11531706  
7000693902 ytfi hypothetical protein ytfi (db:pir2.dat) G69991 G69991 Bacillus subtilis 1423 -11531706 4000714228 ytfi ytfi (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:159667) (re:160347) (di:direct) AF008220 AF008220 g2293236 Bacillus subtilis 1423 -11531706  
7500964700 ytfi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:20080) (re:20760) (di:complement) BSUB0016 Z99119 g2635435 Bacillus subtilis 1423 -11531706

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808909	5663	27819	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808911	5664	27820	1176	391

Description

6500727849 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yteJ yteJ Bacillus subtilis 1423 -11531707  
7000693899 ytej hypothetical protein ytej (db:pir2.dat) F69990 F69990  
Bacillus subtilis 1423 -11531707 4000714227 ytej ytej (db:genpept-bct1)  
(de:bacillus subtilis rrnb-dnab genomic region.) (le:159098) (re:159592)  
(di:direct) AF008220 AF008220 g2293235 Bacillus subtilis 1423 -11531707  
7500964697 ytej (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis  
complete genome (section 16 of 21): from 2997771to 3213410.) (le:20835)  
(re:21329) (di:complement) BSUB0016 Z99119 g2635436 Bacillus subtilis 1423  
-11531707

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808923	5665	27821	306	102

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808936	5666	27822	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808943	5667	27823	942	314

Description

GTC ORF with score 138 to: (sr:thale cress strain=columbia)  
(db:genpept-pln1) (de:arabidopsis thaliana chromosome i cosmid g8261 dna  
(cytosine-5-)methyltransferase, zinc finger protein 1, nucleoporin 98, poly  
a+rna export protein, plasma membrane ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808944	5668	27824	675	224

Description

6500727850 hypothetical protein:similar to protease iv (gtcfc:10.11)  
(ec:3.4.-.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yteI  
yteI Bacillus subtilis 1423 -11531708 7000694463 ytei proteinase iv homolog  
ytei (db:pir2.dat) E69990 E69990 Bacillus subtilis 1423 -11531708  
4000714226 ytei putative protease (db:genpept-bct1) (de:bacillus subtilis  
rrnb-dnab genomic region.) (le:158078) (re:159085) (di:direct) AF008220  
AF008220 g2293234 Bacillus subtilis 1423 -11531708 7500965113 ytei  
(fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome  
(section 16 of 21): from 2997771to 3213410.) (nt:similar to protease iv)  
(le:21342) (re:22349) (di:complement) BSUB0016 Z99119 g2635437 Bacillus  
subtilis 1423 -11531708

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808962	5669	27825	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808968	5670	27826	330	109

Description

6500727851 hypothetical protein:similar to hypothetical proteins  
(gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytdI  
ytdI Bacillus subtilis 1423 -11531709 7000692745 ytdi conserved  
hypothetical protein ytdi (cl:conserved hypothetical protein hi0072)  
(db:pir2.dat) B69990 B69990 Bacillus subtilis 1423 -11531709 4000714225  
ytdi ytdi (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.)  
(nt:similarity to pos5 protein from s.cerevisiae) (le:157089) (re:157892)  
(di:complement) AF008220 AF008220 g2293323 Bacillus subtilis 1423 -11531709  
7500963820 ytdi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis  
complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to  
hypothetical proteins) (le:22535) (re:23338) (di:direct) BSUB0016 Z99119  
g2635438 Bacillus subtilis 1423 -11531709

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808984	5671	27827	417	139

Description

6500727852 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytcJ ytcJ Bacillus subtilis 1423 -11531710 7000692744 ytcj conserved hypothetical protein ytcj (db:pir2.dat) F69989 F69989 Bacillus subtilis 1423 -11531710 4000714224 ytcj ytcj (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:155468) (re:157057) (di:direct) AF008220 AF008220 g2293233 Bacillus subtilis 1423 -11531710 7500963819 ytcj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:23370) (re:24959) (di:complement) BSUB0016 Z99119 g2635439 Bacillus subtilis 1423 -11531710

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808988	5672	27828	189	62

Description

6500727853 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytbJ ytbJ Bacillus subtilis 1423 -11531711 7502851734 thii (de:probable thiamin biosynthesis protein thii) (db:swissprot) THII\_BACSU O34595 BACILLUS SUBTILIS 1423 -11531711 7000692743 ytbj conserved hypothetical protein ytbj (cl:mycoplasma genitalium hypothetical protein mg372) (db:pir2.dat) E69988 E69988 Bacillus subtilis 1423 -11531711 4000714222 ytbj ytbj (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to hypothetical protein mg372 from m.) (le:152168) (re:153244) (di:direct) AF008220 AF008220 g2293230 Bacillus subtilis 1423 -11531711 7500963818 ytbj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:27183) (re:28259) (di:complement) BSUB0016 Z99119 g2635442 Bacillus subtilis 1423 -11531711

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501808989	5673	27829	183	60

Description

GTC ORF with score 92 to: (fn:transfer of acetyl group to coa; binds) (db:genpept-bct2) (ec:2.3.1.12) (de:pseudomonas aeruginosa pyruvate dehydrogenase (acea) anddihydrolipoamide acetyltransferase (aceb) genes, complete cds.) (le:2983) (re:4623) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808992	5674	27830	399	132

Description

6500727854 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytwP ytwP Bacillus subtilis 1423 -11531712  
 7000693932 ytwP hypothetical protein ytwP (db:pir2.dat) G70002 G70002 Bacillus subtilis 1423 -11531712 4000714219 ytwP ytwP (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to fcra protein precursor from) (le:147704) (re:149392) (di:direct) AF008220 AF008220 g2293228 Bacillus subtilis 1423 -11531712 7500964730 ytwP (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:31035) (re:32723) (di:complement) BSUB0016 Z99119 g2635445 Bacillus subtilis 1423 -11531712

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501808995	5675	27831	363	120

Description

6500727855 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytvP ytvP Bacillus subtilis 1423 -11531713 7000692764 ytvP conserved hypothetical protein ytvP (db:pir2.dat) D70002 D70002 Bacillus subtilis 1423 -11531713 4000714218 ytvP ytvP (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to orf13 in the 3' region of hisie from) (le:146701) (re:147507) (di:complement) AF008220 AF008220 g2293321 Bacillus subtilis 1423 -11531713 7500963838 ytvP (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:32920) (re:33726) (di:direct) BSUB0016 Z99119 g2635446 Bacillus subtilis 1423 -11531713

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809005	5676	27832	1161	387

Description

GTC ORF with score 449 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana dna chromosome 4, bac clone f4d11 (essaiiproject).) (nt:similarity to mrna for kiaa0079 gene, homo sapiens;) (le:66563:67101:67394) (re:66743:67189:67573) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809007	5677	27833	348	115

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809014	5678	27834	396	131

Description

6500727856 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yttP yttP Bacillus subtilis 1423 -11531714  
7000693930 yttP hypothetical protein yttP (db:pir2.dat) H70001 H70001 Bacillus subtilis 1423 -11531714 4000714217 yttP putative transcription regulator (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:146081) (re:146704) (di:direct) AF008220 AF008220 g2293227 Bacillus subtilis 1423 -11531714 7500964728 yttP (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:33723) (re:34346) (di:complement) BSUB0016 Z99119 g2635447 Bacillus subtilis 1423 -11531714

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809018	5679	27835	519	173

Description

GTC ORF with score 175 to: (fn:conversion of oxaloacetate to citrate in the) (sr:cucurbita sp. (strain:kurokawa amakuri nankin) cotyledonary stag) (db:genpept-pln1) (ec:4.1.3.7) (de:pumpkin mrna for glyoxysomal citrate synthase, complete cds.) (le:133)...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809023	5680	27836	576	191

Description

6500727857 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytsP ytsP Bacillus subtilis 1423 -11531715 7502851735 ytsP (de:hypothetical 8.7 kd protein in brab-rpsd intergenic region) (db:swissprot) YTSP\_BACSU O34553 BACILLUS SUBTILIS 1423 -11531715 7000692762 ytsP conserved hypothetical protein ytsP (db:pir2.dat) D70001 D70001 Bacillus subtilis 1423 -11531715 4000714216 ytsP ytsP (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to hypothetical protein ykl069w from) (le:145464) (re:145700) (di:complement) AF008220 AF008220 g2293320 Bacillus subtilis 1423 -11531715 7500963836 ytsP (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:34727) (re:34963) (di:direct) BSUB0016 Z99119 g2635448 Bacillus subtilis 1423 -11531715

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809028	5681	27837	1023	341

Description

6500727858 hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytrP ytrP Bacillus subtilis 1423 -11531716 7000694862 ytrp two-component sensor histidine kinase homolog ytrp (db:pir2.dat) F70000 F70000 Bacillus subtilis 1423 -11531716 4000714215 ytrp ytrp (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to hypothetical protein 183 from) (le:143687) (re:145426) (di:direct) AF008220 AF008220 g2293226 Bacillus subtilis 1423 -11531716 7500965416 ytrp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to two-component sensor histidine kinase) (le:35001) (re:36740) (di:complement) BSUB0016 Z99119 g2635449 Bacillus subtilis 1423 -11531716

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809037	5682	27838	567	188

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809054	5683	27839	1002	333

Description

GTC ORF with score 282 to: (fn:helicase, helicase-primase complex) (db:genpept-vr1) (de:human herpesvirus 6 serotype b putative major immediate-earlygenes.) (nt:similar to hhv6a u86, region ie-b) (le:16386) (re:19235) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809058	5684	27840	825	274

Description

5000689697 hypothetical protein:hypothetical 27.6 kd protein in acuc 5region:orfb (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytxE ytxE Bacillus subtilis 1423 -11531717 116458 ytxe (de:hypothetical 27.6 kd protein in acuc 5'region (orfb)) (db:swissprot) YTXE\_BACSU P39064 BACILLUS SUBTILIS 1423 -11531717 7000688618 ytxe motility protein homolog ytxe (db:pir2.dat) S39642 S39642 Bacillus subtilis 1423 -11531717 7500952782 ytxe ytxe (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to b. subtilis motility protein b) (le:135828) (re:136556) (di:direct) AF008220 AF008220 g2293223 Bacillus subtilis 1423 -11531717 215121 (fn:unknown; similar to motb product) (sr:bacillus subtilis (strain wl68) dna) (db:genpept-bct1) (de:bacillus subtilis homologues of mota and motb genes acetoinutilization operon genes acua, acub and acuc, and acetyl-coasynthase (acsa) genes, complete ... BACACUCBA L17309 g348049 Bacillus subtilis 1423 -11531717 4000707473 ytxe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to motility protein) (le:43871) (re:44599) (di:complement) BSUB0016 Z99119 g2635456 Bacillus subtilis 1423 -11531717 170234 ytxe motility protein homolog ytxe (db:pir) S39642 S39642 Bacillus subtilis 1423 -11531717 6500727859 hypothetical protein:hypothetical 27.6 kd protein in acuc 5region:orfb (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytxE ytxE Bacillus subtilis 1423 -11531717



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809060	5685	27841	207	68

Description

5000689696 hypothetical protein:hypothetical 30.1 kd protein in acuc 5region:orfa (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytxD ytxD Bacillus subtilis 1423 -11531718 116456 ytxd (de:hypothetical 30.1 kd protein in acuc 5'region (orfa)) (db:swissprot) YTXD\_BACSU P39063 BACILLUS SUBTILIS 1423 -11531718 7000688617 ytxd flagellar motor apparatus homolog ytxd (cl:flagellar motor rotation protein) (db:pir2.dat) S39641 S39641 Bacillus subtilis 1423 -11531718 7500952781 ytxd ytxd (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to b. subtilis motility protein a) (le:135020) (re:135838) (di:direct) AF008220 AF008220 g2293222 Bacillus subtilis 1423 -11531718 215120 (fn:unknown; similar to mota product) (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis homologues of mota and motb genes acetoinutilization operon genes acua, acub and acuc, and acetyl-coasynthase (acsa) genes, complete ... BACACUCBA L17309 g348048 Bacillus subtilis 1423 -11531718 4000707472 ytxd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to flagellar motor apparatus) (le:44589) (re:45407) (di:complement) BSUB0016 Z99119 g2635457 Bacillus subtilis 1423 -11531718 170231 ytxd flagellar motor apparatus homolog ytxd (db:pir) S39641 S39641 Bacillus subtilis 1423 -11531718 6500727860 hypothetical protein:hypothetical 30.1 kd protein in acuc 5region:orfa (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytxD ytxD Bacillus subtilis 1423 -11531718

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809062	5686	27842	1755	585

Description

6500727861 csb40:ytxj hypothetical protein:hypothetical 12.4 kd protein in murc-aroa intergenic region:orf2:orf3 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytxJ ytxJ Bacillus subtilis 1423 -11531719 219011 ytxj (de:(orf3)) (db:swissprot) YTXJ\_BACSU P39914 BACILLUS SUBTILIS 1423 -11531719 7000688621 ytxj general stress protein homolog ytxj (db:pir2.dat) S21420 S21420 Bacillus subtilis 1423 -11531719 7500952785 ytxj ytxj (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:132039) (re:132365) (di:direct) AF008220 AF008220 g2293219 Bacillus subtilis 1423 -11531719 5000689700 orf::2 (db:genpept-bct1) (de:b.subtilis aroa-arog gene.) (le:105) (re:431) (di:direct) BSAROAG X65945 g39815 Bacillus subtilis 1423 -11531719 4000707475 ytxj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: csb40; similar to general) (le:48061) (re:48387) (di:complement) BSUB0016 Z99119 g2635460 Bacillus subtilis 1423 -11531719 116461 ytxj (de:(orf3)) (db:swissprot) YTXJ\_BACSU P39914 BACILLUS SUBTILIS 1423 -11531719 170198 ytxj general stress protein homolog ytxj (db:pir) S21420 S21420 Bacillus subtilis 1423 -11531719

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809063	5687	27843	996	331

Description

6500727862 csb40:ytXH hypothetical protein:hypothetical 16.7 kd protein in murc-aroa intergenic region:orf2 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytxH ytxH Bacillus subtilis 1423 -11531720 116460 ytxh (de:hypothetical 16.7 kd protein in murc-aroa intergenic region (orf2)) (db:swissprot) YTXH\_BACSU P40780 BACILLUS SUBTILIS 1423 -11531720 7000688620 ytxh general stress protein homolog ytxh (db:pir2.dat) E70003 E70003 Bacillus subtilis 1423 -11531720 217012 (db:genpept-bct1) (de:bacillus subtilis udp-n-acetylmuramate-alanine ligase gene, partialcds, and 3 orf's.) (nt:similar to plant water stress proteins; orf2) (le:1670) (re:2128) (di:direct) BACUNAM L31845 g556016 Bacillus subtilis 1423 -11531720 7500952784 ytxh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: csb40; similar to general) (le:48411) (re:48869) (di:complement) BSUB0016 Z99119 g2635461 Bacillus subtilis 1423 -11531720 5000689699 (de:(ytXH) (pn:hypothetical 16) (gtcfc:13.07) (ec:)) (ytXH\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) ytxH ytxH Bacillus subtilis 1423 10058185

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809079	5688	27844	786	261

Description

6500727863 csb40:ytgx hypothetical protein:hypothetical 15.7 kd protein in murc-aroa intergenic region:orf1 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytxG ytxG Bacillus subtilis 1423 -11531721  
 116459 ytxg (de:hypothetical 15.7 kd protein in murc-aroa intergenic region (orf1)) (db:swissprot) YTXG\_BACSU P40779 BACILLUS SUBTILIS 1423 -11531721  
 7000688619 ytxg general stress protein homolog ytxg (db:pir2.dat) D70003 D70003 Bacillus subtilis 1423 -11531721 217011 ytxg ytxg (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:131098) (re:131529) (di:direct) AF008220 AF008220 g2293217 Bacillus subtilis 1423 -11531721 4000707474 (db:genpept-bct1) (de:bacillus subtilis udp-n-acetylmuramate-alanine ligase gene, partialcds, and 3 orf's.) (nt:orf1) (le:1211) (re:1642) (di:direct) BACUNAM L31845 g556015 Bacillus subtilis 1423 -11531721 7500952783 ytxg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: csb40; similar to general) (le:48897) (re:49328) (di:complement) BSUB0016 Z99119 g2635462 Bacillus subtilis 1423 -11531721 5000689698 (de:(ytgx) (pn:hypothetical 15) (gtcfc:13.07) (ec:) (ytgx\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) ytxG ytxG Bacillus subtilis 1423 10058184

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809083	5689	27845	444	147

Description

GTC ORF with score 263 to: (sr:escherichia coli (strain c600) dna) (db:genpept-bct1) (de:e.coli dmsa, dmsb and dmsh genes encoding anaerobic dimethylsulfoxide reductase, complete cds.) (nt:orf z; putative) (le:4760) (re:5386) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809084	5690	27846	231	76

Description

GTC ORF with score 100 to: (sr:escherichia coli (strain c600) dna) (db:genpept-bct1) (de:e.coli dmsa, dmsb and dmsh genes encoding anaerobic dimethylsulfoxide reductase, complete cds.) (nt:orf z; putative) (le:4760) (re:5386) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809089	5691	27847	189	62

Description

6500727864 hypothetical protein:similar to dna translocase stage iii sporulation protein:spoiie (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytpT ytpT Bacillus subtilis 1423 -11531722 7000692947 ytpT dna translocase stage iii sporulation prot homolog ytpT (db:pir2.dat) C69999 C69999 Bacillus subtilis 1423 -11531722 4000714212 ytpT ytpT (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:strong similarity to ftsk of e. coli and spoiie of) (le:127280) (re:129388) (di:direct) AF008220 AF008220 g2293215 Bacillus subtilis 1423 -11531722 7500963958 ytpT (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to dna translocase stage iii sporulation) (le:51038) (re:53146) (di:complement) BSUB0016 Z99119 g2635464 Bacillus subtilis 1423 -11531722

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809096	5692	27848	441	147

Description

GTC ORF with score 94 to: (or:Caenorhabditis elegans) (db:genpept-inv) (de:caenorhabditis elegans cosmid f25h8, complete sequence.) (nt:cdna est embl:d66541 comes from this gene; cdna est) (le:16095:16195:16361) (re:16141:16314:16447) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809099	5693	27849	636	211

Description

6500727865 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytpS ytpS Bacillus subtilis 1423 -11531723 7000693926 ytpS hypothetical protein ytpS (db:pir2.dat) B69999 B69999 Bacillus subtilis 1423 -11531723 4000714211 ytpS ytpS (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:126531) (re:127325) (di:direct) AF008220 AF008220 g2293214 Bacillus subtilis 1423 -11531723 7500964724 ytpS (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:53101) (re:53895) (di:complement) BSUB0016 Z99119 g2635465 Bacillus subtilis 1423 -11531723

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809100	5694	27850	315	104

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809101	5695	27851	447	148

Description

6500727866 hypothetical protein:similar to phenylalanyl-trna synthetase:beta subunit (gtcfc:10.6) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytpR ytpR Bacillus subtilis 1423 -11531724 7000694391 ytpR phenylalanyl-trna synthetase beta subunit homolog ytpR (db:pir2.dat) A69999 A69999 Bacillus subtilis 1423 -11531724 4000714210 ytpR ytpR (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to phenylalanine trna ligase of e. coli) (le:125766) (re:126371) (di:direct) AF008220 AF008220 g2293213 Bacillus subtilis 1423 -11531724 7500965060 ytpR (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to phenylalanyl-trna synthetase (beta) (le:54055) (re:54660) (di:complement) BSUB0016 Z99119 g2635466 Bacillus subtilis 1423 -11531724

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809108	5696	27852	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809113	5697	27853	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809121	5698	27854	513	170

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809134	5699	27855	270	89

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809156	5700	27856	684	227

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809157	5701	27857	435	144

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809158	5702	27858	279	92

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809172	5703	27859	402	133

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809175	5704	27860	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809176	5705	27861	1008	335

Description

6500727867 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) ytpQ ytpQ Bacillus subtilis 1423 -11531725  
7000693925 ytpq hypothetical protein ytpq (db:pir2.dat) H69998 H69998  
Bacillus subtilis 1423 -11531725 4000714209 ytpq ytpq (db:genpept-bct1)  
(de:bacillus subtilis rrnb-dnab genomic region.) (le:124941) (re:125750)  
(di:direct) AF008220 AF008220 g2293212 Bacillus subtilis 1423 -11531725  
7500964723 ytpq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis  
complete genome (section 16 of 21): from 2997771to 3213410.) (le:54676)  
(re:55485) (di:complement) BSUB0016 Z99119 g2635467 Bacillus subtilis 1423  
-11531725

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809182	5706	27862	1095	365

Description

6500727868 hypothetical protein:similar to thioredoxin h1 (gtcfc:9.13) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytpP ytpP Bacillus subtilis 1423 -11531726 7000694679 ytpP thioredoxin h1 homolog ytpP (cl:thioredoxin:thioredoxin homology) (db:pir2.dat) G69998 G69998 Bacillus subtilis 1423 -11531726 4000714208 ytpP putative thioredoxin (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:124603) (re:124926) (di:direct) AF008220 AF008220 g2293211 Bacillus subtilis 1423 -11531726 7500965264 ytpP (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to thioredoxin h1) (le:55500) (re:55823) (di:complement) BSUB0016 Z99119 g2635468 Bacillus subtilis 1423 -11531726

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809203	5707	27863	807	268

Description

6500727869 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytoQ ytoQ Bacillus subtilis 1423 -11531727 7000693922 ytoQ hypothetical protein ytoQ (db:pir2.dat) C69998 C69998 Bacillus subtilis 1423 -11531727 4000714207 ytoQ ytoQ (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:123922) (re:124368) (di:complement) AF008220 AF008220 g2293315 Bacillus subtilis 1423 -11531727 7500964720 ytoQ (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:56058) (re:56504) (di:direct) BSUB0016 Z99119 g2635469 Bacillus subtilis 1423 -11531727

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809207	5708	27864	672	223

Description

6500727870 hypothetical protein:similar to endo-1:4-beta-glucanase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytoP ytoP Bacillus subtilis 1423 -11531728 7000692960 ytoP endo-1:4-beta-glucanase homolog ytoP (cl:thermophilic aminopeptidase i alpha chain) (db:pir2.dat) B69998 B69998 Bacillus subtilis 1423 -11531728 4000714206 ytoP ytoP (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to hypothetical protein f356 from e. coli) (le:122794) (re:123867) (di:direct) AF008220 AF008220 g2293210 Bacillus subtilis 1423 -11531728 7500963966 ytoP (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to endo-1,4-beta-glucanase) (le:56559) (re:57632) (di:complement) BSUB0016 Z99119 g2635470 Bacillus subtilis 1423 -11531728

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809215	5709	27865	1260	420

Description

6500727871 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytzB ytzB Bacillus subtilis 1423 -11531729  
7000693935 ytzB hypothetical protein ytzB (db:pir2.dat) D70004 D70004 Bacillus subtilis 1423 -11531729 7500964733 ytzB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:57791) (re:58108) (di:direct) BSUB0016 Z99119 g2635471 Bacillus subtilis 1423 -11531729

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809232	5710	27866	1650	550

Description

6500727872 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytnP ytnP Bacillus subtilis 1423 -11531730  
7000693920 ytnP hypothetical protein ytnP (db:pir2.dat) G69997 G69997 Bacillus subtilis 1423 -11531730 4000714204 ytnP ytnP (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:119713) (re:120483) (di:direct) AF008220 AF008220 g2293208 Bacillus subtilis 1423 -11531730 7500964718 ytnP (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:59943) (re:60713) (di:complement) BSUB0016 Z99119 g2635473 Bacillus subtilis 1423 -11531730

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809241	5711	27867	408	135

Description

6500727873 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytmQ ytmQ Bacillus subtilis 1423 -11531731 7000692757 ytmQ conserved hypothetical protein ytmQ (cl:hypothetical protein hi0340) (db:pir2.dat) B69997 B69997 Bacillus subtilis 1423 -11531731 4000714203 ytmQ ytmQ (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to hypothetical protein hi0340 from h.) (le:118926) (re:119567) (di:direct) AF008220 AF008220 g2293207 Bacillus subtilis 1423 -11531731 7500955847 ytmQ (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:60859) (re:61500) (di:complement) BSUB0016 Z99119 g2635474 Bacillus subtilis 1423 -11531731



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809247	5712	27868	276	91

Description

6500727874 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytzH ytzH Bacillus subtilis 1423 -11531732  
7000693938 ytzH hypothetical protein ytzH (db:pir2.dat) B70005 B70005 Bacillus subtilis 1423 -11531732 7500964736 ytzH (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:61707) (re:61985) (di:direct) BSUB0016 Z99119 g2635475 Bacillus subtilis 1423 -11531732

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809248	5713	27869	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809254	5714	27870	270	89

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809274	5715	27871	1677	558

Description

6500727875 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytmP ytmP Bacillus subtilis 1423 -11531733  
7000693917 ytmP hypothetical protein ytmP (db:pir2.dat) A69997 A69997 Bacillus subtilis 1423 -11531733 4000714202 ytmP ytmP (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:117631) (re:118440) (di:direct) AF008220 AF008220 g2293206 Bacillus subtilis 1423 -11531733 7500964715 ytmP (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:61986) (re:62795) (di:complement) BSUB0016 Z99119 g2635476 Bacillus subtilis 1423 -11531733

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809295	5716	27872	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809310	5717	27873	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809314	5718	27874	492	163

Description

6500727876 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytlR ytlR Bacillus subtilis 1423 -11531734  
7000693914 ytlr hypothetical protein ytlr (db:pir2.dat) H69995 H69995 Bacillus subtilis 1423 -11531734 4000714200 ytlr ytlr (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to bmr protein from b. subtilis) (le:114352) (re:115281) (di:direct) AF008220 AF008220 g2293204 Bacillus subtilis 1423 -11531734 7500964712 ytlr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:65145) (re:66074) (di:complement) BSUB0016 Z99119 g2635478 Bacillus subtilis 1423 -11531734

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809334	5719	27875	276	91

Description

6500727877 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytlQ ytlQ Bacillus subtilis 1423 -11531735  
7000693913 ytlq hypothetical protein ytlq (db:pir2.dat) G69995 G69995 Bacillus subtilis 1423 -11531735 4000714199 ytlq ytlq (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to hypothetical protein 3 from) (le:113389) (re:114303) (di:direct) AF008220 AF008220 g2293203 Bacillus subtilis 1423 -11531735 7500964711 ytlq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:66123) (re:67037) (di:complement) BSUB0016 Z99119 g2635479 Bacillus subtilis 1423 -11531735

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809346	5720	27876	264	87

Description

6500727878 hypothetical protein:similar to abc transporter:permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytlP ytlP Bacillus subtilis 1423 -11531736 7000692121 ytlp abc transporter permease homolog ytlp (db:pir2.dat) F69995 F69995 Bacillus subtilis 1423 -11531736 4000714198 ytlp ytlp (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to hypothetical protein 3 from) (le:112812) (re:113363) (di:direct) AF008220 AF008220 g2293202 Bacillus subtilis 1423 -11531736 7500963360 ytlp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to abc transporter (permease)) (le:67063) (re:67614) (di:complement) BSUB0016 Z99119 g2635480 Bacillus subtilis 1423 -11531736

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809347	5721	27877	318	105

Description

6500727879 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytip ytip Bacillus subtilis 1423 -11531737 7000692753 ytip conserved hypothetical protein ytip (cl:conserved hypothetical protein hi0125) (db:pir2.dat) G69993 G69993 Bacillus subtilis 1423 -11531737 4000714195 ytip ytip (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to hypothetical protein hi0125 from h.) (le:108908) (re:110206) (di:complement) AF008220 AF008220 g2293313 Bacillus subtilis 1423 -11531737 7500963828 ytip (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:70220) (re:71518) (di:direct) BSUB0016 Z99119 g2635483 Bacillus subtilis 1423 -11531737

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809357	5722	27878	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809360	5723	27879	573	190

Description

6500727880 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ythQ ythQ Bacillus subtilis 1423 -11531738  
 7000693906 ythq hypothetical protein ythq (db:pir2.dat) D69993 D69993 Bacillus subtilis 1423 -11531738 4000714194 ythq ythq (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to hypothetical protein o716 from e.) (le:107712) (re:108869) (di:direct) AF008220 AF008220 g2293200 Bacillus subtilis 1423 -11531738 7500964704 ythq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:71557) (re:72714) (di:complement) BSUB0016 Z99119 g2635484 Bacillus subtilis 1423 -11531738

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809386	5724	27880	537	178

Description

GTC ORF with score 168 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone\_lib:mizukam) (db:genpept-pln1) (de:schizosaccharomyces pombe 37 kb genomic dna, clone c213.) (nt:similar to s.cerevisiae methionyl-trna synthetase:) (le:14661) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809391	5725	27881	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809392	5726	27882	402	134

Description

6500727881 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ythP ythP Bacillus subtilis 1423 -11531739 7000692097 ythp abc transporter atp-binding protein homolog ythp (cl:atp-binding cassette homology) (db:pir2.dat) C69993 C69993 Bacillus subtilis 1423 -11531739 4000714193 ythp transporter (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:107005) (re:107715) (di:direct) AF008220 AF008220 g2293199 Bacillus subtilis 1423 -11531739 7500963338 ythp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to abc transporter (atp-binding protein)) (le:72711) (re:73421) (di:complement) BSUB0016 Z99119 g2635485 Bacillus subtilis 1423 -11531739

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809395	5727	27883	309	103

Description

6500727882 hypothetical protein:similar to transcriptional regulator:deor family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytzE ytzE Bacillus subtilis 1423 -11531740 7000694726 ytze transcription regulator deor family homolog ytze (db:pir2.dat) G70004 G70004 Bacillus subtilis 1423 -11531740 7500965301 ytze (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to transcriptional regulator (deor family)) (le:73712) (re:73933) (di:direct) BSUB0016 Z99119 g2635486 Bacillus subtilis 1423 -11531740

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809413	5728	27884	1494	497

Description

GTC ORF with score 259 to: (sr:drosophila melanogaster (clone library: brown and kafatos 1988) (db:genpept-inv) (de:drosophila melanogaster chromodomain-helicase-dna-binding (chd-1)mRNA, complete cds.) (le:110) (re:5761) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809420	5729	27885	210	69

Description

6500727883 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytzF ytzF Bacillus subtilis 1423 -11531741 7502851736 ytzf (de:hypothetical 17.7 kd protein in amyX-opuD intergenic region) (db:swissprot) YTZF\_BACSU 032068 BACILLUS SUBTILIS 1423 -11531741 7000692768 ytzf conserved hypothetical protein ytzf (db:pir2.dat) H70004 H70004 Bacillus subtilis 1423 -11531741 7500963841 ytzf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:74054) (re:74527) (di:complement) BSUB0016 Z99119 g2635487 Bacillus subtilis 1423 -11531741

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809468	5730	27886	600	199

Description

6500727884 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytzG ytzG Bacillus subtilis 1423 -11531742 7000692769 ytzg conserved hypothetical protein ytzg (db:pir2.dat) A70005 A70005 Bacillus subtilis 1423 -11531742 7500963842 ytzg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:74512) (re:74772) (di:complement) BSUB0016 Z99119 g2635488 Bacillus subtilis 1423 -11531742

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809474	5731	27887	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809475	5732	27888	804	267

Description

GTC ORF with score 147 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completedcds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809476	5733	27889	231	76

Description

6500727885 hypothetical protein:similar to spore cortex protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytgP ytgP Bacillus subtilis 1423 -11531743 7000694621 ytgP spore cortex protein homolog ytgP (db:pir2.dat) G69992 G69992 Bacillus subtilis 1423 -11531743 4000714192 ytgP ytgP (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to spovb protein from b. subtilis) (le:103951) (re:105585) (di:direct) AF008220 AF008220 g2293198 Bacillus subtilis 1423 -11531743 7500965216 ytgP (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to spore cortex protein) (le:74841) (re:76475) (di:complement) BSUB0016 Z99119 g2635489 Bacillus subtilis 1423 -11531743

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809523	5734	27890	183	60

Description

6500727886 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytfp ytfp Bacillus subtilis 1423 -11531744 7000692750 ytfp conserved hypothetical protein ytfp (db:pir2.dat) A69992 A69992 Bacillus subtilis 1423 -11531744 7500963825 ytfp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:76983) (re:77939) (di:direct) BSUB0016 Z99119 g2635490 Bacillus subtilis 1423 -11531744

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809524	5735	27891	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809530	5736	27892	639	212

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809543	5737	27893	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809558	5738	27894	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809575	5739	27895	1122	373

Description

6500727887 cse60:yteV hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yteV yteV Bacillus subtilis 1423 -11531745 7000693901 yteV hypothetical protein yteV (db:pir2.dat) E69991 E69991 Bacillus subtilis 1423 -11531745 220188 cse60 cse60 (db:genpept-bct1) (de:bacillus subtilis cse60 (cse60) gene, complete cds.) (le:672) (re:854) (di:direct) BSU70041 U70041 g1710300 Bacillus subtilis 1423 -11531745 7500964699 yteV (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: cse60) (le:79703) (re:79885) (di:complement) BSUB0016 Z99119 g2635492 Bacillus subtilis 1423 -11531745

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809576	5740	27896	549	182

Description

6500727888 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yteT yteT Bacillus subtilis 1423 -11531746 7000692748 yteT conserved hypothetical protein yteT (db:pir2.dat) C69991 C69991 Bacillus subtilis 1423 -11531746 4000714189 yteT yteT (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:98497) (re:99783) (di:direct) AF008220 AF008220 g2293196 Bacillus subtilis 1423 -11531746 7500963823 yteT (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:80643) (re:81929) (di:complement) BSUB0016 Z99119 g2635494 Bacillus subtilis 1423 -11531746

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809580	5741	27897	1032	344

Description

6500727889 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yteS yteS Bacillus subtilis 1423 -11531747 7000693900 yteS hypothetical protein yteS (db:pir2.dat) B69991 B69991 Bacillus subtilis 1423 -11531747 4000714188 yteS yteS (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:98006) (re:98485) (di:direct) AF008220 AF008220 g2293195 Bacillus subtilis 1423 -11531747 7500964698 yteS (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:81941) (re:82420) (di:complement) BSUB0016 Z99119 g2635495 Bacillus subtilis 1423 -11531747



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809587	5742	27898	513	170

Description

6500727890 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yter yter Bacillus subtilis 1423 -11531748 7000692747 yter conserved hypothetical protein yter (db:pir2.dat) A69991 A69991 Bacillus subtilis 1423 -11531748 4000714187 yter yter (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to hypothetical protein 1 (pica 5') (le:96864) (re:97985) (di:direct) AF008220 AF008220 g2293194 Bacillus subtilis 1423 -11531748 7500963822 yter (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:82441) (re:83562) (di:complement) BSUB0016 Z99119 g2635496 Bacillus subtilis 1423 -11531748

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809603	5743	27899	573	191

Description

GTC ORF with score 933 to: (fn:required for conidial pigmentation) (db:genpept-pln2) (de:aspergillus fumigatus polyketide synthase (alb1) gene, completedcds.) (nt:alb1) (le:598:932:1268:4755:5584) (re:884:1220:4699:5510:7260) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809604	5744	27900	765	254

Description

GTC ORF with score 1287 to: (fn:required for conidial pigmentation) (db:genpept-pln2) (de:aspergillus fumigatus polyketide synthase (alb1) gene, completedcds.) (nt:alb1) (le:598:932:1268:4755:5584) (re:884:1220:4699:5510:7260) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809623	5745	27901	687	228

Description

GTC ORF with score 150 to: (sr:d.melanogaster dna, clone p4.1) (db:genpept-inv) (de:d.melanogaster rna polymerase ii largest subunit gene, last 2exons.) (nt:rna polymerase ii largest subunit (, ec 2.7.7.6)) (le:<1:379) (re:133:1472) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809641	5746	27902	1830	609

Description

6500727891 hypothetical protein:similar to sugar transport protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yteQ yteQ Bacillus subtilis 1423 -11531749 7000694649 yteq sugar transport protein homolog yteq (db:pir2.dat) H69990 H69990 Bacillus subtilis 1423 -11531749 7500965233 yteq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to sugar transport protein) (le:83570) (re:84061) (di:complement) BSUB0016 Z99119 g2635497 Bacillus subtilis 1423 -11531749

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809643	5747	27903	576	191

Description

6500727892 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yteP yteP Bacillus subtilis 1423 -11531750 7000692746 ytep conserved hypothetical protein ytep (db:pir2.dat) G69990 G69990 Bacillus subtilis 1423 -11531750 4000714185 ytep ytep (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:95890) (re:96270) (di:direct) AF008220 AF008220 g2293192 Bacillus subtilis 1423 -11531750 7500963821 ytep (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins from b. subtilis) (le:84156) (re:84536) (di:complement) BSUB0016 Z99119 g2635498 Bacillus subtilis 1423 -11531750

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809648	5748	27904	507	168

Description

6500727893 hypothetical protein:similar to transcriptional regulator:arac/xyls family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytdP ytdP Bacillus subtilis 1423 -11531751 7000694719 ytdp transcription regulator arac/xyls family homolog ytdp (db:pir2.dat) C69990 C69990 Bacillus subtilis 1423 -11531751 7500965294 ytdp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to transcriptional regulator (arac/xyls) (le:84752) (re:87070) (di:direct) BSUB0016 Z99119 g2635499 Bacillus subtilis 1423 -11531751

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809652	5749	27905	351	116

Description

6500727894 hypothetical protein:similar to lipoprotein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytcQ ytcQ Bacillus subtilis 1423 -11531752 7000694170 ytcq lipoprotein homolog ytcq (cl:bacillus subtilis lipoprotein lpla) (db:pir2.dat) H69989 H69989 Bacillus subtilis 1423 -11531752 4000714182 ytcq ytcq (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to lipoprotein lpla precursor from b.) (le:91848) (re:93170) (di:direct) AF008220 AF008220 g2293191 Bacillus subtilis 1423 -11531752 7500964900 ytcq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to lipoprotein) (le:87257) (re:88579) (di:complement) BSUB0016 Z99119 g2635500 Bacillus subtilis 1423 -11531752

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809661	5750	27906	552	184

Description

6500727895 hypothetical protein:similar to abc transporter:permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytcP ytcP Bacillus subtilis 1423 -11531753 7500952746 ytcp (de:region (orf3)) (db:swissprot) YTCP\_BACSU P53561 BACILLUS SUBTILIS 1423 -11531753 7000692119 ytcp abc transporter permease homolog ytcp (db:pir2.dat) G69989 G69989 Bacillus subtilis 1423 -11531753 4000714181 ytcp transporter (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:90935) (re:91795) (di:direct) AF008220 AF008220 g2293190 Bacillus subtilis 1423 -11531753 7500952749 ytcp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to abc transporter (permease)) (le:88632) (re:89492) (di:complement) BSUB0016 Z99119 g2635501 Bacillus subtilis 1423 -11531753

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809677	5751	27907	930	309

Description

6500727896 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytbQ ytbQ Bacillus subtilis 1423 -11531754 7000693894 ytbq hypothetical protein ytbq (db:pir2.dat) F69988 F69988 Bacillus subtilis 1423 -11531754 4000714180 ytbq ytbq (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:90123) (re:90728) (di:direct) AF008220 AF008220 g2293189 Bacillus subtilis 1423 -11531754 7500964692 ytbq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:89699) (re:90304) (di:complement) BSUB0016 Z99119 g2635502 Bacillus subtilis 1423 -11531754

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809684	5752	27908	444	147

Description

6500727897 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytaP ytaP Bacillus subtilis 1423 -11531755  
7000693893 ytap hypothetical protein ytap (db:pir2.dat) B69988 B69988 Bacillus subtilis 1423 -11531755 4000714177 ytap ytap (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:82552) (re:83451) (di:direct) AF008220 AF008220 g2293182 Bacillus subtilis 1423 -11531755  
7500964691 ytap (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:96976) (re:97875) (di:complement) BSUB0016 Z99119 g2635509 Bacillus subtilis 1423 -11531755

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809685	5753	27909	681	226

Description

6500727898 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytwF ytwF Bacillus subtilis 1423 -11531756 7000692765 ytwf conserved hypothetical protein ytwf (db:pir2.dat) E70002 E70002 Bacillus subtilis 1423 -11531756 7500963839 ytwf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins from b. subtilis) (le:103512) (re:103718) (di:complement) BSUB0016 Z99119 g2635515 Bacillus subtilis 1423 -11531756

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809689	5754	27910	585	194

Description

6500727899 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytvB ytvB Bacillus subtilis 1423 -11531757  
7000693931 ytvb hypothetical protein ytvb (db:pir2.dat) B70002 B70002 Bacillus subtilis 1423 -11531757 4000714170 ytvb ytvb (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:73311) (re:73646) (di:direct) AF008220 AF008220 g2293180 Bacillus subtilis 1423 -11531757  
7500964729 ytvb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:106781) (re:107116) (di:complement) BSUB0016 Z99119 g2635517 Bacillus subtilis 1423 -11531757

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809691	5755	27911	471	156

Description

6500727900 hypothetical protein:similar to protein kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytvA ytvA Bacillus subtilis 1423 -11531758 7000694458 ytvA protein kinase homolog ytvA (db:pir2.dat) A70002 A70002 Bacillus subtilis 1423 -11531758 4000714169 ytvA putative protein kinase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to protein kinases) (le:72121) (re:72906) (di:complement) AF008220 AF008220 g2293304 Bacillus subtilis 1423 -11531758 7500965108 ytvA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to protein kinase) (le:107521) (re:108306) (di:direct) BSUB0016 Z99119 g2635518 Bacillus subtilis 1423 -11531758

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809692	5756	27912	498	165

Description

6500727901 hypothetical protein:similar to multidrug resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yttB yttB Bacillus subtilis 1423 -11531759 7000694247 yttB multidrug resistance protein homolog yttb (db:pir2.dat) F70001 F70001 Bacillus subtilis 1423 -11531759 4000714168 yttb yttb (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to tetracycline resistance protein from) (le:70691) (re:71884) (di:direct) AF008220 AF008220 g2293179 Bacillus subtilis 1423 -11531759 7500964972 yttb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to multidrug resistance protein) (le:108543) (re:109736) (di:complement) BSUB0016 Z99119 g2635519 Bacillus subtilis 1423 -11531759

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809702	5757	27913	408	135

Description

6500727902 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yttA yttA Bacillus subtilis 1423 -11531760 7000693929 yttA hypothetical protein yttA (db:pir2.dat) E70001 E70001 Bacillus subtilis 1423 -11531760 7500964727 yttA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:109931) (re:110671) (di:direct) BSUB0016 Z99119 g2635520 Bacillus subtilis 1423 -11531760

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809706	5758	27914	1041	346

Description

6500727903 hypothetical protein:similar to abc transporter:permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytsD ytsD Bacillus subtilis 1423 -11531761 7000692122 ytsd abc transporter permease homolog ytsd (db:pir2.dat) B70001 B70001 Bacillus subtilis 1423 -11531761 4000714166 ytsd ytsd (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to nadh dehydrogenase) (le:67779) (re:69719) (di:direct) AF008220 AF008220 g2293178 Bacillus subtilis 1423 -11531761 7500963361 ytsd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to abc transporter (permease)) (le:110708) (re:112648) (di:complement) BSUB0016 Z99119 g2635521 Bacillus subtilis 1423 -11531761

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809712	5759	27915	1590	529

Description

6500727904 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytsC ytsC Bacillus subtilis 1423 -11531762 7000692100 ytsc abc transporter atp-binding protein homolog ytsc (cl:atp-binding cassette homology) (db:pir2.dat) A70001 A70001 Bacillus subtilis 1423 -11531762 4000714165 ytsc transporter (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:67028) (re:67789) (di:direct) AF008220 AF008220 g2293177 Bacillus subtilis 1423 -11531762 7500963341 ytsc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to abc transporter (atp-binding protein)) (le:112638) (re:113399) (di:complement) BSUB0016 Z99119 g2635522 Bacillus subtilis 1423 -11531762

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809722	5760	27916	1413	471

Description

6500727905 hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (ec:2.7.3.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytsB ytsB Bacillus subtilis 1423 -11531763 7000694877 ytsb two-component sensor histidine kinase homolog ytsb (db:pir2.dat) H70000 H70000 Bacillus subtilis 1423 -11531763 4000714164 ytsb signal transduction protein kinase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:65922) (re:66926) (di:direct) AF008220 AF008220 g2293176 Bacillus subtilis 1423 -11531763 7500965417 ytsb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to two-component sensor histidine kinase) (le:113501) (re:114505) (di:complement) BSUB0016 Z99119 g2635523 Bacillus subtilis 1423 -11531763

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809733	5761	27917	1179	393

Description

6500727906 hypothetical protein:similar to two-component response regulator (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytsA ytsA Bacillus subtilis 1423 -11531764 7000694848 ytsa two-component response regulator ytsb homolog ytsa) (cl:ompr protein:response regulator homology) (db:pir2.dat) G70000 G70000 Bacillus subtilis 1423 -11531764 4000714163 ytsa signal transduction regulator (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:65234) (re:65929) (di:direct) AF008220 AF008220 g2293175 Bacillus subtilis 1423 -11531764 7500965397 ytsa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to two-component response regulator (ytsb)) (le:114498) (re:115193) (di:complement) BSUB0016 Z99119 g2635524 Bacillus subtilis 1423 -11531764

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809743	5762	27918	1167	389

Description

6500727907 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytrF ytrF Bacillus subtilis 1423 -11531765 7000692761 ytrf conserved hypothetical protein ytrf (db:pir2.dat) D70000 D70000 Bacillus subtilis 1423 -11531765 4000714162 ytrf ytrf (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to hypothetical protein hi1548 from) (le:63827) (re:65137) (di:direct) AF008220 AF008220 g2293174 Bacillus subtilis 1423 -11531765 7500963835 ytrf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:115290) (re:116600) (di:complement) BSUB0016 Z99119 g2635525 Bacillus subtilis 1423 -11531765

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809744	5763	27919	372	123

Description

6500727908 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytrE ytrE Bacillus subtilis 1423 -11531766 7000692099 ytre abc transporter atp-binding protein homolog ytre (cl:atp-binding cassette homology) (db:pir2.dat) C70000 C70000 Bacillus subtilis 1423 -11531766 4000714161 ytre transporter (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:63142) (re:63837) (di:direct) AF008220 AF008220 g2293173 Bacillus subtilis 1423 -11531766 7500963340 ytre (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to abc transporter (atp-binding protein)) (le:116590) (re:117285) (di:complement) BSUB0016 Z99119 g2635526 Bacillus subtilis 1423 -11531766

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809755	5764	27920	663	220

Description

GTC ORF with score 351 to: (db:genpept-inv) (de:caenorhabditis elegans rrm-type rna binding protein, actin-relatedprotein homolog and hypothetical protein 1207-1 polycistronic mrna,complete cds.) (nt:rna recognition motif-type rna binding protein with)...



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809760	5765	27921	399	132

#### Description

6500727909 hypothetical protein:similar to cytochrome c oxidase subunit (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytrD ytrD Bacillus subtilis 1423 -11531767 7000692893 ytrd cytochrome-c oxidase chain i homolog ytrd (db:pir2.dat) B70000 B70000 Bacillus subtilis 1423 -11531767 4000714160 ytrd ytrd (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to cytochrome-c oxidase from rat) (le:62150) (re:63127) (di:direct) AF008220 AF008220 g2293172 Bacillus subtilis 1423 -11531767 7500963922 ytrd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to cytochrome c oxidase subunit) (le:117300) (re:118277) (di:complement) BSUB0016 Z99119 g2635527 Bacillus subtilis 1423 -11531767

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809766	5766	27922	228	75

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809793	5767	27923	312	103

#### Description

6500727910 hypothetical protein:similar to cytochrome c oxidase subunit (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytrC ytrC Bacillus subtilis 1423 -11531768 7000692892 ytrc cytochrome-c oxidase chain i homolog ytrc (db:pir2.dat) A70000 A70000 Bacillus subtilis 1423 -11531768 4000714159 ytrc ytrc (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to nosy protein precursor from) (le:61134) (re:62120) (di:direct) AF008220 AF008220 g2293171 Bacillus subtilis 1423 -11531768 7500963921 ytrc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to cytochrome c oxidase subunit) (le:118307) (re:119293) (di:complement) BSUB0016 Z99119 g2635528 Bacillus subtilis 1423 -11531768

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809799	5768	27924	213	70

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809807	5769	27925	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809813	5770	27926	240	79

Description

6500727911 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytrB ytrB Bacillus subtilis 1423 -11531769 7000692098 ytrb abc transporter atp-binding protein homolog ytrb (cl:atp-binding cassette homology) (db:pir2.dat) H69999 H69999 Bacillus subtilis 1423 -11531769 4000714158 ytrb transporter (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:60262) (re:61140) (di:direct) AF008220 AF008220 g2293170 Bacillus subtilis 1423 -11531769 7500963339 ytrb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to abc transporter (atp-binding protein)) (le:119287) (re:120165) (di:complement) BSUB0016 Z99119 g2635529 Bacillus subtilis 1423 -11531769

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809822	5771	27927	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809842	5772	27928	1632	544

Description

6500727912 hypothetical protein:similar to transcriptional regulator:gntR family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytrA ytrA Bacillus subtilis 1423 -11531770 7000694739 ytra transcription regulator gntR family homolog ytra (db:pir2.dat) G69999 G69999 Bacillus subtilis 1423 -11531770 4000714157 ytra transcription regulator (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:59877) (re:60269) (di:direct) AF008220 AF008220 g2293169 Bacillus subtilis 1423 -11531770 7500965312 ytra (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to transcriptional regulator (gntR family)) (le:120158) (re:120550) (di:complement) BSUB0016 Z99119 g2635530 Bacillus subtilis 1423 -11531770

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809859	5773	27929	405	134

Description

6500727913 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytzC ytzC Bacillus subtilis 1423 -11531771  
7000693936 ytzC hypothetical protein ytzC (db:pir2.dat) E70004 E70004  
Bacillus subtilis 1423 -11531771 7500964734 ytzC (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21):  
from 2997771to 3213410.) (le:120876) (re:121148) (di:complement) BSUB0016  
Z99119 g2635531 Bacillus subtilis 1423 -11531771

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809861	5774	27930	285	94

Description

6500727914 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytqA ytqA Bacillus subtilis 1423 -11531772 7000692759 ytqA conserved hypothetical protein ytqA (cl:methanococcus jannaschii conserved hypothetical protein mj0486) (db:pir2.dat) D69999 D69999 Bacillus subtilis 1423 -11531772 4000714156 ytqA ytqA (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to biotine synthase from b.sphaericus) (le:58149) (re:59117) (di:complement) AF008220 AF008220 g2293302 Bacillus subtilis 1423 -11531772 7500963833 ytqA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:121310) (re:122278) (di:direct) BSUB0016 Z99119 g2635532 Bacillus subtilis 1423 -11531772

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809881	5775	27931	372	123

Description

6500727915 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytqB ytqB Bacillus subtilis 1423 -11531773  
7000693927 ytqB hypothetical protein ytqB (db:pir2.dat) E69999 E69999  
Bacillus subtilis 1423 -11531773 4000714155 ytqB ytqB (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:57568) (re:58152) (di:complement) AF008220 AF008220 g2293301 Bacillus subtilis 1423 -11531773  
7500964725 ytqB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:122275) (re:122859) (di:direct) BSUB0016 Z99119 g2635533 Bacillus subtilis 1423 -11531773

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809886	5776	27932	1491	497

Description

6500727916 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytpB ytpB Bacillus subtilis 1423 -11531774  
7000693923 ytpb hypothetical protein ytpb (db:pir2.dat) E69998 E69998 Bacillus subtilis 1423 -11531774 4000714154 ytpb ytpb (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:56475) (re:57578) (di:direct) AF008220 AF008220 g2293168 Bacillus subtilis 1423 -11531774  
7500964721 ytpb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:122849) (re:123952) (di:complement) BSUB0016 Z99119 g2635534 Bacillus subtilis 1423 -11531774

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809891	5777	27933	624	207

Description

6500727917 hypothetical protein:similar to lysophospholipase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytpA ytpA Bacillus subtilis 1423 -11531775 7000694175 ytpA lysophospholipase homolog ytpa (db:pir2.dat) D69998 D69998 Bacillus subtilis 1423 -11531775 4000714153 ytpa probable lysophospholipase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:55675) (re:56454) (di:direct) AF008220 AF008220 g2293167 Bacillus subtilis 1423 -11531775 7500964905 ytpa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to lysophospholipase) (le:123973) (re:124752) (di:complement) BSUB0016 Z99119 g2635535 Bacillus subtilis 1423 -11531775

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809894	5778	27934	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809924	5779	27935	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809939	5780	27936	1002	334

Description

6500727918 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytoA ytoA Bacillus subtilis 1423 -11531776 7000692758 ytoa conserved hypothetical protein ytoa (cl:ferripyochelin binding protein) (db:pir2.dat) H69997 H69997 Bacillus subtilis 1423 -11531776 4000714152 ytoa ytoa (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to ferripyochelin binding protein from p.) (le:55111) (re:55626) (di:complement) AF008220 AF008220 g2293300 Bacillus subtilis 1423 -11531776 7500963832 ytoa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:124801) (re:125316) (di:direct) BSUB0016 Z99119 g2635536 Bacillus subtilis 1423 -11531776

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809947	5781	27937	465	154

Description

6500727919 hypothetical protein:similar to proline permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytnA ytnA Bacillus subtilis 1423 -11531777 7000694449 ytna probable proline transport protein:probable proline-specific permease (cl:arginine permease) (db:pir2.dat) C69997 C69997 Bacillus subtilis 1423 -11531777 4000714151 ytna amino acid transporter (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:53475) (re:54866) (di:direct) AF008220 AF008220 g2293166 Bacillus subtilis 1423 -11531777 7500965102 ytna (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to proline permease) (le:125561) (re:126952) (di:complement) BSUB0016 Z99119 g2635537 Bacillus subtilis 1423 -11531777

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809956	5782	27938	438	145

Description

6500727920 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytmB ytmB Bacillus subtilis 1423 -11531778  
 7502851737 ytmB (de:hypothetical 9.3 kd protein in pcka-dps intergenic region) (db:swissprot) YTM\_BACSU 034365 BACILLUS SUBTILIS 1423 -11531778  
 7000693916 ytmB hypothetical protein ytmB (db:pir2.dat) B69996 B69996 Bacillus subtilis 1423 -11531778 4000714147 ytmB ytmB (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:47722) (re:47964) (di:direct) AF008220 AF008220 g2293163 Bacillus subtilis 1423 -11531778  
 7500964714 ytmB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:132463) (re:132705) (di:complement) BSUB0016 Z99119 g2635541 Bacillus subtilis 1423 -11531778

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809957	5783	27939	522	173

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809969	5784	27940	648	215

Description

6500727921 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytmA ytmA Bacillus subtilis 1423 -11531779  
 7000693915 ytmA hypothetical protein ytmA (db:pir2.dat) A69996 A69996 Bacillus subtilis 1423 -11531779 4000714146 ytmA putative peptidase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:46897) (re:47670) (di:direct) AF008220 AF008220 g2293162 Bacillus subtilis 1423 -11531779 7500964713 ytmA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:132757) (re:133530) (di:complement) BSUB0016 Z99119 g2635542 Bacillus subtilis 1423 -11531779

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501809971	5785	27941	189	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809992	5786	27942	1119	372

Description

GTC ORF with score 784 to: (fn:dna repair) (sr:neurospora crassa  
(strain:74-or23-1a) germinating conidia cdna t) (db:genpept-pln1)  
(de:neurospora crassa mrna for uv-endonuclease.) (nt:start codon putative)  
(le:148) (re:2118) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501809999	5787	27943	720	239

Description

6500727922 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) ytlA ytlA Bacillus subtilis 1423 -11531780  
7000693911 ytlA hypothetical protein ytlA (db:pir2.dat) A69995 A69995  
Bacillus subtilis 1423 -11531780 4000714145 ytlA putative transcription  
regulator (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.)  
(le:46057) (re:46746) (di:complement) AF008220 AF008220 g2293298 Bacillus  
subtilis 1423 -11531780 7500964709 ytlA (fn:unknown) (db:genpept-bct1)  
(de:bacillus subtilis complete genome (section 16 of 21): from 2997771to  
3213410.) (le:133681) (re:134370) (di:direct) BSUB0016 Z99119 g2635543  
Bacillus subtilis 1423 -11531780

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810007	5788	27944	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810014	5789	27945	513	170

Description

6500727923 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) ytlB ytlB Bacillus subtilis 1423 -11531781  
7000693912 ytlB hypothetical protein ytlb (db:pir2.dat) B69995 B69995  
Bacillus subtilis 1423 -11531781 4000714144 ytlb ytlb (db:genpept-bct1)  
(de:bacillus subtilis rrnb-dnab genomic region.) (le:45743) (re:46060)  
(di:complement) AF008220 AF008220 g2293297 Bacillus subtilis 1423 -11531781  
7500964710 ytlb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis  
complete genome (section 16 of 21): from 2997771to 3213410.) (le:134367)  
(re:134684) (di:direct) BSUB0016 Z99119 g2635544 Bacillus subtilis 1423  
-11531781

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810017	5790	27946	282	93

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810026	5791	27947	636	212

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810044	5792	27948	1143	380

Description

6500727924 hypothetical protein:similar to anion transport abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytlC ytlC Bacillus subtilis 1423 -11531782 7000692209 ytlc anion transport abc transporter atp-bindi homolog ytlc (cl:atp-binding cassette homology) (db:pir2.dat) C69995 C69995 Bacillus subtilis 1423 -11531782 4000714143 ytlc putative transporter (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:44948) (re:45730) (di:complement) AF008220 AF008220 g2293296 Bacillus subtilis 1423 -11531782 7500963416 ytlc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to anion transport abc transporter) (le:134697) (re:135479) (di:direct) BSUB0016 Z99119 g2635545 Bacillus subtilis 1423 -11531782

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810054	5793	27949	387	128

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810055	5794	27950	834	277

Description

GTC ORF with score 135 to: (db:genpept-bct2) (ec:3.1.1.24:4.1.1.44) (de:rhodococcus opacus succinyl coa:3-oxoadipate coa transferasesubunit homolog (pcai') gene, partial cds, protococatechuatedioxygenase beta subunit (pcah), protococatechuate dioxygenase ...



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810072	5795	27951	318	105

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810074	5796	27952	645	215

Description

6500727925 hypothetical protein:similar to abc transporter:permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytld ytld Bacillus subtilis 1423 -11531783 7000692120 ytld abc transporter permease homolog ytld (db:pir2.dat) D69995 D69995 Bacillus subtilis 1423 -11531783 4000714142 ytld ytld (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to dciac protein from b. subtilis) (le:44161) (re:44973) (di:complement) AF008220 AF008220 g2293295 Bacillus subtilis 1423 -11531783 7500963359 ytld (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to abc transporter (permease)) (le:135454) (re:136266) (di:direct) BSUB0016 Z99119 g2635546 Bacillus subtilis 1423 -11531783

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810094	5797	27953	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810098	5798	27954	333	110

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810099	5799	27955	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810112	5800	27956	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810118	5801	27957	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810126	5802	27958	1635	545

Description

6500727926 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytkD ytkD Bacillus subtilis 1423 -11531784  
7000693910 ytkd hypothetical protein ytkd (db:pir2.dat) E69994 E69994 Bacillus subtilis 1423 -11531784 4000714141 ytkd ytkd (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:43658) (re:44134) (di:direct) AF008220 AF008220 g2293161 Bacillus subtilis 1423 -11531784 7500964708 ytkd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:136293) (re:136769) (di:complement) BSUB0016 Z99119 g2635547 Bacillus subtilis 1423 -11531784

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810135	5803	27959	408	135

Description

6500727927 hypothetical protein:similar to autolytic amidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytkC ytkC Bacillus subtilis 1423 -11531785 7000692253 ytkc autolytic amidase homolog ytkc (db:pir2.dat) D69994 D69994 Bacillus subtilis 1423 -11531785 4000714140 ytkc ytkc (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to hypothetical protein d from c.) (le:43045) (re:43449) (di:direct) AF008220 AF008220 g2293160 Bacillus subtilis 1423 -11531785 7500963442 ytkc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to autolytic amidase) (le:136978) (re:137382) (di:complement) BSUB0016 Z99119 g2635548 Bacillus subtilis 1423 -11531785

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810138	5804	27960	705	234

Description

6500727928 ytkb:dps hypothetical protein:stress-and starvation-induced gene controlled by sigma-b (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) dps dps Bacillus subtilis 1423 -11531786  
7000694633 dps stress-and starvation-induced gene controlled by sigma-b dps (cl:hypothetical protein hi1349) (db:pir2.dat) H69618 H69618 Bacillus subtilis 1423 -11531786 4000714139 ytkb (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to hi1349 from h. influenzae) (le:42442) (re:42879) (di:direct) AF008220 AF008220 g2293159 Bacillus subtilis 1423 -11531786 7500965225 dps (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: ytkb; stress- and) (le:137548) (re:137985) (di:complement) BSUB0016 Z99119 g2635549 Bacillus subtilis 1423 -11531786

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810141	5805	27961	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810142	5806	27962	2073	691

Description

6500727929 yzna:ytkA hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytkA ytkA Bacillus subtilis 1423 -11531787 7000693909 ytkA hypothetical protein ytkA (db:pir2.dat) C69994 C69994 Bacillus subtilis 1423 -11531787 4000714138 ytkA ytkA (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity with the n-part of the metalloprotease) (le:41742) (re:42179) (di:direct) AF008220 AF008220 g2293158 Bacillus subtilis 1423 -11531787 7500964707 ytkA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: yzna) (le:138248) (re:138685) (di:complement) BSUB0016 Z99119 g2635550 Bacillus subtilis 1423 -11531787

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810146	5807	27963	573	190

Description

6500727930 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytjB ytjB Bacillus subtilis 1423 -11531788  
7000693908 ytjb hypothetical protein ytjb (cl:conserved hypothetical protein hi0491) (db:pir2.dat) A69994 A69994 Bacillus subtilis 1423 -11531788  
4000714137 ytjb ytjb (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to hypothetical protein hi0491 from h.) (le:41149) (re:41622) (di:direct) AF008220 AF008220 g2293157 Bacillus subtilis 1423 -11531788 7500964706 ytjb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:138805) (re:139278) (di:complement) BSUB0016 Z99119 g2635551 Bacillus subtilis 1423 -11531788

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810158	5808	27964	480	159

Description

6500727931 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytjA ytjA Bacillus subtilis 1423 -11531789  
7000693907 ytja hypothetical protein ytja (cl:conserved hypothetical protein hi1000) (db:pir2.dat) H69993 H69993 Bacillus subtilis 1423 -11531789  
4000714136 ytja ytja (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to hypothetical 9.3 kd protein from p.) (le:40793) (re:41020) (di:complement) AF008220 AF008220 g2293294 Bacillus subtilis 1423 -11531789 7500964705 ytja (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:139407) (re:139634) (di:direct) BSUB0016 Z99119 g2635552 Bacillus subtilis 1423 -11531789

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810163	5809	27965	849	282

Description

6500727932 hypothetical protein:similar to carbonic anhydrase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytiB ytiB Bacillus subtilis 1423 -11531790 7000692319 ytib carbonic anhydrase homolog ytib (cl:methanobacterium thermoautotrophicum carbonic anhydrase) (db:pir2.dat) F69993 F69993 Bacillus subtilis 1423 -11531790 4000714135 ytib ytib (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to carbonic anhydrase of e. coli) (le:40233) (re:40796) (di:direct) AF008220 AF008220 g2293156 Bacillus subtilis 1423 -11531790 7500963488 ytib (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to carbonic anhydrase) (le:139631) (re:140194) (di:complement) BSUB0016 Z99119 g2635553 Bacillus subtilis 1423 -11531790

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810169	5810	27966	555	184

Description

6500727933 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytiA ytiA Bacillus subtilis 1423 -11531791 7502851738 ytiA (de:hypothetical ribosomal protein in dps-mene intergenic region) (db:swissprot) YTIA\_BACSU 034967 BACILLUS SUBTILIS 1423 -11531791 7000692752 ytiA conserved hypothetical protein ytiA (cl:escherichia coli ribosomal protein l31) (db:pir2.dat) E69993 E69993 Bacillus subtilis 1423 -11531791 4000714134 ytiA ytiA (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:homology with the ribosomal protein l31) (le:39891) (re:40139) (di:direct) AF008220 AF008220 g2293155 Bacillus subtilis 1423 -11531791 7500963827 ytiA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:140288) (re:140536) (di:complement) BSUB0016 Z99119 g2635554 Bacillus subtilis 1423 -11531791

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810180	5811	27967	312	103

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810186	5812	27968	204	67

Description

GTC ORF with score 113 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana chromosome ii bac t06b20 genomic sequence,complete sequence.) (nt:yeast hypothetical protein ydb1\_schpo isolog) (le:74887:75256:76460:76808) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810194	5813	27969	507	168

Description

6500727934 hypothetical protein:similar to cytochrome d oxidase subunit (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ythA ythA Bacillus subtilis 1423 -11531792 7000692898 ytha cytochrome d oxidase subunit homolog ytha (cl:cytochrome d complex terminal oxidase chain i) (db:pir2.dat) H69992 H69992 Bacillus subtilis 1423 -11531792 4000714133 ytha ytha (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to cytochrome oxidase d subunit i) (le:38355) (re:39671) (di:complement) AF008220 AF008220 g2293293 Bacillus subtilis 1423 -11531792 7500963924 ytha (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to cytochrome d oxidase subunit) (le:140756) (re:142072) (di:direct) BSUB0016 Z99119 g2635555 Bacillus subtilis 1423 -11531792

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810207	5814	27970	264	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810208	5815	27971	795	265

Description

6500727935 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ythB ythB Bacillus subtilis 1423 -11531793 7000693904 ythb hypothetical protein ythb (db:pir2.dat) A69993 A69993 Bacillus subtilis 1423 -11531793 4000714132 ythb ythb (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to nadh dehydrogenases) (le:37271) (re:38311) (di:complement) AF008220 AF008220 g2293292 Bacillus subtilis 1423 -11531793 7500964702 ythb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:142116) (re:143156) (di:direct) BSUB0016 Z99119 g2635556 Bacillus subtilis 1423 -11531793

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810212	5816	27972	681	226

Description

6500727936 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ythC ythC Bacillus subtilis 1423 -11531794  
7000693905 ythc hypothetical protein ythc (db:pir2.dat) B69993 B69993 Bacillus subtilis 1423 -11531794 4000714131 ythc ythc (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:37055) (re:37222) (di:complement) AF008220 AF008220 g2293291 Bacillus subtilis 1423 -11531794  
7500964703 ythc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:143205) (re:143372) (di:direct) BSUB0016 Z99119 g2635557 Bacillus subtilis 1423 -11531794

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810216	5817	27973	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810224	5818	27974	1122	373

Description

6500727937 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytgD ytgD Bacillus subtilis 1423 -11531795 7000692751 ytgD conserved hypothetical protein ytgD (db:pir2.dat) E69992 E69992 Bacillus subtilis 1423 -11531795 4000714130 ytgD ytgD (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to membrane proteins) (le:36153) (re:37040) (di:direct) AF008220 AF008220 g2293154 Bacillus subtilis 1423 -11531795 7500963826 ytgD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:143387) (re:144274) (di:complement) BSUB0016 Z99119 g2635558 Bacillus subtilis 1423 -11531795

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810233	5819	27975	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810252	5820	27976	678	225
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810255	5821	27977	273	90
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810260	5822	27978	555	184
<u>Description</u>				

6500727938 hypothetical protein:similar to abc transporter:membrane protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytgC ytgC Bacillus subtilis 1423 -11531796 7000692116 ytgC abc transporter membrane protein homolog ytgC (db:pir2.dat) D69992 D69992 Bacillus subtilis 1423 -11531796 4000714129 ytgC ytgC (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to hypothetical protein hi0359 from h.) (le:34856) (re:36163) (di:direct) AF008220 AF008220 g2293153 Bacillus subtilis 1423 -11531796 7500963355 ytgC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to abc transporter (membrane protein)) (le:144264) (re:145571) (di:complement) BSUB0016 Z99119 g2635559 Bacillus subtilis 1423 -11531796

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810264	5823	27979	198	65
<u>Description</u>				

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810300	5824	27980	276	91

Description

6500727939 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytgB ytgB Bacillus subtilis 1423 -11531797 7000692096 ytgB abc transporter atp-binding protein homolog ytgB (cl:atp-binding cassette homology) (db:pir2.dat) C69992 C69992 Bacillus subtilis 1423 -11531797 4000714128 ytgB putative transporter (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to iron (iii) dicitrate transporter of e.) (le:34098) (re:34850) (di:direct) AF008220 AF008220 g2293152 Bacillus subtilis 1423 -11531797 7500963337 ytgB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to abc transporter (atp-binding protein)) (le:145577) (re:146329) (di:complement) BSUB0016 Z99119 g2635560 Bacillus subtilis 1423 -11531797

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810301	5825	27981	690	229

Description

6500727940 hypothetical protein:similar to abc transporter:membrane protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytgA ytgA Bacillus subtilis 1423 -11531798 7000692115 ytgA abc transporter membrane protein homolog ytgA (db:pir2.dat) B69992 B69992 Bacillus subtilis 1423 -11531798 4000714127 ytgA ytgA (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to adhesin b precursor of s. sanguis) (le:33159) (re:34079) (di:direct) AF008220 AF008220 g2293151 Bacillus subtilis 1423 -11531798 7500963354 ytgA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to abc transporter (membrane protein)) (le:146348) (re:147268) (di:complement) BSUB0016 Z99119 g2635561 Bacillus subtilis 1423 -11531798

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810310	5826	27982	303	101

Description

6500727941 hypothetical protein:similar to n-acylamino acid racemase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytfD ytfD Bacillus subtilis 1423 -11531799 7000694286 ytfD n-acylamino acid racemase homolog ytfD (cl:muconate cycloisomerase) (db:pir2.dat) F69991 F69991 Bacillus subtilis 1423 -11531799 4000714126 ytfD ytfD (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to muconate cycloisomerase of p. putida;) (le:31764) (re:32879) (di:direct) AF008220 AF008220 g2293150 Bacillus subtilis 1423 -11531799 7500954465 ytfD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to n-acylamino acid racemase) (le:147548) (re:148663) (di:complement) BSUB0016 Z99119 g2635562 Bacillus subtilis 1423 -11531799

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810316	5827	27983	699	233

Description

6500727942 ytfb:ytxm hypothetical protein:similar to prolyl aminopeptidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytxM ytxM Bacillus subtilis 1423 -11531800 7000694453 ytxM probable prolyl aminopeptidase:ytxm:cytosol aminopeptidase v:pro-x aminopeptidase:proline aminopeptidase:proline iminopeptidase (ec:3.4.11.5) (db:pir2.dat) H70003 H70003 Bacillus subtilis 1423 -11531800 4000714123 ytxM ytxM (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity with 2-hydroxy-6-oxo-2,4-heptadienoate) (le:28542) (re:29366) (di:direct) AF008220 AF008220 g2293147 Bacillus subtilis 1423 -11531800 7500965104 ytxM (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: ytfb; similar to prolyl) (le:151061) (re:151885) (di:complement) BSUB0016 Z99119 g2635565 Bacillus subtilis 1423 -11531800

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810333	5828	27984	285	94

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810353	5829	27985	1095	364

Description

GTC ORF with score 352 to: (sr:baker's yeast strain=s288c (ab972))  
(db:genpept-pln1) (de:saccharomyces cerevisiae chromosome viii cosmid 9196.)  
(nt:member of the atp-binding transport protein family) (le:27976)  
(re:32754) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810367	5830	27986	303	100

Description

6500727943 yzwb:ytea hypothetical protein (gtcfc:14.1) (keggfc:14.2)  
(bsorffc:8.1.1) (db:gtc-bacillus subtilis) yteA yteA Bacillus subtilis 1423  
-11531801 7000693898 ytea hypothetical protein ytea (db:pir2.dat) D69990  
D69990 Bacillus subtilis 1423 -11531801 4000714121 ytea ytea  
(db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.)  
(nt:similarity with dosage-dependent dnaK suppressor) (le:24566) (re:25111)  
(di:complement) AF008220 AF008220 g2293290 Bacillus subtilis 1423 -11531801  
7500964696 ytea (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis  
complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate  
gene name: yzwb) (le:155316) (re:155861) (di:direct) BSUB0016 Z99119  
g2635568 Bacillus subtilis 1423 -11531801

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810368	5831	27987	1263	420

Description

6500727944 hypothetical protein:similar to ndp-sugar dehydrogenase  
(gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytca  
ytca Bacillus subtilis 1423 -11531802 7000694312 ytca ndp-sugar  
dehydrogenase homolog ytca (cl:gdpmannose dehydrogenase) (db:pir2.dat)  
G69988 G69988 Bacillus subtilis 1423 -11531802 4000714120 ytca ytca  
(db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.)  
(nt:similar to udp glucose dehydrogenase of x.) (le:22108) (re:23394)  
(di:complement) AF008220 AF008220 g2293289 Bacillus subtilis 1423 -11531802  
7500965013 ytca (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis  
complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to  
ndp-sugar dehydrogenase) (le:157033) (re:158319) (di:direct) BSUB0016 Z99119  
g2635570 Bacillus subtilis 1423 -11531802

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810372	5832	27988	381	126

Description

6500727945 hypothetical protein:similar to lipopolysaccharide n-acetylglucosaminyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytcC ytcC Bacillus subtilis 1423 -11531803 7000694169 ytcc lipopolysaccharide n-acetylglucosaminyltra homolog ytcc (cl:lps biosynthesis related protein) (db:pir2.dat) A69989 A69989 Bacillus subtilis 1423 -11531803 4000714118 ytcc ytcc (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity with lipopolysaccharide) (le:19935) (re:21158) (di:complement) AF008220 AF008220 g2293287 Bacillus subtilis 1423 -11531803 7500954011 ytcc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to lipopolysaccharide) (le:159269) (re:160492) (di:direct) BSUB0016 Z99119 g2635572 Bacillus subtilis 1423 -11531803

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810375	5833	27989	204	67

Description

6500727946 ytbb:ytso hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytxO ytxO Bacillus subtilis 1423 -11531804 7000693934 ytso hypothetical protein ytso (db:pir2.dat) B70004 B70004 Bacillus subtilis 1423 -11531804 4000714117 ytso ytso (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:19430) (re:19861) (di:direct) AF008220 AF008220 g2293143 Bacillus subtilis 1423 -11531804 7500964732 ytso (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: ytbb) (le:160566) (re:160997) (di:complement) BSUB0016 Z99119 g2635573 Bacillus subtilis 1423 -11531804

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810377	5834	27990	294	97

Description

6500727947 ytba:ytxn hypothetical protein:hypothetical 42.9 kd protein in cots 5region:orfx (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytxN ytxN Bacillus subtilis 1423 -11531805 116464 ytxn (de:hypothetical 42.9 kd protein in cots 5'region (orfx)) (db:swissprot) YTXN\_BACSU P46915 BACILLUS SUBTILIS 1423 -11531805 7000688622 ytxn lipopolysaccharide n-acetylglucosaminyltra homolog ytxn (cl:lps biosynthesis related protein) (db:pir2.dat) A70004 A70004 Bacillus subtilis 1423 -11531805 215386 ytxn (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity with probable lipopolysaccharide) (le:17225) (re:18358) (di:direct) AF008220 AF008220 g2293141 Bacillus subtilis 1423 -11531805 4000707476 orfx (sr:bacillus subtilis (strain:60015) dna) (db:genpept-bct1) (de:bacillus subtilis cots gene for spore coat protein cots, completecds.) (le:240) (re:1373) (di:direct) BACCOTS D31847 g1197085 Bacillus subtilis 1423 -11531805 7500952786 ytxn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: ytba; similar to) (le:162069) (re:163202) (di:complement) BSUB0016 Z99119 g2635575 Bacillus subtilis 1423 -11531805 5000689703 (de:(ytxn) (pn:hypothetical 42) (gtcfc:13.07) (ec:) (ytxn\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) ytxN ytxN Bacillus subtilis 1423 10058189

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810378	5835	27991	576	191

Description

6500727948 hypothetical protein:similar to spore coat protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytaA ytaA Bacillus subtilis 1423 -11531806 7000694619 ytaa spore coat protein homolog ytaa (db:pir2.dat) F69987 F69987 Bacillus subtilis 1423 -11531806 4000714116 ytaa ytaa (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:homology to the spore coat protein cots) (le:15962) (re:17035) (di:complement) AF008220 AF008220 g2293286 Bacillus subtilis 1423 -11531806 7500965214 ytaa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to spore coat protein) (le:163392) (re:164465) (di:direct) BSUB0016 Z99119 g2635576 Bacillus subtilis 1423 -11531806

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810379	5836	27992	282	93

Description

6500727949 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytaB ytaB Bacillus subtilis 1423 -11531807  
7000693891 ytab hypothetical protein ytab (db:pir2.dat) G69987 G69987 Bacillus subtilis 1423 -11531807 4000714115 ytab ytab (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to benzodiazepine receptor 1 from mus) (le:15415) (re:15882) (di:complement) AF008220 AF008220 g2293285 Bacillus subtilis 1423 -11531807 7500964689 ytab (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:164545) (re:165012) (di:direct) BSUB0016 Z99119 g2635577 Bacillus subtilis 1423 -11531807

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810382	5837	27993	282	93

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810384	5838	27994	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810392	5839	27995	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810396	5840	27996	1308	435

Description

6500727950 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuaJ yuaJ Bacillus subtilis 1423 -11531808 7000692773 yuaj conserved hypothetical protein yuaj (db:pir2.dat) C70006 C70006 Bacillus subtilis 1423 -11531808 7500963844 yuaj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:180606) (re:181184) (di:direct) BSUB0016 Z99119 g2635583 Bacillus subtilis 1423 -11531808

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810405	5841	27997	633	210

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810406	5842	27998	1032	343

Description

6500727951 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuaI yuaI Bacillus subtilis 1423 -11531809  
7000693942 yuai hypothetical protein yuai (db:pir2.dat) B70006 B70006  
Bacillus subtilis 1423 -11531809 7500964740 yuai (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21):  
from 2997771to 3213410.) (le:181226) (re:181747) (di:complement) BSUB0016  
Z99119 g2635584 Bacillus subtilis 1423 -11531809

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810421	5843	27999	786	262

Description

6500727952 yuah:yuag hypothetical protein:similar to epidermal surface  
antigen (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus  
subtilis) yuaG yuaG Bacillus subtilis 1423 -11531810 7502851739 yuag  
(de:hypothetical 56.0 kd protein in glgb-gbsb intergenic region)  
(db:swissprot) YUAG\_BACSU O32076 BACILLUS SUBTILIS 1423 -11531810  
7000692967 yuag epidermal surface antigen homolog yuag (db:pir2.dat) A70006  
A70006 Bacillus subtilis 1423 -11531810 7500963971 yuag (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21):  
from 2997771to 3213410.) (nt:alternate gene name: yuah; similar to  
epidermal) (le:181765) (re:183294) (di:complement) BSUB0016 Z99119 g2635585  
Bacillus subtilis 1423 -11531810

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810431	5844	28000	279	92

Description

6500727953 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yuaF yuaF Bacillus subtilis 1423 -11531811  
7000693941 yuaf hypothetical protein yuaf (db:pir2.dat) H70005 H70005  
Bacillus subtilis 1423 -11531811 7500964739 yuaf (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21):  
from 2997771to 3213410.) (le:183315) (re:183839) (di:complement) BSUB0016  
Z99119 g2635586 Bacillus subtilis 1423 -11531811

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810432	5845	28001	471	156

Description

6500727954 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuaE yuaE Bacillus subtilis 1423 -11531812  
7000693940 yuae hypothetical protein yuae (db:pir2.dat) G70005 G70005  
Bacillus subtilis 1423 -11531812 7500964738 yuae (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21):  
from 2997771to 3213410.) (le:184007) (re:184495) (di:direct) BSUB0016 Z99119  
g2635587 Bacillus subtilis 1423 -11531812

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810440	5846	28002	447	148

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810443	5847	28003	669	222

Description

6500727955 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuaD yuaD Bacillus subtilis 1423 -11531813  
7000693939 yuad hypothetical protein yuad (db:pir2.dat) F70005 F70005  
Bacillus subtilis 1423 -11531813 7500964737 yuad (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21):  
from 2997771to 3213410.) (le:184501) (re:185079) (di:complement) BSUB0016  
Z99119 g2635588 Bacillus subtilis 1423 -11531813



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810452	5848	28004	264	87

Description

6500727956 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuaC yuaC Bacillus subtilis 1423 -11531814 7500952792 yuac (de:hypothetical 21.1 kd protein in gbsa-tlpb intergenic region (orf2)) (db:swissprot) YUAC\_BACSU P71015 BACILLUS SUBTILIS 1423 -11531814 7000692772 yuac conserved hypothetical protein yuac (db:pir2.dat) E70005 E70005 Bacillus subtilis 1423 -11531814 7500952794 yuac (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:188063) (re:188605) (di:direct) BSUB0016 Z99119 g2635591 Bacillus subtilis 1423 -11531814 220030 (db:genpept-bct2) (de:bacillus subtilis gbsab operon, glycine betaine aldehydedehydrogenase gbsa, alcohol dehydrogenase gbsb genes, complete cds.) (nt:orf-2 upstream of gbsab operon) (le:522) (re:1064) (di:complement) BSU47861 U47861 g1524394 Bacillus subtilis 1423 -11531814

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810454	5849	28005	540	179

Description

6500727957 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuaB yuaB Bacillus subtilis 1423 -11531815 7500952789 yuab (de:hypothetical 19.3 kd protein in gbsa-tlpb intergenic region (orf-1)) (db:swissprot) YUAB\_BACSU P71014 BACILLUS SUBTILIS 1423 -11531815 7000692771 yuab conserved hypothetical protein yuab (db:pir2.dat) D70005 D70005 Bacillus subtilis 1423 -11531815 7500952791 yuab (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins from b. subtilis) (le:188803) (re:189348) (di:direct) BSUB0016 Z99119 g2635592 Bacillus subtilis 1423 -11531815

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810457	5850	28006	606	201

Description

6500727958 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuaA yuaA Bacillus subtilis 1423 -11531816 7000692770 yuaa conserved hypothetical protein yuaa (cl:conserved hypothetical protein mg323) (db:pir2.dat) C70005 C70005 Bacillus subtilis 1423 -11531816 7500963843 yuaa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:189714) (re:190382) (di:direct) BSUB0016 Z99119 g2635593 Bacillus subtilis 1423 -11531816

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810462	5851	28007	966	321

Description

6500727959 hypothetical protein:similar to na+-transporting atp synthase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yubG yubG Bacillus subtilis 1423 -11531817 7000694290 yubg na+-transporting atp synthase homolog yubg (cl:na+-atp synthase chain j) (db:pir2.dat) B70007 B70007 Bacillus subtilis 1423 -11531817 7500964999 yubg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to na+-transporting atp synthase) (le:190389) (re:191726) (di:direct) BSUB0016 Z99119 g2635594 Bacillus subtilis 1423 -11531817

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810463	5852	28008	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810486	5853	28009	1590	529

Description

6500727960 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yubF yubF Bacillus subtilis 1423 -11531818 7000693943 yubf hypothetical protein yubf (db:pir2.dat) A70007 A70007 Bacillus subtilis 1423 -11531818 7500964741 yubf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:191762) (re:192025) (di:complement) BSUB0016 Z99119 g2635595 Bacillus subtilis 1423 -11531818

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810493	5854	28010	1068	356

Description

GTC ORF with score 520 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid f55b11, complete sequence.) (nt:predicted using genefinder; cdna est yk369e7.5) (le:24426:24649:24927:26086) (re:24572:24870:25233:26255) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810495	5855	28011	639	212

Description

6500727961 hypothetical protein:similar to n-acetylmuramoyl-l-alanine amidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yubE yubE Bacillus subtilis 1423 -11531819 7000694285 yube n-acetylmuramoyl-l-alanine amidase homolog yube (db:pir2.dat) H70006 H70006 Bacillus subtilis 1423 -11531819 7500964996 yube (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to n-acetylmuramoyl-l-alanine amidase) (le:192134) (re:192982) (di:complement) BSUB0016 Z99119 g2635596 Bacillus subtilis 1423 -11531819

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810496	5856	28012	693	230

Description

6500727962 hypothetical protein:similar to multidrug resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yubD yubD Bacillus subtilis 1423 -11531820 7000694248 yubd multidrug resistance protein homolog yubd (db:pir2.dat) G70006 G70006 Bacillus subtilis 1423 -11531820 7500964973 yubd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to multidrug resistance protein) (le:193143) (re:194678) (di:complement) BSUB0016 Z99119 g2635597 Bacillus subtilis 1423 -11531820

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810498	5857	28013	1068	356

Description

GTC ORF with score 256 to: (sr:dog) (db:genpept-mam) (de:canis familiaris keratin (krt9) gene, complete cds.) (nt:found in intermediate filaments of epidermal cells) (le:356:2486:2687:3120:4046) (re:949:2568:2843:3281:4171) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810504	5858	28014	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810508	5859	28015	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810518	5860	28016	408	135

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810519	5861	28017	480	159

Description

6500727963 hypothetical protein:similar to cysteine dioxygenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yubC yubC Bacillus subtilis 1423 -11531821 7000692887 yubc cysteine dioxygenase homolog yubc (db:pir2.dat) F70006 F70006 Bacillus subtilis 1423 -11531821 7500963917 yubc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to cysteine dioxygenase) (le:195163) (re:195648) (di:direct) BSUB0016 Z99119 g2635598 Bacillus subtilis 1423 -11531821

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810524	5862	28018	312	103

Description

6500727964 hypothetical protein:similar to bacitracin resistance protein:undecaprenol kinase (gtcfc:14.1) (ec:2.7.1.66) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yubB yubB Bacillus subtilis 1423 -11531822 7000692254 yubb probable bacitracin resistance protein undecapreno yubb (cl:escherichia coli bacitracin resistance protein baca) (db:pir2.dat) E70006 E70006 Bacillus subtilis 1423 -11531822 7500963443 yubb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to bacitracin resistance protein) (le:195935) (re:196765) (di:complement) BSUB0016 Z99119 g2635599 Bacillus subtilis 1423 -11531822

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810525	5863	28019	369	123

Description

GTC ORF with score 92 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid y51a2d, complete sequence.) (nt:predicted using genefinder; similar to sugar (and) (le:45748:46209:46825:47593) (re:45976:46412:47178:48174) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810533	5864	28020	1026	341

Description

GTC ORF with score 603 to: (sr:schizosaccharomyces pombe dna)  
(db:genpept-pln2) (ec:3.1.3.16) (de:yeast pab1+ gene for protein phosphatase  
2a 55kd regulatory subunit(b subunit), complete cds.)  
(1e:1245:1333:1451:2777) (re:1288:1373:2733:2800) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810538	5865	28021	495	164

Description

6500727965 hypothetical protein:similar to hypothetical proteins  
(gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yubA  
yubA Bacillus subtilis 1423 -11531823 7000692774 yuba conserved  
hypothetical protein yuba (db:pir2.dat) D70006 D70006 Bacillus subtilis 1423  
-11531823 7500963845 yuba (fn:unknown) (db:genpept-bct1) (de:bacillus  
subtilis complete genome (section 16 of 21): from 2997771to 3213410.)  
(nt:similar to hypothetical proteins) (1e:196858) (re:198024)  
(di:complement) BSUB0016 Z99119 g2635600 Bacillus subtilis 1423 -11531823

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810539	5866	28022	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810543	5867	28023	555	184

Description

6500727966 hypothetical protein:similar to hypothetical proteins  
(gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yulF  
yulF Bacillus subtilis 1423 -11531824 7502851740 yulf (de:hypothetical 36.5  
kd protein in gbsa-tlpb intergenic region) (db:swissprot) YULF\_BACSU 005265  
BACILLUS SUBTILIS 1423 -11531824 7000692790 yulf conserved hypothetical  
protein yulf (cl:escherichia coli ygjr protein) (db:pir2.dat) H70014 H70014  
Bacillus subtilis 1423 -11531824 7500963856 yulf (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21):  
from 2997771to 3213410.) (nt:similar to hypothetical proteins) (1e:198206)  
(re:199192) (di:direct) BSUB0016 Z99119 g2635601 Bacillus subtilis 1423  
-11531824

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810560	5868	28024	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810561	5869	28025	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810575	5870	28026	1326	441

Description

GTC ORF with score 131 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid f28c1, complete sequence.) (nt:weak similarity to pig ribonuclease inhibitor) (le:19785:20331:20796:20970) (re:20246:20753:20927:21186) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810576	5871	28027	699	232

Description

GTC ORF with score 117 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f59a6.) (nt:similar to glycoproteins) (le:13300:13899:15490:15579) (re:13615:15440:15533:15701) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810577	5872	28028	1338	445

Description

6500727967 hypothetical protein:similar to hypothetical proteins  
(gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yulD  
yulD Bacillus subtilis 1423 -11531825 7000692789 yulD conserved  
hypothetical protein yulD (db:pir2.dat) F70014 F70014 Bacillus subtilis 1423  
-11531825 1500693711 yulD (fn:unknown) (db:genpept-bct1) (de:bacillus  
subtilis complete genome (section 16 of 21): from 2997771to 3213410.)  
(nt:similar to hypothetical proteins) (le:200533) (re:200847)  
(di:complement) BSUB0016 Z99119 g2635603 Bacillus subtilis 1423 -11531825  
6000691372 yulD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis  
complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to  
hypothetical proteins) (le:1303) (re:1617) (di:complement) BSUB0017 Z99120  
g2635615 Bacillus subtilis 1423 -11531825 7500963855 yulD unknown  
(db:genpept-bct1) (de:bacillus subtilis genomic dna fragment from yula to yulf.)  
(le:4612) (re:4926) (di:direct) BSZ93938 Z93938 g1934824 Bacillus subtilis  
1423 -11531825

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810582	5873	28029	819	272

Description

6500727968 hypothetical protein:similar to transcriptional regulator:deor  
family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis)  
yulB yulB Bacillus subtilis 1423 -11531826 7500952810 yulB (de:hypothetical  
transcriptional regulator in gbsa-tlpb intergenic region) (db:swissprot)  
YULB\_BACSU 005261 BACILLUS SUBTILIS 1423 -11531826 7000694727 yulB  
transcription regulator deor family homolog yulB (cl:regulatory protein  
gutr) (db:pir2.dat) D70014 D70014 Bacillus subtilis 1423 -11531826  
6000691376 yulB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis  
complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to  
transcriptional regulator (deor family)) (le:202327) (re:203103)  
(di:complement) BSUB0016 Z99119 g2635605 Bacillus subtilis 1423 -11531826  
7500952812 yulB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis  
complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to  
transcriptional regulator (deor family)) (le:3097) (re:3873) (di:complement)  
BSUB0017 Z99120 g2635617 Bacillus subtilis 1423 -11531826 1500693709 yulB  
unknown (db:genpept-bct1) (de:bacillus subtilis genomic dna fragment from yula to  
yulf.) (nt:potential regulatory protein of glucitol operon) (le:2356)  
(re:3132) (di:direct) BSZ93938 Z93938 g1934822 Bacillus subtilis 1423  
-11531826

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810593	5874	28030	324	107

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810596	5875	28031	621	206

Description

GTC ORF with score 241 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 0438.) (nt:unnamed protein product) (le:141) (re:1340) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810607	5876	28032	237	78

Description

GTC ORF with score 337 to: (fn:controls germ tube growth and pathogenicity of) (db:genpept-pln1) (de:magnaporthe grisea putative transcriptional regulator (con7) gene,complete cds.) (nt:has zinc-finger motif and nuclear localization) (le:298:1253:1920)...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810613	5877	28033	372	123

Description

GTC ORF with score 208 to: (fn:controls germ tube growth and pathogenicity of) (db:genpept-pln1) (de:magnaporthe grisea putative transcriptional regulator (con7) gene,complete cds.) (nt:has zinc-finger motif and nuclear localization) (le:298:1253:1920)...



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810614	5878	28034	1365	454

Description

6500727969 yula:yuxg hypothetical protein:similar to sorbitol-6-phosphate 2-dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuxG yuxG Bacillus subtilis 1423 -11531827 7500952822 yuxg:yula (ec:1.-.-.-) (de:(ec 1.-.-.-) (orf2)) (db:swissprot) YUXG\_BACSU P40747 BACILLUS SUBTILIS 1423 -11531827 7000694599 yuxg sorbitol-6-phosphate 2-dehydrogenase homolog yuxg (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) H70024 H70024 Bacillus subtilis 1423 -11531827 6000691378 yuxg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: yula; similar to) (le:203160) (re:205229) (di:complement) BSUB0016 Z99119 g2635606 Bacillus subtilis 1423 -11531827 7500952824 yuxg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate gene name: yula; similar to) (le:3930) (re:5999) (di:complement) BSUB0017 Z99120 g2635618 Bacillus subtilis 1423 -11531827 1500693708 yula unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yula to yulf.) (le:230) (re:2299) (di:direct) BSZ93938 Z93938 g1934821 Bacillus subtilis 1423 -11531827

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810630	5879	28035	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810678	5880	28036	228	76

Description

6500727970 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yugU yugU Bacillus subtilis 1423 -11531828 7500952806 yugu (de:hypothetical 16.3 kd protein in tgl-pgi intergenic region) (db:swissprot) YUGU\_BACSU 005243 BACILLUS SUBTILIS 1423 -11531828 7000692781 yugu conserved hypothetical protein yugu (cl:hypothetical protein mj1081) (db:pir2.dat) A70012 A70012 Bacillus subtilis 1423 -11531828 6000691382 yugu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins) (le:215153) (re:215581) (di:complement) BSUB0016 Z99119 g2635612 Bacillus subtilis 1423 -11531828 7500952808 yugu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins) (le:15923) (re:16351) (di:complement) BSUB0017 Z99120 g2635624 Bacillus subtilis 1423 -11531828 1500693688 yugu unknown (db:genpept-bct1) (de:bacillus subtilis genomic dna fragment from yugs to mcpb.) (le:3231) (re:3659) (di:direct) BSZ93935 Z93935 g1934798 Bacillus subtilis 1423 -11531828

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810685	5881	28037	852	283

Description

6500727971 hypothetical protein:similar to exo-alpha-1:4-glucosidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yugT yugT Bacillus subtilis 1423 -11531829 7000692974 yugt exo-alpha-1:4-glucosidase homolog yugt (cl:alpha-glucosidase:alpha-amylase core homology) (db:pir2.dat) H70011 H70011 Bacillus subtilis 1423 -11531829 1500693687 yugt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to exo-alpha-1,4-glucosidase) (le:16441) (re:18105) (di:complement) BSUB0017 Z99120 g2635625 Bacillus subtilis 1423 -11531829 7500963975 yugt unknown (db:genpept-bct1) (de:bacillus subtilis genomic dna fragment from yugs to mcpb.) (le:1477) (re:3141) (di:direct) BSZ93935 Z93935 g1934797 Bacillus subtilis 1423 -11531829

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810691	5882	28038	1275	424

Description

6500727972 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yugS yugS Bacillus subtilis 1423 -11531830 7500952802 yugs (de:hypothetical 49.5 kd protein in tgl-pgi intergenic region) (db:swissprot) YUGS\_BACSU 005241 BACILLUS SUBTILIS 1423 -11531830 7000692780 yugs conserved hypothetical protein yugs (cl:hypothetical protein hi0107) (db:pir2.dat) G70011 G70011 Bacillus subtilis 1423 -11531830 7500952804 yugs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins from b. subtilis) (le:18232) (re:19536) (di:complement) BSUB0017 Z99120 g2635626 Bacillus subtilis 1423 -11531830 1500693686 yugs unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yugs to mcpb.) (le:46) (re:1350) (di:direct) BSZ93935 Z93935 g1934796 Bacillus subtilis 1423 -11531830

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810694	5883	28039	441	146

Description

6500727973 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yugP yugP Bacillus subtilis 1423 -11531831 7000693955 yugp hypothetical protein yugp (db:pir2.dat) F70011 F70011 Bacillus subtilis 1423 -11531831 1500693695 yugp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:19564) (re:20241) (di:complement) BSUB0017 Z99120 g2635627 Bacillus subtilis 1423 -11531831 7500964753 yugp unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yugl to yugp.) (le:4045) (re:4722) (di:direct) BSZ93936 Z93936 g1934806 Bacillus subtilis 1423 -11531831

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810713	5884	28040	285	94

Description

6500727974 hypothetical protein:similar to potassium channel protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yugO yugO Bacillus subtilis 1423 -11531832 7000694439 yugo potassium channel protein homolog yugo (db:pir2.dat) E70011 E70011 Bacillus subtilis 1423 -11531832 1500693694 yugo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to potassium channel protein) (le:20593) (re:21720) (di:direct) BSUB0017 Z99120 g2635628 Bacillus subtilis 1423 -11531832 7500965094 yugo unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yugl to yugp.) (le:2566) (re:3693) (di:complement) BSZ93936 Z93936 g1934805 Bacillus subtilis 1423 -11531832

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810718	5885	28041	762	253

Description

6500727975 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yugN yugN Bacillus subtilis 1423 -11531833 7000693954 yugn hypothetical protein yugn (db:pir2.dat) D70011 D70011 Bacillus subtilis 1423 -11531833 1500693693 yugn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:21905) (re:22309) (di:complement) BSUB0017 Z99120 g2635629 Bacillus subtilis 1423 -11531833 7500964752 yugn unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yugl to yugp.) (le:1977) (re:2381) (di:direct) BSZ93936 Z93936 g1934804 Bacillus subtilis 1423 -11531833

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810729	5886	28042	795	264

Description

6500727976 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yugM yugM Bacillus subtilis 1423 -11531834 7000693953 yugm hypothetical protein yugm (db:pir2.dat) C70011 C70011 Bacillus subtilis 1423 -11531834 1500693692 yugm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:22369) (re:22740) (di:complement) BSUB0017 Z99120 g2635630 Bacillus subtilis 1423 -11531834 7500964751 yugm unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yugl to yugp.) (le:1546) (re:1917) (di:direct) BSZ93936 Z93936 g1934803 Bacillus subtilis 1423 -11531834

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810741	5887	28043	1230	409

Description

6500727977 hypothetical protein:similar to nadh-dependent butanol dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yugK yugK Bacillus subtilis 1423 -11531835 7500876584 yugk (ec:1.1.1.-) (de:probable nadh-dependent butanol dehydrogenase 2,) (db:swissprot) ADHB\_BACSU O05240 BACILLUS SUBTILIS 1423 -11531835 7000694309 yugk nadh-dependent butanol dehydrogenase homolog yugk (cl:lactaldehyde reductase:lactaldehyde reductase homology) (db:pir2.dat) B70011 B70011 Bacillus subtilis 1423 -11531835 7500876586 yugk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to nadh-dependent butanol dehydrogenase) (le:24266) (re:25438) (di:complement) BSUB0017 Z99120 g2635632 Bacillus subtilis 1423 -11531835 1500693685 yugk nadh-dependent butanol dehydrogenase (db:genpept-bct1) (de:b.subtilis genomic dna fragment from patb to yugk.) (nt:putative) (le:6702) (re:7874) (di:direct) BSZ93934 Z93934 g1934794 Bacillus subtilis 1423 -11531835

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810743	5888	28044	351	116

Description

6500727978 hypothetical protein:similar to nadh-dependent butanol dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yugJ yugJ Bacillus subtilis 1423 -11531836 7500876580 yugj (ec:1.1.1.-) (de:probable nadh-dependent butanol dehydrogenase 1,) (db:swissprot) ADHA\_BACSU O05239 BACILLUS SUBTILIS 1423 -11531836 7000694308 yugj nadh-dependent butanol dehydrogenase homolog yugj (cl:lactaldehyde reductase:lactaldehyde reductase homology) (db:pir2.dat) A70011 A70011 Bacillus subtilis 1423 -11531836 7500876582 yugj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to nadh-dependent butanol dehydrogenase) (le:25542) (re:26705) (di:complement) BSUB0017 Z99120 g2635633 Bacillus subtilis 1423 -11531836 1500693684 yugj nadh-dependent butanol dehydrogenase (db:genpept-bct1) (de:b.subtilis genomic dna fragment from patb to yugk.) (nt:putative) (le:5435) (re:6598) (di:direct) BSZ93934 Z93934 g1934793 Bacillus subtilis 1423 -11531836

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810762	5889	28045	369	122

Description

6500727979 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuzA yuzA Bacillus subtilis 1423 -11531837  
7000693986 yuza hypothetical protein yuza (db:pir2.dat) H70025 H70025 Bacillus subtilis 1423 -11531837 7500964778 yuza (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:26935) (re:27171) (di:direct) BSUB0017 Z99120 g2635634 Bacillus subtilis 1423 -11531837

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810764	5890	28046	258	85

Description

6500727980 hypothetical protein:similar to polyribonucleotide nucleotidyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yugI yugI Bacillus subtilis 1423 -11531838  
7000694434 yugi polyribonucleotide nucleotidyltransferase homolog yugi (cl:polyribonucleotide nucleotidyltransferase homolog yabr) (db:pir2.dat) H70010 H70010 Bacillus subtilis 1423 -11531838 1500693683 yugi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to polyribonucleotide) (le:27249) (re:27641) (di:complement) BSUB0017 Z99120 g2635635 Bacillus subtilis 1423 -11531838 7500965090 yugi unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from patb to yugk.) (le:4499) (re:4891) (di:direct) BSZ93934 Z93934 g1934792 Bacillus subtilis 1423 -11531838

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810769	5891	28047	1458	486

Description

6500727981 hypothetical protein:similar to transcriptional regulator:lrp/asnc family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yugG yugG Bacillus subtilis 1423 -11531839  
7000694750 yugg transcription regulator lrp/asnc family homolog yugg (cl:transcription regulator yugg) (db:pir2.dat) F70010 F70010 Bacillus subtilis 1423 -11531839 3000694825 yugg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to transcriptional regulator (lrp/asnc) (le:29010) (re:29510) (di:complement) BSUB0017 Z99120 g2635637 Bacillus subtilis 1423 -11531839 7500955509 yugg unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from patb to yugk.) (le:2630) (re:3130) (di:direct) BSZ93934 Z93934 g2125791 Bacillus subtilis 1423 -11531839

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810814	5892	28048	492	163

Description

6500727982 hypothetical protein:similar to dihydrolipoamide s-acetyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yugF yugF Bacillus subtilis 1423 -11531840 7000692920 yugf dihydrolipoamide s-acetyltransferase homolog yugf (db:pir2.dat) E70010 E70010 Bacillus subtilis 1423 -11531840 1500693680 yugf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to dihydrolipoamide s-acetyltransferase) (le:29658) (re:30479) (di:direct) BSUB0017 Z99120 g2635638 Bacillus subtilis 1423 -11531840 7500963938 yugf unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from patb to yugk.) (le:1661) (re:2482) (di:complement) BSZ93934 Z93934 g1934789 Bacillus subtilis 1423 -11531840

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810838	5893	28049	735	244

Description

6500727983 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yugE yugE Bacillus subtilis 1423 -11531841 7000693952 yuge hypothetical protein yuge (db:pir2.dat) D70010 D70010 Bacillus subtilis 1423 -11531841 1500693679 yuge (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:30508) (re:30774) (di:complement) BSUB0017 Z99120 g2635639 Bacillus subtilis 1423 -11531841 7500964750 yuge unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from patb to yugk.) (nt:in the original sequence a partial open reading) (le:1366) (re:1632) (di:direct) BSZ93934 Z93934 g1934788 Bacillus subtilis 1423 -11531841

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810841	5894	28050	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810859	5895	28051	321	106

Description

6500727984 yugb:kapd hypothetical protein:inhibition of the kina pathway to sporulation (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) kapD kapD Bacillus subtilis 1423 -11531842 7000694106 kapd inhibitor of the kina pathway to sporulation kapd (db:pir2.dat) B69647 B69647 Bacillus subtilis 1423 -11531842 1500694333 kapd (fn:inhibition of the kina pathway to sporulation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate gene name: yugb) (le:33892) (re:34509) (di:complement) BSUB0017 Z99120 g2635643 Bacillus subtilis 1423 -11531842 7500964865 yugb unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yuga to yugd.) (le:3325) (re:3942) (di:complement) BSZ93933 Z93933 g1934782 Bacillus subtilis 1423 -11531842

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810860	5896	28052	1191	396

Description

6500727985 yugc:yuxj hypothetical protein:similar to multidrug-efflux transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuxJ yuxJ Bacillus subtilis 1423 -11531843 7500952827 yuxj (de:hypothetical 39.1 kd protein in kapd-pbpd intergenic region (orf1)) (db:swissprot) YUXJ\_BACSU P40760 BACILLUS SUBTILIS 1423 -11531843 7000694257 yuxj multidrug-efflux transporter homolog yuxj:msyb homolog:pbpd 5-region (cl:escherichia coli probable integral membrane protein) (db:pir2.dat) C70025 C70025 Bacillus subtilis 1423 -11531843 7500952829 yuxj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate gene name: yugc; similar to) (le:34827) (re:35897) (di:direct) BSUB0017 Z99120 g2635644 Bacillus subtilis 1423 -11531843 1500694334 yugc unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yuga to yugd.) (le:4260) (re:5330) (di:direct) BSZ93933 Z93933 g1934783 Bacillus subtilis 1423 -11531843



ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501810877	5897	28053	552	183

#### Description

6500727986 yugd:yuxk hypothetical protein:hypothetical 15.7 kd protein in pbpd 3region:orf2 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuxK yuxK Bacillus subtilis 1423 -11531844 116484 yuxk (de:hypothetical 15.7 kd protein in pbpd-coma intergenic region (orf2)) (db:swissprot) YUXK\_BACSU P40761 BACILLUS SUBTILIS 1423 -11531844 7000688624 yuxk hypothetical protein yuxk:pbpd 3-region hypothetical protein (db:pir2.dat) B55220 B55220 Bacillus subtilis 1423 -11531844 7500952831 pbpd unknown (db:genpept-bct1) (de:bacillus subtilis orf1, partial cds, penicillin-binding protein 4(pbpd) gene, complete cds, and orf2, complete cds.) (nt:orf2) (le:2760) (re:3173) (di:direct) BSU11882 U11882 g520537 Bacillus subtilis 1423 -11531844 219801 yuxk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate gene name: yugd) (le:37885) (re:38298) (di:direct) BSUB0017 Z99120 g2635646 Bacillus subtilis 1423 -11531844 1500685732 yugd unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yuga to yugd.) (le:7318) (re:7731) (di:direct) BSZ93933 Z93933 g1934785 Bacillus subtilis 1423 -11531844 170417 yuxk hypothetical protein yuxk:pbpd 3-region hypothetical protein (db:pir) B55220 B55220 Bacillus subtilis 1423 -11531844 5000689709 (de:(yuxk) (pn:hypothetical 15) (gtcfc:13.07) (ec:) (yuxk\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yuxK yuxK Bacillus subtilis 1423 10058209

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501810903	5898	28054	825	275

#### Description

6500727987 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yufK yufK Bacillus subtilis 1423 -11531845 7000693950 yufk hypothetical protein yufk (db:pir2.dat) H70008 H70008 Bacillus subtilis 1423 -11531845 1500693696 yufk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:38501) (re:39115) (di:complement) BSUB0017 Z99120 g2635647 Bacillus subtilis 1423 -11531845 7500964748 yufk unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yufk to yufv.) (le:289) (re:903) (di:complement) BSZ93937 Z93937 g1934808 Bacillus subtilis 1423 -11531845

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501810906	5899	28055	255	84

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810917	5900	28056	837	278

Description

6500727988 hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yufL yufL Bacillus subtilis 1423 -11531846 7000694878 yufL two-component sensor histidine kinase homolog yufL (cl:two-component sensor histidine kinase:sensor histidine kinase homology) (db:pir2.dat) A70009 A70009 Bacillus subtilis 1423 -11531846 1500693697 yufL (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to two-component sensor histidine kinase) (le:39236) (re:40837) (di:direct) BSUB0017 Z99120 g2635648 Bacillus subtilis 1423 -11531846 7500955340 yufL unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yufk to yufv.) (le:1024) (re:2625) (di:direct) BSZ93937 Z93937 g1934809 Bacillus subtilis 1423 -11531846

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810918	5901	28057	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810924	5902	28058	1518	505

Description

6500727989 hypothetical protein:similar to two-component response regulator (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yufM yufM Bacillus subtilis 1423 -11531847 7000694849 yufM two-component response regulator yufL homolog yufM) (cl:transcription regulator crir:response regulator homology) (db:pir2.dat) B70009 B70009 Bacillus subtilis 1423 -11531847 1500693698 yufM (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to two-component response regulator (yufL)) (le:40830) (re:41537) (di:direct) BSUB0017 Z99120 g2635649 Bacillus subtilis 1423 -11531847 7500965398 yufM unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yufk to yufv.) (le:2618) (re:3325) (di:direct) BSZ93937 Z93937 g1934810 Bacillus subtilis 1423 -11531847

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810934	5903	28059	189	62

Description

6500727990 hypothetical protein:similar to abc transporter:lipoprotein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yufN yufN Bacillus subtilis 1423 -11531848 7502851741 yufn (de:hypothetical lipoprotein yufn precursor) (db:swissprot) YUFN\_BACSU 005252 BACILLUS SUBTILIS 1423 -11531848 7000692114 yufn abc transporter lipoprotein homolog yufn (cl:abc transporter yufn) (db:pir2.dat) C70009 C70009 Bacillus subtilis 1423 -11531848 1500693699 yufn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to abc transporter (lipoprotein)) (le:42036) (re:43088) (di:direct) BSUB0017 Z99120 g2635650 Bacillus subtilis 1423 -11531848 7500955883 yufn unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yufk to yufv.) (nt:potential membrane protein) (le:3824) (re:4876) (di:direct) BSZ93937 Z93937 g1934811 Bacillus subtilis 1423 -11531848

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810935	5904	28060	414	137

Description

6500727991 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yufo yufo Bacillus subtilis 1423 -11531849 7000692101 yufo abc transporter atp-binding protein homolog yufo (cl:atp-binding cassette homology) (db:pir2.dat) D70009 D70009 Bacillus subtilis 1423 -11531849 1500693700 yufo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to abc transporter (atp-binding protein)) (le:43164) (re:44696) (di:direct) BSUB0017 Z99120 g2635651 Bacillus subtilis 1423 -11531849 7500963342 yufo unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yufk to yufv.) (nt:potential methylgalactoside transport atp binding) (le:4952) (re:6484) (di:direct) BSZ93937 Z93937 g1934812 Bacillus subtilis 1423 -11531849

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810936	5905	28061	339	112

Description

6500727992 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yufP yufP Bacillus subtilis 1423 -11531850 7000692778 yufp conserved hypothetical protein yufp (db:pir2.dat) E70009 E70009 Bacillus subtilis 1423 -11531850 1500693701 yufp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins) (le:44689) (re:45735) (di:direct) BSUB0017 Z99120 g2635652 Bacillus subtilis 1423 -11531850 7500963849 yufp unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yufk to yufv.) (le:6477) (re:7523) (di:direct) BSZ93937 Z93937 g1934813 Bacillus subtilis 1423 -11531850

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810937	5906	28062	351	116

Description

6500727993 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yufQ yufQ Bacillus subtilis 1423 -11531851 7000692779 yufq conserved hypothetical protein yufq (cl:probable ribose abc transporter rbsc-2) (db:pir2.dat) F70009 F70009 Bacillus subtilis 1423 -11531851 1500693702 yufq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins) (le:45736) (re:46695) (di:direct) BSUB0017 Z99120 g2635653 Bacillus subtilis 1423 -11531851 7500963850 yufq unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yufk to yufv.) (le:7524) (re:8483) (di:direct) BSZ93937 Z93937 g1934814 Bacillus subtilis 1423 -11531851

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810938	5907	28063	216	71

Description

6500727994 hypothetical protein:similar to organic acid transport protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yufR yufR Bacillus subtilis 1423 -11531852 7000694346 yufR organic acid transport protein homolog yufR (cl:citrate transport protein citc) (db:pir2.dat) G70009 G70009 Bacillus subtilis 1423 -11531852 1500693703 yufR (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to organic acid transport protein) (le:46849) (re:48195) (di:direct) BSUB0017 Z99120 g2635654 Bacillus subtilis 1423 -11531852 7500965036 yufR unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yufk to yufv.) (nt:potential malate permease or citrate transporter) (le:8637) (re:9983) (di:direct) BSZ93937 Z93937 g1934815 Bacillus subtilis 1423 -11531852

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810958	5908	28064	411	136

Description

6500727995 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yufs yufs Bacillus subtilis 1423 -11531853  
7000693951 yufs hypothetical protein yufs (db:pir2.dat) H70009 H70009  
Bacillus subtilis 1423 -11531853 1500693704 yufs (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21):  
from 3197001to 3414420.) (le:48231) (re:48446) (di:complement) BSUB0017  
Z99120 g2635655 Bacillus subtilis 1423 -11531853 7500964749 yufs unknown  
(db:genpept-bct1) (de:b.subtilis genomic dna fragment from yufk to yufv.)  
(le:10019) (re:10234) (di:complement) BSZ93937 Z93937 g1934816 Bacillus  
subtilis 1423 -11531853

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810961	5909	28065	366	121

Description

6500727996 hypothetical protein:similar to na+/h+ antiporter (gtcfc:12.6) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yufU yufU Bacillus subtilis 1423 -11531854 7000694294 yufu na+/h+ antiporter homolog yufu (db:pir2.dat) B70010 B70010 Bacillus subtilis 1423 -11531854 1500693706 yufu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to na+/h+ antiporter) (le:51075) (re:51506) (di:direct) BSUB0017 Z99120 g2635657 Bacillus subtilis 1423 -11531854 7500965003 yufu unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yufk to yufv.) (nt:potential na/h antiporter system orf2 or phab) (le:12863) (re:13294) (di:direct) BSZ93937 Z93937 g1934818 Bacillus subtilis 1423 -11531854

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501810962	5910	28066	234	77

Description

6500727997 hypothetical protein:similar to na+/h+ antiporter (gtcfc:12.6) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yufV yufV Bacillus subtilis 1423 -11531855 7000694295 yufv na+/h+ antiporter homolog yufv (db:pir2.dat) C70010 C70010 Bacillus subtilis 1423 -11531855 1500693707 yufv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to na+/h+ antiporter) (le:51506) (re:51847) (di:direct) BSUB0017 Z99120 g2635658 Bacillus subtilis 1423 -11531855 7500965004 yufv unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yufk to yufv.) (nt:potential na/h antiporter system orf3 or phac) (le:13294) (re:13635) (di:direct) BSZ93937 Z93937 g1934819 Bacillus subtilis 1423 -11531855

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810967	5911	28067	510	169

Description

6500727998 hypothetical protein:similar to nadh dehydrogenase:ubiquinone (gtcfc:9.12) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yufD yufD Bacillus subtilis 1423 -11531856 7000694303 yufD nadh dehydrogenase ubiquinone homolog yufD (db:pir2.dat) G70008 G70008 Bacillus subtilis 1423 -11531856 7500965010 yufD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to nadh dehydrogenase (ubiquinone)) (le:51840) (re:53282) (di:direct) BSUB0017 Z99120 g2635659 Bacillus subtilis 1423 -11531856

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810972	5912	28068	303	100

Description

6500727999 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yufC yufC Bacillus subtilis 1423 -11531857 7000693949 yufC hypothetical protein yufC (db:pir2.dat) F70008 F70008 Bacillus subtilis 1423 -11531857 1500694330 yufC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:53800) (re:54084) (di:direct) BSUB0017 Z99120 g2635660 Bacillus subtilis 1423 -11531857 7500964747 yufC unknown (db:genpept-bct1) (de:bacillus subtilis genomic dna fragment from yufa to yufe.) (le:7444) (re:7728) (di:complement) BSZ93932 Z93932 g1934775 Bacillus subtilis 1423 -11531857

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810975	5913	28069	360	119

Description

6500728000 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yufB yufB Bacillus subtilis 1423 -11531858 7000692777 yufB conserved hypothetical protein yufB (db:pir2.dat) E70008 E70008 Bacillus subtilis 1423 -11531858 1500694329 yufB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins) (le:54068) (re:54442) (di:direct) BSUB0017 Z99120 g2635661 Bacillus subtilis 1423 -11531858 7500963848 yufB unknown (db:genpept-bct1) (de:bacillus subtilis genomic dna fragment from yufa to yufe.) (le:7086) (re:7460) (di:complement) BSZ93932 Z93932 g1934774 Bacillus subtilis 1423 -11531858

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810978	5914	28070	645	214

Description

6500728001 srfb:comab:coma2:yuxo hypothetical protein:coma operon protein 2 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuxO yuxO Bacillus subtilis 1423 -11531859 64865 comab:coma2 (de:coma operon protein 2) (db:swissprot) CMA2\_BACSU P14205 BACILLUS SUBTILIS 1423 -11531859 7000684843 yuxo conserved hypothetical protein yuxo:hypothetical 14k protein coma 3 region (db:pir2.dat) B33591 B33591 Bacillus subtilis 1423 -11531859 7500878893 (sr:b.subtilis (strain 168) dna) (db:genpept-bct1) (de:b.subtilis comp and coma genes encoding competence proteins, complete cds.) (nt:a competence protein 2) (le:3388) (re:3768) (di:direct) BACCOMBA2 M22856 g142702 Bacillus subtilis 1423 -11531859 215364 yuxo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate gene name: srfb, comab; similar to) (le:54481) (re:54861) (di:complement) BSUB0017 Z99120 g2635662 Bacillus subtilis 1423 -11531859 1500685154 comab (fn:competence; early block) (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yufa to yufe.) (le:6667) (re:7047) (di:direct) BSZ93932 Z93932 g1934773 Bacillus subtilis 1423 -11531859 170043 yuxo conserved hypothetical protein yuxo:hypothetical 14k protein coma 3 region (db:pir) B33591 B33591 Bacillus subtilis 1423 -11531859 5000689908 (de:(comab) (pn:coma operon protein 2:coma operon protein 2) (gn:coma2) (gtcfc:13.12) (ec:) (cma2\_bacsu) (keggfc:11.2) (bsorffc:6.6.0) (db:gtc-bacillus subtilis)) comAB comAB Bacillus subtilis 1423 10007526

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810982	5915	28071	498	166

Description

6500728002 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuzC yuzC Bacillus subtilis 1423 -11531860 7000693988 yuzc hypothetical protein yuzc (db:pir2.dat) B70026 B70026 Bacillus subtilis 1423 -11531860 7500964780 yuzc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:59769) (re:60137) (di:direct) BSUB0017 Z99120 g2635668 Bacillus subtilis 1423 -11531860

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810985	5916	28072	456	152

Description

6500728003 comb:yufa:yuxh hypothetical protein:hypothetical 47.9 kd protein in degq 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuxH yuxH Bacillus subtilis 1423 -11531861 116481 yuxh (de:hypothetical 47.9 kd protein in degq 5'region) (db:swissprot) YUXH\_BACSU P14203 BACILLUS SUBTILIS 1423 -11531861 131476 yuxh:comb competence protein comb yuxh (cl:comb protein) (db:pir1.dat) BVBSB C33591 Bacillus subtilis 1423 -11531861 215361 (sr:b.subtilis dna) (db:genpept-bct1) (de:b.subtilis comb gene encoding b competence protein, complete cds.) (nt:b competence protein) (le:186) (re:1415) (di:direct) BACCOMBA1 M22855 g142699 Bacillus subtilis 1423 -11531861 1500685731 yuxh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate gene name: comb, yufa) (le:60113) (re:61342) (di:complement) BSUB0017 Z99120 g2635669 Bacillus subtilis 1423 -11531861 7500952826 yufa unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yufa to yufe.) (le:186) (re:1415) (di:direct) BSZ93932 Z93932 g1934768 Bacillus subtilis 1423 -11531861 5000689706 (de:(yuxh) (pn:hypothetical 47) (gtcfc:13.07) (ec:) (yuxh\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yuxH yuxH Bacillus subtilis 1423 10058206

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810995	5917	28073	1695	564

Description

6500728004 hypothetical protein:similar to nicotinate phosphoribosyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yueK yueK Bacillus subtilis 1423 -11531862 7000694315 yueK nicotinate phosphoribosyltransferase homolog yueK (db:pir2.dat) D70008 D70008 Bacillus subtilis 1423 -11531862 7500965016 yueK (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to nicotinate phosphoribosyltransferase) (le:61479) (re:62951) (di:complement) BSUB0017 Z99120 g2635670 Bacillus subtilis 1423 -11531862

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501810996	5918	28074	228	75

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811036	5919	28075	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811039	5920	28076	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811040	5921	28077	417	138

Description

6500728005 hypothetical protein:similar to pyrazinamidase/nicotinamidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yueJ yueJ Bacillus subtilis 1423 -11531863 7000694477 yuej pyrazinamidase/nicotinamidase homolog yuej (cl:hypothetical protein b1011) (db:pir2.dat) C70008 C70008 Bacillus subtilis 1423 -11531863 7500955930 yuej (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to pyrazinamidase/nicotinamidase) (le:62967) (re:63518) (di:complement) BSUB0017 Z99120 g2635671 Bacillus subtilis 1423 -11531863

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811044	5922	28078	213	70

Description

6500728006 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yueI yueI Bacillus subtilis 1423 -11531864 7000693948 yuei hypothetical protein yuei (db:pir2.dat) B70008 B70008 Bacillus subtilis 1423 -11531864 7500964746 yuei (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:63615) (re:64013) (di:complement) BSUB0017 Z99120 g2635672 Bacillus subtilis 1423 -11531864

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811046	5923	28079	696	231

Description

6500728007 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yueH yueH Bacillus subtilis 1423 -11531865  
7000693947 yueh hypothetical protein yueh (db:pir2.dat) A70008 A70008 Bacillus subtilis 1423 -11531865 7500964745 yueh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:64085) (re:64333) (di:complement) BSUB0017 Z99120 g2635673 Bacillus subtilis 1423 -11531865

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811049	5924	28080	234	77

Description

6500728008 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yueG yueG Bacillus subtilis 1423 -11531866 7000692776 yueg conserved hypothetical protein yueg (cl:bacillus subtilis conserved hypothetical protein yish) (db:pir2.dat) H70007 H70007 Bacillus subtilis 1423 -11531866 7500963847 yueg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins from b. subtilis) (le:64406) (re:64627) (di:complement) BSUB0017 Z99120 g2635674 Bacillus subtilis 1423 -11531866

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811072	5925	28081	882	294

Description

6500728009 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yueF yueF Bacillus subtilis 1423 -11531867 7000692775 yuef conserved hypothetical protein yuef (db:pir2.dat) G70007 G70007 Bacillus subtilis 1423 -11531867 7500963846 yuef (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins) (le:64687) (re:65796) (di:complement) BSUB0017 Z99120 g2635675 Bacillus subtilis 1423 -11531867

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811073	5926	28082	288	95

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811086	5927	28083	471	156

Description

6500728010 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuzE yuzE Bacillus subtilis 1423 -11531868  
7000693990 yuze hypothetical protein yuze (db:pir2.dat) D70026 D70026 Bacillus subtilis 1423 -11531868 7500964782 yuze (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:65911) (re:66300) (di:direct) BSUB0017 Z99120 g2635676 Bacillus subtilis 1423 -11531868

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811087	5928	28084	690	230

Description

6500728011 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuzF yuzF Bacillus subtilis 1423 -11531869  
7000693991 yuzf hypothetical protein yuzf (db:pir2.dat) E70026 E70026 Bacillus subtilis 1423 -11531869 7500964783 yuzf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:66341) (re:66577) (di:complement) BSUB0017 Z99120 g2635677 Bacillus subtilis 1423 -11531869

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811106	5929	28085	345	114

Description

6500728012 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yueE yueE Bacillus subtilis 1423 -11531870  
7000693946 yuee hypothetical protein yuee (db:pir2.dat) F70007 F70007 Bacillus subtilis 1423 -11531870 7500964744 yuee (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:66754) (re:67284) (di:complement) BSUB0017 Z99120 g2635678 Bacillus subtilis 1423 -11531870

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811111	5930	28086	399	132

Description

6500728013 hypothetical protein:similar to sepiapterin reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yueD yueD Bacillus subtilis 1423 -11531871 7000694577 yueD sepiapterin reductase homolog yueD (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) E70007 E70007 Bacillus subtilis 1423 -11531871 7500965176 yueD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to sepiapterin reductase) (le:67482) (re:68213) (di:complement) BSUB0017 Z99120 g2635679 Bacillus subtilis 1423 -11531871

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811130	5931	28087	1155	384

Description

6500728014 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yueC yueC Bacillus subtilis 1423 -11531872 7000693945 yueC hypothetical protein yueC (db:pir2.dat) D70007 D70007 Bacillus subtilis 1423 -11531872 7500964743 yueC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:68276) (re:68731) (di:complement) BSUB0017 Z99120 g2635680 Bacillus subtilis 1423 -11531872

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811134	5932	28088	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811139	5933	28089	1071	356

Description

6500728015 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yueB yueB Bacillus subtilis 1423 -11531873 7000693944 yueB hypothetical protein yueB (db:pir2.dat) C70007 C70007 Bacillus subtilis 1423 -11531873 7500964742 yueB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:68763) (re:71993) (di:complement) BSUB0017 Z99120 g2635681 Bacillus subtilis 1423 -11531873

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811145	5934	28090	351	116

Description

6500728016 yuea:yuka hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuka yuka Bacillus subtilis 1423 -11531874 7000692787 yuka conserved hypothetical protein yuka (db:pir2.dat) C70013 C70013 Bacillus subtilis 1423 -11531874 7500963854 yuka (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate gene name: yuea; similar to hypothetical) (le:71990) (re:75613) (di:complement) BSUB0017 Z99120 g2635682 Bacillus subtilis 1423 -11531874

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811154	5935	28091	222	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811165	5936	28092	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811170	5937	28093	300	99

Description

6500728017 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yukB yukB Bacillus subtilis 1423 -11531875 7000693957 yukb hypothetical protein yukb (db:pir2.dat) D70013 D70013 Bacillus subtilis 1423 -11531875 220360 yukb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:75613) (re:76488) (di:complement) BSUB0017 Z99120 g2635683 Bacillus subtilis 1423 -11531875 307778 yukb (db:genpept-bct1) (de:bacillus subtilis yuk(a,b,c,d,e,f), yuk(i,j,k,l,m) and ald genes.) (le:1844) (re:2719) (di:complement) BSZ82015 Z82015 g1665847 Bacillus subtilis 1423 -11531875

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811178	5938	28094	333	110

Description

6500728018 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yukC yukC Bacillus subtilis 1423 -11531876  
 7000693958 yukc hypothetical protein yukc (db:pir2.dat) E70013 E70013  
 Bacillus subtilis 1423 -11531876 220361 yukc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:76516) (re:77871) (di:complement) BSUB0017 Z99120 g2635684  
 Bacillus subtilis 1423 -11531876 307779 yukc (db:genpept-bct1) (de:b.subtilis yuk(a,b,c,d,e,f), yuk(i,j,k,l,m) and ald genes.) (le:2747) (re:4102) (di:complement) BSZ82015 Z82015 g1665848 Bacillus subtilis 1423 -11531876

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811188	5939	28095	825	274

Description

6500728019 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yukD yukD Bacillus subtilis 1423 -11531877  
 7000693959 yukd hypothetical protein yukd (db:pir2.dat) F70013 F70013  
 Bacillus subtilis 1423 -11531877 220362 yukd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:77886) (re:78125) (di:complement) BSUB0017 Z99120 g2635685  
 Bacillus subtilis 1423 -11531877 307780 yukd (db:genpept-bct1) (de:b.subtilis yuk(a,b,c,d,e,f), yuk(i,j,k,l,m) and ald genes.) (le:4117) (re:4356) (di:complement) BSZ82015 Z82015 g1665849 Bacillus subtilis 1423 -11531877

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811192	5940	28096	216	71

Description

6500728020 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yukE yukE Bacillus subtilis 1423 -11531878  
 7000693960 yuke hypothetical protein yuke (db:pir2.dat) G70013 G70013  
 Bacillus subtilis 1423 -11531878 220363 yuke (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:78269) (re:78511) (di:complement) BSUB0017 Z99120 g2635686  
 Bacillus subtilis 1423 -11531878 307781 yuke (db:genpept-bct1) (de:b.subtilis yuk(a,b,c,d,e,f), yuk(i,j,k,l,m) and ald genes.) (le:4500) (re:4742) (di:complement) BSZ82015 Z82015 g1665850 Bacillus subtilis 1423 -11531878

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811193	5941	28097	306	101

#### Description

6500728021 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yukF yukF Bacillus subtilis 1423 -11531879 7000692788 yukf conserved hypothetical protein yukf (db:pir2.dat) H70013 H70013 Bacillus subtilis 1423 -11531879 220364 yukf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins from b. subtilis) (le:79008) (re:80312) (di:direct) BSUB0017 Z99120 g2635687 Bacillus subtilis 1423 -11531879 307782 yukf (db:genpept-bct1) (de:b.subtilis yuk(a,b,c,d,e,f), yuk(i,j,k,l,m) and ald genes.) (le:5239) (re:6543) (di:direct) BSZ82015 Z82015 g1665851 Bacillus subtilis 1423 -11531879

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811194	5942	28098	258	85

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811215	5943	28099	837	278

#### Description

6500728022 yuki:yuxi hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuxI yuxI Bacillus subtilis 1423 -11531880 7000693985 yuxi hypothetical protein yuxi (db:pir2.dat) B70025 B70025 Bacillus subtilis 1423 -11531880 220366 yuxi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate gene name: yuki) (le:81629) (re:81952) (di:direct) BSUB0017 Z99120 g2635689 Bacillus subtilis 1423 -11531880 307784 yuki (db:genpept-bct1) (de:b.subtilis yuk(a,b,c,d,e,f), yuk(i,j,k,l,m) and ald genes.) (nt:yuki is new name for yuxi) (le:7860) (re:8183) (di:direct) BSZ82015 Z82015 g1665853 Bacillus subtilis 1423 -11531880

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811230	5944	28100	627	208

Description

6500728023 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yukJ yukJ Bacillus subtilis 1423 -11531881  
7000693961 yukj hypothetical protein yukj (db:pir2.dat) A70014 A70014 Bacillus subtilis 1423 -11531881 220367 yukj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:81870) (re:82307) (di:direct) BSUB0017 Z99120 g2635690 Bacillus subtilis 1423 -11531881 307785 yukj (db:genpept-bct1) (de:bacillus subtilis yuk(a,b,c,d,e,f), yuk(i,j,k,l,m) and ald genes.) (le:8101) (re:8538) (di:direct) BSZ82015 Z82015 g1665854 Bacillus subtilis 1423 -11531881

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811231	5945	28101	363	120

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811245	5946	28102	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811250	5947	28103	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811258	5948	28104	525	174

Description

6500728024 hypothetical protein:similar to antibiotic synthetase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yukL yukL Bacillus subtilis 1423 -11531882 7000692219 yukl antibiotic synthetase homolog yukl (cl:acetate--coa ligase homology:acyl carrier protein homology:gramicidin s synthetase i repeat homology) (db:pir2.dat) B70014 B70014 Bacillus subtilis 1423 -11531882 7500963424 yukl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to antibiotic synthetase) (le:82576) (re:85215) (di:complement) BSUB0017 Z99120 g2635691 Bacillus subtilis 1423 -11531882



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811263	5949	28105	405	134

Description

6500728025 hypothetical protein:similar to antibiotic synthetase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yukM yukM Bacillus subtilis 1423 -11531883 7000692220 yukm antibiotic synthetase homolog yukm (db:pir2.dat) C70014 C70014 Bacillus subtilis 1423 -11531883 220370 yukm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to antibiotic synthetase) (le:85303) (re:85518) (di:complement) BSUB0017 Z99120 g2635692 Bacillus subtilis 1423 -11531883 307788 yukm (db:genpept-bct1) (de:b.subtilis yuk(a,b,c,d,e,f), yuk(i,j,k,l,m) and ald genes.) (le:11533) (re:11748) (di:complement) BSZ82015 Z82015 g1665857 Bacillus subtilis 1423 -11531883

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811265	5950	28106	327	108

Description

6500728026 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuiI yuiI Bacillus subtilis 1423 -11531884 7000693956 yuii hypothetical protein yuii (db:pir2.dat) B70013 B70013 Bacillus subtilis 1423 -11531884 7500964754 yuii (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:94547) (re:95491) (di:complement) BSUB0017 Z99120 g2635698 Bacillus subtilis 1423 -11531884

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811272	5951	28107	960	319

Description

6500728027 hypothetical protein:similar to sulfite oxidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuiH yuiH Bacillus subtilis 1423 -11531885 7000694655 yuih sulfite oxidase homolog yuih (cl:hypothetical protein af0171) (db:pir2.dat) A70013 A70013 Bacillus subtilis 1423 -11531885 7500965239 yuih (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to sulfite oxidase) (le:95630) (re:96226) (di:complement) BSUB0017 Z99120 g2635699 Bacillus subtilis 1423 -11531885

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811276	5952	28108	489	163

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811277	5953	28109	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811289	5954	28110	195	64

Description

6500728028 hypothetical protein:similar to biotin metabolism (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuiG yuiG Bacillus subtilis 1423 -11531886 7000692288 yuig biotin metabolism homolog yuig (db:pir2.dat) H70012 H70012 Bacillus subtilis 1423 -11531886 7500963458 yuig (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to biotin metabolism) (le:96327) (re:96929) (di:direct) BSUB0017 Z99120 g2635700 Bacillus subtilis 1423 -11531886

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811292	5955	28111	804	268

Description

6500728029 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuiF yuiF Bacillus subtilis 1423 -11531887 7000692786 yuif conserved hypothetical protein yuif (cl:conserved integral membrane protein hp0758) (db:pir2.dat) G70012 G70012 Bacillus subtilis 1423 -11531887 7500955227 yuif (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins) (le:96999) (re:98327) (di:complement) BSUB0017 Z99120 g2635701 Bacillus subtilis 1423 -11531887

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811308	5956	28112	1140	380

Description

6500728030 hypothetical protein:similar to leucyl aminopeptidase (gtcfc:14.1) (ec:3.4.11.1) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuiE yuiE Bacillus subtilis 1423 -11531888 7000694160 yuie leucyl aminopeptidase homolog yuie (cl:cytosol aminopeptidase) (db:pir2.dat) F70012 F70012 Bacillus subtilis 1423 -11531888 7500964893 yuie (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to leucyl aminopeptidase) (le:98474) (re:99976) (di:complement) BSUB0017 Z99120 g2635702 Bacillus subtilis 1423 -11531888

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811323	5957	28113	324	107

Description

6500728031 hypothetical protein:similar to hypothetical proteins  
(gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuiD  
yuiD Bacillus subtilis 1423 -11531889 7000692785 yuid conserved  
hypothetical protein yuid (cl:hypothetical protein yuid) (db:pir2.dat)  
E70012 E70012 Bacillus subtilis 1423 -11531889 7500955903 yuid (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21):  
from 3197001to 3414420.) (nt:similar to hypothetical proteins) (le:100134)  
(re:100610) (di:direct) BSUB0017 Z99120 g2635703 Bacillus subtilis 1423  
-11531889

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811324	5958	28114	291	96

Description

6500728032 hypothetical protein:similar to hypothetical proteins  
(gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuiC  
yuiC Bacillus subtilis 1423 -11531890 7000692784 yuic conserved  
hypothetical protein yuic (db:pir2.dat) D70012 D70012 Bacillus subtilis 1423  
-11531890 7500963853 yuic (fn:unknown) (db:genpept-bct1) (de:bacillus  
subtilis complete genome (section 17 of 21): from 3197001to 3414420.)  
(nt:similar to hypothetical proteins) (le:100641) (re:101297)  
(di:complement) BSUB0017 Z99120 g2635704 Bacillus subtilis 1423 -11531890

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811327	5959	28115	573	190

Description

6500728033 hypothetical protein:similar to hypothetical proteins from  
b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus  
subtilis) yuiB yuiB Bacillus subtilis 1423 -11531891 7000692783 yuib  
conserved hypothetical protein yuib (db:pir2.dat) C70012 C70012 Bacillus  
subtilis 1423 -11531891 7500963852 yuib (fn:unknown) (db:genpept-bct1)  
(de:bacillus subtilis complete genome (section 17 of 21): from 3197001to  
3414420.) (nt:similar to hypothetical proteins from b. subtilis) (le:101401)  
(re:101721) (di:complement) BSUB0017 Z99120 g2635705 Bacillus subtilis 1423  
-11531891

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811331	5960	28116	516	171

Description

6500728034 yuma:yuia hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuiA yuiA Bacillus subtilis 1423 -11531892 7000692782 yuia conserved hypothetical protein yuia (db:pir2.dat) B70012 B70012 Bacillus subtilis 1423 -11531892 7500963851 yuia (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate gene name: yuma; similar to hypothetical) (le:101775) (re:101918) (di:complement) BSUB0017 Z99120 g2635706 Bacillus subtilis 1423 -11531892

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811333	5961	28117	1404	467

Description

GTC ORF with score 387 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone\_lib:mizukam) (db:genpept-pln2) (de:schizosaccharomyces pombe 42.8 kb genomic dna, clone c973.) (nt:similar to s.cerevisiae hypothetical 105.9 kd) (le:35939:36599) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811346	5962	28118	261	86

Description

6500728035 hypothetical protein:similar to nadh dehydrogenase (gtcfc:14.1) (ec:1.6.99.3) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yumB yumB Bacillus subtilis 1423 -11531893 7000694306 yumb nadh dehydrogenase homolog yumb (cl:nadh dehydrogenase) (db:pir2.dat) A70015 A70015 Bacillus subtilis 1423 -11531893 1500693715 yumb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to nadh dehydrogenase) (le:102091) (re:103311) (di:complement) BSUB0017 Z99120 g2635707 Bacillus subtilis 1423 -11531893 7500953890 yumb nadh dehydrogenase (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yuma to yulf.) (nt:putative; unknown) (le:528) (re:1748) (di:complement) BSZ93939 Z93939 g1934829 Bacillus subtilis 1423 -11531893

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811348	5963	28119	330	109

Description

6500728036 hypothetical protein:similar to thioredoxin reductase (gtcfc:9.13) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yumC yumC Bacillus subtilis 1423 -11531894 7000694689 yumc thioredoxin reductase homolog yumc (db:pir2.dat) B70015 B70015 Bacillus subtilis 1423 -11531894 1500693716 yumc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to thioredoxin reductase) (le:103643) (re:104641) (di:direct) BSUB0017 Z99120 g2635708 Bacillus subtilis 1423 -11531894 7500965272 yumc thioredoxine reductase (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yuma to yulf.) (nt:putative) (le:2080) (re:3078) (di:direct) BSZ93939 Z93939 g1934830 Bacillus subtilis 1423 -11531894

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811349	5964	28120	390	129

Description

6500728037 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuzG yuzG Bacillus subtilis 1423 -11531895 7000693992 yuzg hypothetical protein yuzg (db:pir2.dat) F70026 F70026 Bacillus subtilis 1423 -11531895 7500964784 yuzg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:104680) (re:104820) (di:complement) BSUB0017 Z99120 g2635709 Bacillus subtilis 1423 -11531895

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811366	5965	28121	648	215

Description

6500728038 hypothetical protein:similar to gmp reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yumD yumD Bacillus subtilis 1423 -11531896 7000693072 yumd gmp reductase:homolog yumd (ec:1.6.6.8) (db:pir2.dat) C70015 C70015 Bacillus subtilis 1423 -11531896 1500693717 yumd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to gmp reductase) (le:105099) (re:106079) (di:direct) BSUB0017 Z99120 g2635710 Bacillus subtilis 1423 -11531896 7500964039 yumd unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yuma to yulf.) (nt:potential inosine or guanosine 5' monophosphate) (le:3536) (re:4516) (di:direct) BSZ93939 Z93939 g1934831 Bacillus subtilis 1423 -11531896

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811380	5966	28122	765	254

Description

6500728039 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yutM yutM Bacillus subtilis 1423 -11531897 7000692798 yutM conserved hypothetical protein yutM (cl:conserved hypothetical protein hi0376) (db:pir2.dat) G70024 G70024 Bacillus subtilis 1423 -11531897 7500963864 yutM (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins) (le:107656) (re:108018) (di:complement) BSUB0017 Z99120 g2635713 Bacillus subtilis 1423 -11531897

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811400	5967	28123	366	121

Description

6500728040 hypothetical protein:similar to na+/nucleoside cotransporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yutK yutK Bacillus subtilis 1423 -11531898 7000694296 yutK na+/nucleoside cotransporter homolog yutK (cl:pyrimidine nucleoside transport protein nupc) (db:pir2.dat) E70024 E70024 Bacillus subtilis 1423 -11531898 7500965005 yutK (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to na+/nucleoside cotransporter) (le:109074) (re:110288) (di:complement) BSUB0017 Z99120 g2635715 Bacillus subtilis 1423 -11531898

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811402	5968	28124	879	292

Description

6500728041 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuzB yuzB Bacillus subtilis 1423 -11531899 7000693987 yuzB hypothetical protein yuzB (db:pir2.dat) A70026 A70026 Bacillus subtilis 1423 -11531899 7500964779 yuzB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:110425) (re:110661) (di:complement) BSUB0017 Z99120 g2635716 Bacillus subtilis 1423 -11531899

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811421	5969	28125	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811423	5970	28126	2088	695

Description

6500728042 hypothetical protein:similar to nadh dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yutJ yutJ Bacillus subtilis 1423 -11531900 7000694307 yutj nadh dehydrogenase homolog yutj (db:pir2.dat) D70024 D70024 Bacillus subtilis 1423 -11531900 7500965012 yutj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to nadh dehydrogenase) (le:110924) (re:111916) (di:direct) BSUB0017 Z99120 g2635717 Bacillus subtilis 1423 -11531900

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811430	5971	28127	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811431	5972	28128	1740	580

Description

6500728043 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuzD yuzD Bacillus subtilis 1423 -11531901 7000693989 yuzd hypothetical protein yuzd (db:pir2.dat) C70026 C70026 Bacillus subtilis 1423 -11531901 7500964781 yuzd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:112018) (re:112344) (di:complement) BSUB0017 Z99120 g2635718 Bacillus subtilis 1423 -11531901

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811438	5973	28129	288	95

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811445	5974	28130	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811464	5975	28131	888	295

Description

6500728044 hypothetical protein:similar to nifu protein homolog (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yutI yutI Bacillus subtilis 1423 -11531902 7000694322 yuti nifu protein homolog homolog yuti (cl:conserved hypothetical nifu-like protein hp1492) (db:pir2.dat) C70024 C70024 Bacillus subtilis 1423 -11531902 7500955772 yuti (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to nifu protein homolog) (le:112444) (re:112779) (di:direct) BSUB0017 Z99120 g2635719 Bacillus subtilis 1423 -11531902

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811505	5976	28132	621	206

Description

GTC ORF with score 106 to: (sr:d.melanogaster dna, clone p4.1) (db:genpept-inv) (de:d.melanogaster rna polymerase ii largest subunit gene, last 2exons.) (nt:rna polymerase ii largest subunit (, ec 2.7.7.6)) (le:<1:379) (re:133:1472) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811513	5977	28133	867	288

Description

6500728045 hypothetical protein:similar to acylaminoacyl-peptidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuxL yuxL Bacillus subtilis 1423 -11531903 7000692152 yuxl probable acylaminoacyl-peptidase:yuxl (ec:3.4.19.1) (db:pir2.dat) E70025 E70025 Bacillus subtilis 1423 -11531903 7500963379 yuxl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to acylaminoacyl-peptidase) (le:112821) (re:114794) (di:complement) BSUB0017 Z99120 g2635720 Bacillus subtilis 1423 -11531903

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811518	5978	28134	339	113

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811533	5979	28135	348	115

Description

6500728046 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yutH yutH Bacillus subtilis 1423 -11531904  
 7000693984 yuth hypothetical protein yuth (db:pir2.dat) B70024 B70024 Bacillus subtilis 1423 -11531904 7500964777 yuth (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:118388) (re:119407) (di:complement) BSUB0017 Z99120 g2635724 Bacillus subtilis 1423 -11531904

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811543	5980	28136	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811548	5981	28137	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811550	5982	28138	447	148

Description

GTC ORF with score 158 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f56a11.) (nt:coded for by c. elegans cdna yk171d3.5) (le:32282:33079:33163) (re:33024:33112:33414) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811559	5983	28139	495	164

Description

GTC ORF with score 176 to: (sr:homo sapiens (tissue library: primary b cell) cdna to mrna) (db:genpept-pr11) (de:human splicing factor sc35 mrna, complete cds.) (nt:the aas encoded by bases 200-218 and 315-341 bind) (le:156) (re:821) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811562	5984	28140	183	60
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811579	5985	28141	705	234
<u>Description</u>				

6500728047 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yutG yutG Bacillus subtilis 1423 -11531905 7000692797 yutg conserved hypothetical protein yutg (db:pir2.dat) A70024 A70024 Bacillus subtilis 1423 -11531905 7500963863 yutg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins from b. subtilis) (le:119560) (re:120060) (di:direct) BSUB0017 Z99120 g2635725 Bacillus subtilis 1423 -11531905

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811605	5986	28142	999	332
<u>Description</u>				

6500728048 hypothetical protein:similar to n-acetyl-glucosamine catabolism (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yutF yutF Bacillus subtilis 1423 -11531906 7000694274 yutf n-acetyl-glucosamine catabolism homolog yutf (cl:nagd protein) (db:pir2.dat) H70023 H70023 Bacillus subtilis 1423 -11531906 7500955837 yutf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to n-acetyl-glucosamine catabolism) (le:120087) (re:120857) (di:complement) BSUB0017 Z99120 g2635726 Bacillus subtilis 1423 -11531906

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811607	5987	28143	288	96
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811608	5988	28144	483	160

Description

6500728049 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yutE yutE Bacillus subtilis 1423 -11531907  
7000693983 yute hypothetical protein yute (db:pir2.dat) G70023 G70023  
Bacillus subtilis 1423 -11531907 7500964776 yute (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21):  
from 3197001to 3414420.) (le:120886) (re:121320) (di:complement) BSUB0017  
Z99120 g2635727 Bacillus subtilis 1423 -11531907

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811613	5989	28145	738	246

Description

6500728050 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yutD yutD Bacillus subtilis 1423 -11531908  
7000693982 yutd hypothetical protein yutd (db:pir2.dat) F70023 F70023  
Bacillus subtilis 1423 -11531908 7500964775 yutd (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21):  
from 3197001to 3414420.) (le:121344) (re:121652) (di:complement) BSUB0017  
Z99120 g2635728 Bacillus subtilis 1423 -11531908

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811631	5990	28146	573	190

Description

6500728051 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yutC yutC Bacillus subtilis 1423 -11531909  
7000693981 yutc hypothetical protein yutc (db:pir2.dat) E70023 E70023  
Bacillus subtilis 1423 -11531909 7500964774 yutc (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21):  
from 3197001to 3414420.) (le:121734) (re:122366) (di:direct) BSUB0017 Z99120  
g2635729 Bacillus subtilis 1423 -11531909

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811637	5991	28147	540	179

#### Description

6500728052 hypothetical protein:similar to lipoic acid synthetase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yutB yutB Bacillus subtilis 1423 -11531910 7000694167 yutb lipoic acid synthetase:yutb (cl:lipoic acid synthase) (ec:2.8.1.-) (db:pir2.dat) D70023 D70023 Bacillus subtilis 1423 -11531910 7500964898 yutb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to lipoic acid synthetase) (le:122382) (re:123188) (di:complement) BSUB0017 Z99120 g2635730 Bacillus subtilis 1423 -11531910

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811641	5992	28148	291	96

#### Description

6500728053 yuta:yuna hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yunA yunA Bacillus subtilis 1423 -11531911 7000693962 yuna hypothetical protein yuna (db:pir2.dat) D70015 D70015 Bacillus subtilis 1423 -11531911 7500964755 yuna (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate gene name: yuta) (le:123444) (re:124493) (di:direct) BSUB0017 Z99120 g2635731 Bacillus subtilis 1423 -11531911

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811648	5993	28149	237	78

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811655	5994	28150	663	220

#### Description

GTC ORF with score 112 to: (fn:gel formation, gastric epithelial protection) (sr:pig) (db:genpept-mam) (de:sus scrofa yorkshire/chester white/hampshire clone pgm-ss-2agastic mucin mrna, partial cds.) (nt:bases 1-105 encode a cysteine rich, non-repeat)...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811672	5995	28151	297	99

Description

6500728054 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yunB yunB Bacillus subtilis 1423 -11531912  
 7000693963 yunb hypothetical protein yunb (db:pir2.dat) E70015 E70015 Bacillus subtilis 1423 -11531912 7500964756 yunb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:124521) (re:125285) (di:complement) BSUB0017 Z99120 g2635732 Bacillus subtilis 1423 -11531912

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811687	5996	28152	408	135

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811688	5997	28153	840	279

Description

6500728055 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yunC yunC Bacillus subtilis 1423 -11531913  
 7000693964 yunc hypothetical protein yunc (db:pir2.dat) F70015 F70015 Bacillus subtilis 1423 -11531913 7500964757 yunc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:125358) (re:125663) (di:complement) BSUB0017 Z99120 g2635733 Bacillus subtilis 1423 -11531913

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811724	5998	28154	1377	459

Description

6500728056 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yunD yunD Bacillus subtilis 1423 -11531914 7000692791 yund conserved hypothetical protein yund (db:pir2.dat) G70015 G70015 Bacillus subtilis 1423 -11531914 7500963857 yund (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins) (le:125728) (re:127116) (di:complement) BSUB0017 Z99120 g2635734 Bacillus subtilis 1423 -11531914

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811728	5999	28155	636	211

Description

6500728057 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yunE yunE Bacillus subtilis 1423 -11531915  
 7000693965 yune hypothetical protein yune (db:pir2.dat) H70015 H70015  
 Bacillus subtilis 1423 -11531915 7500964758 yune (fn:unknown)  
 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21):  
 from 3197001to 3414420.) (le:127136) (re:127957) (di:complement) BSUB0017  
 Z99120 g2635735 Bacillus subtilis 1423 -11531915

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811735	6000	28156	375	124

Description

6500728058 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yunF yunF Bacillus subtilis 1423 -11531916  
 7000693966 yunf hypothetical protein yunf (db:pir2.dat) A70016 A70016  
 Bacillus subtilis 1423 -11531916 7500964759 yunf (fn:unknown)  
 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21):  
 from 3197001to 3414420.) (le:127975) (re:128829) (di:complement) BSUB0017  
 Z99120 g2635736 Bacillus subtilis 1423 -11531916

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811737	6001	28157	429	142

Description

6500728059 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yunG yunG Bacillus subtilis 1423 -11531917  
 7000693967 yung hypothetical protein yung (db:pir2.dat) B70016 B70016  
 Bacillus subtilis 1423 -11531917 7500964760 yung (fn:unknown)  
 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21):  
 from 3197001to 3414420.) (le:128861) (re:129208) (di:complement) BSUB0017  
 Z99120 g2635737 Bacillus subtilis 1423 -11531917

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811759	6002	28158	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811782	6003	28159	630	210

Description

6500728060 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yunI yunI Bacillus subtilis 1423 -11531918  
7000693968 yuni hypothetical protein yuni (db:pir2.dat) D70016 D70016  
Bacillus subtilis 1423 -11531918 7500964761 yuni (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21):  
from 3197001to 3414420.) (le:130820) (re:132415) (di:direct) BSUB0017 Z99120  
g2635739 Bacillus subtilis 1423 -11531918

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811793	6004	28160	243	80

Description

GTC ORF with score 114 to: (sr:thale cress) (db:genpept-pln2)  
(de:arabidopsis thaliana dihydrolipoylacyltransferase subunit of  
thebranched-chain alpha-keto acid dehydrogenase complex (lta1) mrna,complete  
cds.) (nt:e2 subunit) (le:34) (re:1485) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811809	6005	28161	189	62

Description

6500728061 hypothetical protein:similar to purine permease (gtcfc:14.1)  
(keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yunJ yunJ Bacillus  
subtilis 1423 -11531919 7500952814 yunj (de:hypothetical 47.1 kd protein in  
hom-mrga intergenic region) (db:swissprot) YUNJ\_BACSU 032139 BACILLUS  
SUBTILIS 1423 -11531919 7000694474 yunj purine permease homolog yunj  
(cl:xanthine permease pbux) (db:pir2.dat) E70016 E70016 Bacillus subtilis  
1423 -11531919 7500952816 yunj (fn:unknown) (db:genpept-bct1) (de:bacillus  
subtilis complete genome (section 17 of 21): from 3197001to 3414420.)  
(nt:similar to purine permease) (le:132560) (re:133909) (di:direct) BSUB0017  
Z99120 g2635740 Bacillus subtilis 1423 -11531919

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811811	6006	28162	231	76

#### Description

6500728062 hypothetical protein:similar to purine permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yunK yunK Bacillus subtilis 1423 -11531920 7500952817 yunk (de:hypothetical 44.9 kd protein in hom-mrga intergenic region) (db:swissprot) YUNK\_BACSU 032140 BACILLUS SUBTILIS 1423 -11531920 7000694475 yunk purine permease homolog yunk (cl:xanthine permease pbux) (db:pir2.dat) F70016 Bacillus subtilis 1423 -11531920 7500952819 yunk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to purine permease) (le:133915) (re:135207) (di:direct) BSUB0017 Z99120 g2635741 Bacillus subtilis 1423 -11531920

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811829	6007	28163	744	247

#### Description

6500728063 hypothetical protein:similar to uricase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yunL yunL Bacillus subtilis 1423 -11531921 7000694892 yunl uricase homolog yunl (db:pir2.dat) G70016 G70016 Bacillus subtilis 1423 -11531921 7500965429 yunl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to uricase) (le:135220) (re:136704) (di:direct) BSUB0017 Z99120 g2635742 Bacillus subtilis 1423 -11531921

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811831	6008	28164	186	61

#### Description

6500728064 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yunM yunM Bacillus subtilis 1423 -11531922 7502851742 yunm (de:hypothetical transthyretin-like protein in hom-mrga intergenic region) (db:swissprot) YUNM\_BACSU 032142 BACILLUS SUBTILIS 1423 -11531922 7000692792 yunm conserved hypothetical protein yunm (cl:escherichia coli hypothetical protein b1970) (db:pir2.dat) H70016 H70016 Bacillus subtilis 1423 -11531922 7500963858 yunm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins) (le:136683) (re:137048) (di:direct) BSUB0017 Z99120 g2635743 Bacillus subtilis 1423 -11531922



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811833	6009	28165	933	310

Description

6500728065 hypothetical protein:similar to 4-hydroxybenzoyl-coa reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurB yurB Bacillus subtilis 1423 -11531923 7000692063 yurb 4-hydroxybenzoyl-coa reductase homolog yurb (cl:isoquinoline 1-oxidoreductase alpha chain) (db:pir2.dat) A70017 A70017 Bacillus subtilis 1423 -11531923 7500963307 yurb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to 4-hydroxybenzoyl-coa reductase) (le:137809) (re:138330) (di:complement) BSUB0017 Z99120 g2635744 Bacillus subtilis 1423 -11531923

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811838	6010	28166	429	143

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811853	6011	28167	1242	413

Description

6500728066 hypothetical protein:similar to 4-hydroxybenzoyl-coa reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurC yurC Bacillus subtilis 1423 -11531924 7000692064 yurc xanthine dehydrogenase homolog (db:pir2.dat) B70017 B70017 Bacillus subtilis 1423 -11531924 7500963308 yurc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to 4-hydroxybenzoyl-coa reductase) (le:138321) (re:140558) (di:complement) BSUB0017 Z99120 g2635745 Bacillus subtilis 1423 -11531924

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811864	6012	28168	270	89

Description

6500728067 hypothetical protein:similar to 4-hydroxybenzoyl-coa reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurD yurD Bacillus subtilis 1423 -11531925 7000692065 yurd 4-hydroxybenzoyl-coa reductase homolog yurd (db:pir2.dat) C70017 C70017 Bacillus subtilis 1423 -11531925 7500963309 yurd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to 4-hydroxybenzoyl-coa reductase) (le:140559) (re:141392) (di:complement) BSUB0017 Z99120 g2635746 Bacillus subtilis 1423 -11531925

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811867	6013	28169	1317	438

Description

6500728068 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurE yurE Bacillus subtilis 1423 -11531926  
 7000693969 yure hypothetical protein yure (db:pir2.dat) D70017 D70017 Bacillus subtilis 1423 -11531926 7500964762 yure (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:141414) (re:142007) (di:complement) BSUB0017 Z99120 g2635747 Bacillus subtilis 1423 -11531926

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811884	6014	28170	579	192

Description

6500728069 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurF yurF Bacillus subtilis 1423 -11531927  
 7000693970 yurf hypothetical protein yurf (db:pir2.dat) E70017 E70017 Bacillus subtilis 1423 -11531927 7500964763 yurf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:142004) (re:142996) (di:complement) BSUB0017 Z99120 g2635748 Bacillus subtilis 1423 -11531927

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811903	6015	28171	378	125

Description

6500728070 hypothetical protein:similar to aspartate aminotransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurG yurG Bacillus subtilis 1423 -11531928 7000692239 yurg aspartate aminotransferase homolog yurg (db:pir2.dat) F70017 F70017 Bacillus subtilis 1423 -11531928 7500963437 yurg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to aspartate aminotransferase) (le:143225) (re:144475) (di:complement) BSUB0017 Z99120 g2635749 Bacillus subtilis 1423 -11531928

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811928	6016	28172	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811935	6017	28173	408	135

Description

6500728071 hypothetical protein:similar to n-carbamyl-l-amino acid amidohydrolase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurH yurH Bacillus subtilis 1423 -11531929 7000694287 yurh n-carbamyl-l-amino acid amidohydrolase homolog yurh (cl:n-carbamyl-l-amino acid amidohydrolase) (db:pir2.dat) G70017 G70017 Bacillus subtilis 1423 -11531929 7500954315 yurh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to n-carbamyl-l-amino acid amidohydrolase) (le:144492) (re:145730) (di:complement) BSUB0017 Z99120 g2635750 Bacillus subtilis 1423 -11531929

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811940	6018	28174	402	133

Description

6500728072 hypothetical protein:similar to ribonuclease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurI yurI Bacillus subtilis 1423 -11531930 7000694514 yuri ribonuclease:yuri precursor (ec:3.2.-.-) (db:pir2.dat) H70017 H70017 Bacillus subtilis 1423 -11531930 7500965147 yuri (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to ribonuclease) (le:146172) (re:147038) (di:direct) BSUB0017 Z99120 g2635751 Bacillus subtilis 1423 -11531930

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501811960	6019	28175	480	159

Description

6500728073 hypothetical protein:similar to multiple sugar abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurJ yurJ Bacillus subtilis 1423 -11531931 7000694262 yurj multiple sugar abc transporter atp-bindin homolog yurj (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) A70018 A70018 Bacillus subtilis 1423 -11531931 7500955213 yurj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to multiple sugar abc transporter) (le:147072) (re:148175) (di:complement) BSUB0017 Z99120 g2635752 Bacillus subtilis 1423 -11531931

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811964	6020	28176	642	214

Description

6500728074 hypothetical protein:similar to transcriptional regulator:gntr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurK yurK Bacillus subtilis 1423 -11531932 7502851743 yurk (de:hypothetical transcriptional regulator in hom-mrga intergenic region) (db:swissprot) YURK\_BACSU 032152 BACILLUS SUBTILIS 1423 -11531932 7000694740 yurk transcription regulator gntr family homolog yurk (cl:transcription regulator gntr) (db:pir2.dat) B70018 B70018 Bacillus subtilis 1423 -11531932 7500955356 yurk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to transcriptional regulator (gntr family)) (le:148357) (re:149085) (di:direct) BSUB0017 Z99120 g2635753 Bacillus subtilis 1423 -11531932

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811979	6021	28177	414	138

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811981	6022	28178	432	143

Description

6500728075 hypothetical protein:similar to opine catabolism (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurL yurL Bacillus subtilis 1423 -11531933 7502851744 yurl (de:hypothetical sugar kinase in hom-mrga intergenic region) (db:swissprot) YURL\_BACSU 032153 BACILLUS SUBTILIS 1423 -11531933 7000694343 yurl opine catabolism homolog yurl (db:pir2.dat) C70018 C70018 Bacillus subtilis 1423 -11531933 7500965033 yurl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to opine catabolism) (le:149110) (re:149964) (di:complement) BSUB0017 Z99120 g2635754 Bacillus subtilis 1423 -11531933

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501811983	6023	28179	768	255

Description

6500728076 hypothetical protein:similar to sugar permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurM yurM Bacillus subtilis 1423 -11531934 7502851745 yurm (de:hypothetical abc transporter permease protein yurm) (db:swissprot) YURM\_BACSU O32154 BACILLUS SUBTILIS 1423 -11531934 7000694646 yurm sugar permease homolog yurm (cl:maltose transport protein malg) (db:pir2.dat) D70018 D70018 Bacillus subtilis 1423 -11531934 7500965230 yurm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to sugar permease) (le:149978) (re:150880) (di:complement) BSUB0017 Z99120 g2635755 Bacillus subtilis 1423 -11531934

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812006	6024	28180	846	281

Description

6500728077 hypothetical protein:similar to sugar permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurN yurN Bacillus subtilis 1423 -11531935 7502851746 yurn (de:hypothetical abc transporter permease protein yurn) (db:swissprot) YURN\_BACSU O32155 BACILLUS SUBTILIS 1423 -11531935 7000694647 yurn sugar permease homolog yurn (cl:inner membrane protein ugpa) (db:pir2.dat) E70018 E70018 Bacillus subtilis 1423 -11531935 7500965231 yurn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to sugar permease) (le:150884) (re:151762) (di:complement) BSUB0017 Z99120 g2635756 Bacillus subtilis 1423 -11531935

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812022	6025	28181	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812029	6026	28182	234	77

Description

6500728078 hypothetical protein:similar to multiple sugar-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurO yurO Bacillus subtilis 1423 -11531936 7502851747 yuro (de:precursor) (db:swissprot) YURO\_BACSU O32156 BACILLUS SUBTILIS 1423 -11531936 7000694263 yuro multiple sugar-binding protein homolog yuro (db:pir2.dat) F70018 F70018 Bacillus subtilis 1423 -11531936 7500964981 yuro (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to multiple sugar-binding protein) (le:151820) (re:153088) (di:complement) BSUB0017 Z99120 g2635757 Bacillus subtilis 1423 -11531936

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812031	6027	28183	774	258

Description

6500728079 hypothetical protein:similar to opine catabolism (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurP yurP Bacillus subtilis 1423 -11531937 7000694344 yurp opine catabolism homolog yurp (db:pir2.dat) G70018 G70018 Bacillus subtilis 1423 -11531937 7500965034 yurp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to opine catabolism) (le:153169) (re:154155) (di:complement) BSUB0017 Z99120 g2635758 Bacillus subtilis 1423 -11531937

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812036	6028	28184	330	109

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812042	6029	28185	585	194

Description

6500728080 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurQ yurQ Bacillus subtilis 1423 -11531938 7502851748 yurq (de:hypothetical 14.8 kd protein in hom-mrga intergenic region) (db:swissprot) YURQ\_BACSU O32158 BACILLUS SUBTILIS 1423 -11531938 7000693971 yurq hypothetical protein yurq (db:pir2.dat) H70018 H70018 Bacillus subtilis 1423 -11531938 7500964764 yurq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:154371) (re:154745) (di:complement) BSUB0017 Z99120 g2635759 Bacillus subtilis 1423 -11531938

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812044	6030	28186	294	97

Description

6500728081 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurS yurS Bacillus subtilis 1423 -11531939  
7502851749 yurs (de:hypothetical 10.4 kd protein in hom-mrga intergenic region) (db:swissprot) YURS\_BACSU 032160 BACILLUS SUBTILIS 1423 -11531939  
7000693972 yurs hypothetical protein yurs (db:pir2.dat) B70019 B70019 Bacillus subtilis 1423 -11531939 7500964765 yurs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:156271) (re:156546) (di:direct) BSUB0017 Z99120 g2635761 Bacillus subtilis 1423 -11531939

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812050	6031	28187	477	158

Description

6500728082 hypothetical protein:similar to methylglyoxalase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurT yurT Bacillus subtilis 1423 -11531940 7000694217 yurt methylglyoxalase homolog yurt (db:pir2.dat) C70019 C70019 Bacillus subtilis 1423 -11531940 7500964942 yurt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to methylglyoxalase) (le:156610) (re:156993) (di:complement) BSUB0017 Z99120 g2635762 Bacillus subtilis 1423 -11531940

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812060	6032	28188	666	221

Description

6500728083 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurU yurU Bacillus subtilis 1423 -11531941 7000692793 yuru conserved hypothetical protein yuru (cl:methanobacterium thermoautotrophicum abc transporter chain ycf24) (db:pir2.dat) D70019 D70019 Bacillus subtilis 1423 -11531941 7500963859 yuru (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins) (le:157652) (re:159049) (di:complement) BSUB0017 Z99120 g2635763 Bacillus subtilis 1423 -11531941

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812064	6033	28189	300	99

Description

6500728084 hypothetical protein:similar to nifu protein homolog (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurV yurV Bacillus subtilis 1423 -11531942 7000694321 yurv nifu protein homolog homolog yurv (cl:yeast nitrogen fixation protein:nitrogen fixation protein homology) (db:pir2.dat) E70019 E70019 Bacillus subtilis 1423 -11531942 7500953960 yurv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to nifu protein homolog) (le:159070) (re:159513) (di:complement) BSUB0017 Z99120 g2635764 Bacillus subtilis 1423 -11531942

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812066	6034	28190	183	60

Description

GTC ORF with score 106 to: (gtcfc:8.5:9.4:10.1:10.10:10.2:12.13:12.8) (ec:2.7.1.-) (keggfc:8.5:9.4:13.3) (sgdfc:9.5.0:11.2.1:15.0.0) (db:gtc-saccharomyces cerevisiae) (keggfc:metabolism of complex lipids-sphingoglycolipid metabolism:nicotinate and ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812073	6035	28191	579	192

Description

6500728085 hypothetical protein:similar to nifs protein homolog (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurW yurW Bacillus subtilis 1423 -11531943 7000694319 yurw nifs protein homolog homolog yurw (cl:nifs protein) (db:pir2.dat) F70019 F70019 Bacillus subtilis 1423 -11531943 7500965018 yurw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to nifs protein homolog) (le:159503) (re:160723) (di:complement) BSUB0017 Z99120 g2635765 Bacillus subtilis 1423 -11531943



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812077	6036	28192	759	252

Description

6500728086 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurX yurX Bacillus subtilis 1423 -11531944 7000692794 yurX conserved hypothetical protein yurX (db:pir2.dat) G70019 G70019 Bacillus subtilis 1423 -11531944 7500963860 yurX (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins) (le:160723) (re:162036) (di:complement) BSUB0017 Z99120 g2635766 Bacillus subtilis 1423 -11531944

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812078	6037	28193	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812096	6038	28194	399	132

Description

6500728087 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurY yurY Bacillus subtilis 1423 -11531945 7000692102 yury abc transporter atp-binding protein homolog yury (cl:atp-binding cassette homology) (db:pir2.dat) H70019 H70019 Bacillus subtilis 1423 -11531945 7500963343 yury (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to abc transporter (atp-binding protein)) (le:162054) (re:162839) (di:complement) BSUB0017 Z99120 g2635767 Bacillus subtilis 1423 -11531945

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812106	6039	28195	522	174

Description

6500728088 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurZ yurZ Bacillus subtilis 1423 -11531946 7000693973 yurz hypothetical protein yurz (cl:haemophilus influenzae conserved hypothetical protein hi1053) (db:pir2.dat) A70020 A70020 Bacillus subtilis 1423 -11531946 7500964766 yurz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:163364) (re:163741) (di:complement) BSUB0017 Z99120 g2635768 Bacillus subtilis 1423 -11531946

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812109	6040	28196	420	140

#### Description

6500728089 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusa yusa Bacillus subtilis 1423 -11531947 7000692795 yusa conserved hypothetical protein yusa (cl:lipoprotein-28) (db:pir2.dat) B70020 B70020 Bacillus subtilis 1423 -11531947 7500963861 yusa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins) (le:163826) (re:164650) (di:complement) BSUB0017 Z99120 g2635769 Bacillus subtilis 1423 -11531947

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812119	6041	28197	201	66

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812120	6042	28198	765	254

#### Description

6500728090 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusB yusB Bacillus subtilis 1423 -11531948 7000692796 yusB conserved hypothetical protein yusB (cl:probable transport protein yaeE) (db:pir2.dat) C70020 C70020 Bacillus subtilis 1423 -11531948 7500963862 yusB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins) (le:164664) (re:165332) (di:complement) BSUB0017 Z99120 g2635770 Bacillus subtilis 1423 -11531948

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812139	6043	28199	1575	525

#### Description

6500728091 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusC yusC Bacillus subtilis 1423 -11531949 7000692103 yusC abc transporter atp-binding protein homolog yusC (cl:atp-binding cassette homology) (db:pir2.dat) D70020 D70020 Bacillus subtilis 1423 -11531949 7500963344 yusC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to abc transporter (atp-binding protein)) (le:165325) (re:166350) (di:complement) BSUB0017 Z99120 g2635771 Bacillus subtilis 1423 -11531949

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812142	6044	28200	195	64

Description

6500728092 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusD yusD Bacillus subtilis 1423 -11531950  
7000693974 yusd hypothetical protein yusd (db:pir2.dat) E70020 E70020 Bacillus subtilis 1423 -11531950 7500964767 yusd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:166677) (re:167021) (di:complement) BSUB0017 Z99120 g2635772 Bacillus subtilis 1423 -11531950

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812146	6045	28201	777	258

Description

6500728093 hypothetical protein:similar to thioredoxin (gtcfc:9.13) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusE yusE Bacillus subtilis 1423 -11531951 7000694687 yuse thioredoxin homolog yuse (db:pir2.dat) F70020 F70020 Bacillus subtilis 1423 -11531951 7500965270 yuse (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to thioredoxin) (le:167128) (re:167448) (di:complement) BSUB0017 Z99120 g2635773 Bacillus subtilis 1423 -11531951

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812154	6046	28202	339	112

Description

6500728094 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusF yusF Bacillus subtilis 1423 -11531952  
7000693975 yusf hypothetical protein yusf (db:pir2.dat) G70020 G70020 Bacillus subtilis 1423 -11531952 7500964768 yusf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:167450) (re:167890) (di:complement) BSUB0017 Z99120 g2635774 Bacillus subtilis 1423 -11531952

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812155	6047	28203	381	126

Description

6500728095 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusG yusG Bacillus subtilis 1423 -11531953  
7000693976 yusg hypothetical protein yusg (db:pir2.dat) H70020 H70020  
Bacillus subtilis 1423 -11531953 7500964769 yusg (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21):  
from 3197001to 3414420.) (le:167890) (re:168126) (di:complement) BSUB0017  
Z99120 g2635775 Bacillus subtilis 1423 -11531953

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812158	6048	28204	303	100

Description

6500728096 hypothetical protein:similar to glycine cleavage system protein h (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusH yusH Bacillus subtilis 1423 -11531954 7000693066 yush glycine cleavage system protein h homolog yush (cl:glycine cleavage system protein h:lipoyl/biotin-binding homology) (db:pir2.dat) A70021 A70021 Bacillus subtilis 1423 -11531954 7500955056 yush (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to glycine cleavage system protein h) (le:168182) (re:168565) (di:complement) BSUB0017 Z99120 g2635776 Bacillus subtilis 1423 -11531954

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812162	6049	28205	717	238

Description

6500728097 hypothetical protein:similar to arsenate reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusI yusI Bacillus subtilis 1423 -11531955 7000692229 yusi arsenate reductase homolog yusi (cl:hypothetical protein yjbd) (db:pir2.dat) B70021 B70021 Bacillus subtilis 1423 -11531955 7500955937 yusi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to arsenate reductase) (le:168632) (re:168988) (di:complement) BSUB0017 Z99120 g2635777 Bacillus subtilis 1423 -11531955

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812175	6050	28206	261	86

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812181	6051	28207	864	287

Description

GTC ORF with score 928 to: (fn:controls entry into the asexual developmental) (db:genpept-pln2) (de:neurospora crassa mapkk kinase (nrc-1) gene, complete cds.) (nt:nrc-1; similar to ste11 of saccharomyces) (le:232) (re:2232) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812187	6052	28208	264	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812193	6053	28209	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812212	6054	28210	1464	487

Description

6500728098 hypothetical protein:similar to butyryl-coa dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusJ yusJ Bacillus subtilis 1423 -11531956 7000692298 yusj butyryl-coa dehydrogenase homolog yusj (db:pir2.dat) C70021 C70021 Bacillus subtilis 1423 -11531956 7500963468 yusj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to butyryl-coa dehydrogenase) (le:169099) (re:170883) (di:complement) BSUB0017 Z99120 g2635778 Bacillus subtilis 1423 -11531956

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812216	6055	28211	267	89

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812226	6056	28212	207	68

Description

6500728099 hypothetical protein:similar to 3-hydroxyacyl-coa dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusL yusL Bacillus subtilis 1423 -11531957 7000692044 yusl 3-hydroxyacyl-coa dehydrogenase homolog yusl (cl:enoyl-coa hydratase homology) (db:pir2.dat) E70021 E70021 Bacillus subtilis 1423 -11531957 7500963295 yusl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to 3-hydroxyacyl-coa dehydrogenase) (le:172084) (re:174531) (di:complement) BSUB0017 Z99120 g2635780 Bacillus subtilis 1423 -11531957

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812247	6057	28213	264	87

Description

6500728100 hypothetical protein:similar to proline dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusM yusM Bacillus subtilis 1423 -11531958 7000694445 yusm proline dehydrogenase homolog yusm (cl:proline dehydrogenase homolog yusm) (db:pir2.dat) F70021 F70021 Bacillus subtilis 1423 -11531958 7500953854 yusm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to proline dehydrogenase) (le:174799) (re:175707) (di:complement) BSUB0017 Z99120 g2635781 Bacillus subtilis 1423 -11531958

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812248	6058	28214	318	106

Description

6500728101 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusN yusN Bacillus subtilis 1423 -11531959 7000693977 yusn hypothetical protein yusn (db:pir2.dat) G70021 G70021 Bacillus subtilis 1423 -11531959 7500964770 yusn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:176060) (re:176392) (di:direct) BSUB0017 Z99120 g2635782 Bacillus subtilis 1423 -11531959

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812259	6059	28215	333	110

Description

6500728102 hypothetical protein:similar to transcriptional regulator:marr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusO yusO Bacillus subtilis 1423 -11531960 7000694772 yuso transcription regulator marr family homolog yuso (cl:transcription regulator yfiv) (db:pir2.dat) H70021 H70021 Bacillus subtilis 1423 -11531960 7500955935 yuso (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to transcriptional regulator (marr family)) (le:176551) (re:177018) (di:direct) BSUB0017 Z99120 g2635783 Bacillus subtilis 1423 -11531960

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812260	6060	28216	246	81

Description

6500728103 hypothetical protein:similar to multidrug-efflux transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusP yusP Bacillus subtilis 1423 -11531961 7000694256 yusp multidrug-efflux transporter homolog yusp (cl:multidrug-efflux transporter) (db:pir2.dat) A70022 A70022 Bacillus subtilis 1423 -11531961 7500955415 yusp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to multidrug-efflux transporter) (le:177015) (re:178640) (di:direct) BSUB0017 Z99120 g2635784 Bacillus subtilis 1423 -11531961

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812261	6061	28217	192	63

Description

6500728104 hypothetical protein:similar to acyloate catabolism (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusQ yusQ Bacillus subtilis 1423 -11531962 7000692153 yusq acyloate catabolism homolog yusq (cl:hypothetical protein yrdn) (db:pir2.dat) B70022 B70022 Bacillus subtilis 1423 -11531962 7500963380 yusq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to acyloate catabolism) (le:178676) (re:179059) (di:complement) BSUB0017 Z99120 g2635785 Bacillus subtilis 1423 -11531962

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812263	6062	28218	345	114

Description

6500728105 hypothetical protein:similar to 3-oxoacyl-acyl-carrier protein reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusR yusR Bacillus subtilis 1423 -11531963 7000692055 yusr 3-oxoacyl-acyl-carrier protein reductase homolog yusr (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) C70022 C70022 Bacillus subtilis 1423 -11531963 7500963300 yusr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to 3-oxoacyl-acyl-carrier protein) (le:179078) (re:179467) (di:complement) BSUB0017 Z99120 g2635786 Bacillus subtilis 1423 -11531963

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812279	6063	28219	1020	339

Description

GTC ORF with score 1127 to: (sr:grass mildew) (db:genpept) (ec:1.14.14.1) (de:erysiphe graminis f. sp. hordei eburicol 14alpha demethylase(cyp51) gene, complete cds.) (nt:cytochrome p450 sterol 14-demethylase) (le:164:461:711) (re:409:658:1835) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812289	6064	28220	219	72

Description

6500728106 hypothetical protein:similar to 3-oxoacyl-acyl-carrier protein reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusS yusS Bacillus subtilis 1423 -11531964 7000692056 yuss 3-oxoacyl-acyl-carrier protein reductase homolog yuss (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) D70022 D70022 Bacillus subtilis 1423 -11531964 7500963301 yuss (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to 3-oxoacyl-acyl-carrier protein) (le:179489) (re:179818) (di:complement) BSUB0017 Z99120 g2635787 Bacillus subtilis 1423 -11531964



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812314	6065	28221	483	160

Description

6500728107 hypothetical protein:similar to transcriptional regulator:lysr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusT yusT Bacillus subtilis 1423 -11531965 7000694760 yust transcription regulator lysr family homolog yust (cl:pseudomonas putida regulatory protein catr) (db:pir2.dat) E70022 E70022 Bacillus subtilis 1423 -11531965 7500965330 yust (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to transcriptional regulator (lysr family)) (le:179952) (re:180839) (di:direct) BSUB0017 Z99120 g2635788 Bacillus subtilis 1423 -11531965

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812331	6066	28222	480	159

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812341	6067	28223	1569	522

Description

6500728108 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusU, yusU Bacillus subtilis 1423 -11531966 7000693978 yusu hypothetical protein yusu (db:pir2.dat) F70022 F70022 Bacillus subtilis 1423 -11531966 7500964771 yusu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:180859) (re:181146) (di:complement) BSUB0017 Z99120 g2635789 Bacillus subtilis 1423 -11531966

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812344	6068	28224	360	119

Description

6500728109 hypothetical protein:similar to iron:iii dicitrate transport permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusV yusV Bacillus subtilis 1423 -11531967 7000694131 yusv iron iii dicitrate transport permease homolog yusv (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) G70022 G70022 Bacillus subtilis 1423 -11531967 7500955193 yusv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to iron(iii) dicitrate transport permease) (le:181171) (re:181998) (di:complement) BSUB0017 Z99120 g2635790 Bacillus subtilis 1423 -11531967

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812352	6069	28225	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812359	6070	28226	1509	503

Description

6500728110 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yusW yusW Bacillus subtilis 1423 -11531968  
7000693979 yusw hypothetical protein yusw (db:pir2.dat) H70022 H70022  
Bacillus subtilis 1423 -11531968 7500964772 yusw (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21):  
from 3197001to 3414420.) (le:182216) (re:182653) (di:complement) BSub0017  
Z99120 g2635791 Bacillus subtilis 1423 -11531968

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812362	6071	28227	279	92

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812369	6072	28228	465	154

Description

GTC ORF with score 161 to: (sr:caenorhabditis elegans strain=bristol n2)  
(db:genpept-inv) (de:caenorhabditis elegans cosmid f41e6.) (nt:coded for by  
c. elegans cDNA yk9a5.5; coded for by) (le:19297:20061:20687:20987)  
(re:19568:20637:20941:21895) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812384	6073	28229	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812387	6074	28230	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812390	6075	28231	363	120

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812425	6076	28232	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812431	6077	28233	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812433	6078	28234	810	269

Description

6500728111 hypothetical protein:similar to oligoendopeptidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusX yusX Bacillus subtilis 1423 -11531969 7000694335 yusx oligoendopeptidase homolog yusx (db:pir2.dat) A70023 A70023 Bacillus subtilis 1423 -11531969 7500965029 yusx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to oligoendopeptidase) (le:182763) (re:184265) (di:complement) BSUB0017 Z99120 g2635792 Bacillus subtilis 1423 -11531969

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812435	6079	28235	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812436	6080	28236	345	114

Description

6500728112 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusY yusY Bacillus subtilis 1423 -11531970  
7000693980 yusy conserved hypothetical protein yusy (db:pir2.dat) B70023  
B70023 Bacillus subtilis 1423 -11531970 7500964773 yusy (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21):  
from 3197001to 3414420.) (le:184262) (re:184558) (di:complement) BSUB0017  
Z99120 g2635793 Bacillus subtilis 1423 -11531970

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812441	6081	28237	258	85

Description

6500728113 yvxa:yusz hypothetical protein:similar to retinol dehydrogenase  
(gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusZ  
yusZ Bacillus subtilis 1423 -11531971 7000694507 yusz retinol dehydrogenase  
homolog yusz (cl:retinol dehydrogenase:short-chain alcohol dehydrogenase  
homology) (db:pir2.dat) C70023 C70023 Bacillus subtilis 1423 -11531971  
6000691537 yusz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis  
complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate  
gene name: yvxa; similar to retinol) (le:184692) (re:185534) (di:direct)  
BSUB0017 Z99120 g2635794 Bacillus subtilis 1423 -11531971 7500965145 yuxa  
(db:genpept-bct1) (de:b.subtilis genomic dna fragment from citg to yirg.)  
(nt:putative orf) (le:6270) (re:7112) (di:complement) BSZ93941 Z93941  
g2624002 Bacillus subtilis 1423 -11531971

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812450	6082	28238	480	159

Description

6500728114 hypothetical protein:similar to serine protease do (gtcfc:10.11)  
(keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvtB yvtB Bacillus  
subtilis 1423 -11531972 7000694579 yvtb serine proteinase do homolog yvtb  
(db:pir2.dat) F70048 F70048 Bacillus subtilis 1423 -11531972 6000691539  
yvtb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome  
(section 17 of 21): from 3197001to 3414420.) (nt:similar to serine protease  
do) (le:186129) (re:186803) (di:complement) BSUB0017 Z99120 g2635796  
Bacillus subtilis 1423 -11531972 7500965178 yirf (db:genpept-bct1)  
(de:b.subtilis genomic dna fragment from citg to yirg.) (nt:putative orf)  
(le:5001) (re:5675) (di:direct) BSZ93941 Z93941 g2624000 Bacillus subtilis  
1423 -11531972

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812453	6083	28239	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812454	6084	28240	486	162

Description

6500728115 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvtA yvtA Bacillus subtilis 1423 -11531973  
7000694035 yvta hypothetical protein yvta (db:pir2.dat) E70048 E70048 Bacillus subtilis 1423 -11531973 6000691541 yvta (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:187140) (re:187505) (di:complement) BSUB0017 Z99120 g2635797 Bacillus subtilis 1423 -11531973 7500964820 yire (db:genpept-bct1) (de:b.subtilis genomic dna fragment from citg to yirg.) (nt:putative orf) (le:4299) (re:4664) (di:direct) BSZ93941 Z93941 g2623999 Bacillus subtilis 1423 -11531973

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812455	6085	28241	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812466	6086	28242	813	270

Description

6500728116 hypothetical protein:similar to two-component response regulator (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvqA yvqA Bacillus subtilis 1423 -11531974 7000694852 yvqa two-component response regulator yvqb homolog yvqa) (cl:ompr protein:response regulator homology) (db:pir2.dat) C70045 C70045 Bacillus subtilis 1423 -11531974 7000694853 yvqa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to two-component response regulator (yvqb)) (le:187783) (re:188460) (di:direct) BSUB0017 Z99120 g2635798 Bacillus subtilis 1423 -11531974 7500965401 yvqa putative transcriptional regulatory protein (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:41827) (re:42504) (di:complement) BS43KBDNA AJ223978 g2832828 Bacillus subtilis 1423 -11531974

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812472	6087	28243	297	98

Description

6500728117 hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvqB yvqB Bacillus subtilis 1423 -11531975 7000694881 yvqb two-component sensor histidine kinase homolog yvqb (db:pir2.dat) D70045 D70045 Bacillus subtilis 1423 -11531975 7000694882 yvqb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to two-component sensor histidine kinase) (le:188457) (re:189812) (di:direct) BSUB0017 Z99120 g2635799 Bacillus subtilis 1423 -11531975 7500965420 yvqb putative sensory protein kinase:yvqb (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:40475) (re:41830) (di:complement) BS43KBDNA AJ223978 g2832827 Bacillus subtilis 1423 -11531975

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812473	6088	28244	210	69

Description

6500728118 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yuxN yuxN Bacillus subtilis 1423 -11531976 7000692799 yuxn conserved hypothetical protein yuxn (db:pir2.dat) F70025 F70025 Bacillus subtilis 1423 -11531976 7000692800 yuxn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins from b. subtilis) (le:190172) (re:191047) (di:direct) BSUB0017 Z99120 g2635800 Bacillus subtilis 1423 -11531976 7500963865 yuxn yuxn protein (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:39240) (re:40115) (di:complement) BS43KBDNA AJ223978 g2832826 Bacillus subtilis 1423 -11531976

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812474	6089	28245	219	72

Description

6500728119 hypothetical protein:similar to two-component response regulator (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvqC yvqC Bacillus subtilis 1423 -11531977 7000694854 yvqc two-component response regulator yvqe homolog yvqc) (cl:regulatory protein coma:response regulator homology) (db:pir2.dat) E70045 E70045 Bacillus subtilis 1423 -11531977 7000694855 yvqc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to two-component response regulator (yvqe)) (le:196481) (re:197116) (di:complement) BSUB0017 Z99120 g2635805 Bacillus subtilis 1423 -11531977 7500965402 yvqc yvqc protein (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:33171) (re:33806) (di:direct) BS43KBDNA AJ223978 g2832821 Bacillus subtilis 1423 -11531977

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812475	6090	28246	333	110

Description

6500728120 hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvqE yvqE Bacillus subtilis 1423 -11531978 7000694883 yvqe two-component sensor histidine kinase homolog yvqe (db:pir2.dat) F70045 F70045 Bacillus subtilis 1423 -11531978 7000694884 yvqe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to two-component sensor histidine kinase) (le:197094) (re:198176) (di:complement) BSUB0017 Z99120 g2635806 Bacillus subtilis 1423 -11531978 7500965421 yvqe yvqe protein (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:32111) (re:33193) (di:direct) BS43KBDNA AJ223978 g2832820 Bacillus subtilis 1423 -11531978

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812476	6091	28247	255	84

Description

6500728121 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvqF yvqF Bacillus subtilis 1423 -11531979 7000694026 yvqf hypothetical protein yvqf (db:pir2.dat) G70045 G70045 Bacillus subtilis 1423 -11531979 7000694027 yvqf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:198173) (re:198898) (di:complement) BSUB0017 Z99120 g2635807 Bacillus subtilis 1423 -11531979 7500964815 yvqf yvqf protein (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:31389) (re:32114) (di:direct) BS43KBDNA AJ223978 g2832819 Bacillus subtilis 1423 -11531979

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812484	6092	28248	1314	438

Description

6500728122 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvqG yvqG Bacillus subtilis 1423 -11531980  
7000694028 yvqg hypothetical protein yvqg (db:pir2.dat) H70045 H70045  
Bacillus subtilis 1423 -11531980 7000694029 yvqg (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21):  
from 3197001to 3414420.) (le:198932) (re:199654) (di:complement) BSUB0017  
Z99120 g2635808 Bacillus subtilis 1423 -11531980 7500964816 yvqg yvqg  
protein (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from  
yvsa to yvqa.) (le:30633) (re:31355) (di:direct) BS43KBDNA AJ223978 g2832818  
Bacillus subtilis 1423 -11531980

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812501	6093	28249	2364	788

Description

GTC ORF with score 644 to: (fn:involved in production of the virulence  
factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide  
synthase (pksl) gene,complete cds.) (le:1324:1599:2141:2703)  
(re:1524:2083:2661:3353) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812518	6094	28250	306	101

Description

6500728123 hypothetical protein:similar to hypothetical proteins from  
b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus  
subtilis) yvqH yvqH Bacillus subtilis 1423 -11531981 7500952857 yvqh  
(de:hypothetical 25.7 kd protein in gerac-fhuc intergenic region)  
(db:swissprot) YVQH\_BACSU O32201 BACILLUS SUBTILIS 1423 -11531981  
7000692840 yvqh conserved hypothetical protein yvqh (db:pir2.dat) A70046  
A70046 Bacillus subtilis 1423 -11531981 7500952859 yvqh (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21):  
from 3197001to 3414420.) (nt:similar to hypothetical proteins from b.  
subtilis) (le:199904) (re:200581) (di:complement) BSUB0017 Z99120 g2635809  
Bacillus subtilis 1423 -11531981 7000692841 yvqh yvqh protein  
(db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to  
yvqa.) (le:29706) (re:30383) (di:direct) BS43KBDNA AJ223978 g2832817  
Bacillus subtilis 1423 -11531981



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812526	6095	28251	549	183

Description

6500728124 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvqI yvqI Bacillus subtilis 1423 -11531982  
7000694030 yvqi hypothetical protein yvqi (db:pir2.dat) B70046 B70046 Bacillus subtilis 1423 -11531982 7000694031 yvqi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:200608) (re:200988) (di:complement) BSUB0017 Z99120 g2635810 Bacillus subtilis 1423 -11531982 7500964817 yvqi yvqi protein (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:29299) (re:29679) (di:direct) BS43KBDNA AJ223978 g2832816 Bacillus subtilis 1423 -11531982

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812542	6096	28252	630	210

Description

6500728125 hypothetical protein:similar to macrolide-efflux protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvqJ yvqJ Bacillus subtilis 1423 -11531983 7000694181 yvqj macrolide-efflux protein homolog yvqj (db:pir2.dat) C70046 C70046 Bacillus subtilis 1423 -11531983 7000694182 yvqj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to macrolide-efflux protein) (le:201150) (re:202418) (di:complement) BSUB0017 Z99120 g2635811 Bacillus subtilis 1423 -11531983 7500964908 yvqj putative macrolide-efflux determinant:yvqj (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:27869) (re:29137) (di:direct) BS43KBDNA AJ223978 g2832815 Bacillus subtilis 1423 -11531983

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812550	6097	28253	435	144

Description

6500728126 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvqK yvqK Bacillus subtilis 1423 -11531984 7000692842 yvqk conserved hypothetical protein yvqk (db:pir2.dat) D70046 D70046 Bacillus subtilis 1423 -11531984 6000691556 yvqk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins) (le:202595) (re:203176) (di:complement) BSUB0017 Z99120 g2635812 Bacillus subtilis 1423 -11531984 7000692843 yvqk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:45) (re:626) (di:complement) BSUB0018 Z99121 g2635828 Bacillus subtilis 1423 -11531984 7500963891 yvqk yvqk protein (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:27111) (re:27692) (di:direct) BS43KBDNA AJ223978 g2832814 Bacillus subtilis 1423 -11531984

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812552	6098	28254	432	143

Description

6500728127 hypothetical protein:similar to iron transport system (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvrA yvrA Bacillus subtilis 1423 -11531985 7000694123 yvrA iron transport system homolog yvrA (cl:atp-binding cassette homology) (db:pir2.dat) E70046 E70046 Bacillus subtilis 1423 -11531985 6000691558 yvrA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to iron transport system) (le:203199) (re:204527) (di:complement) BSUB0017 Z99120 g2635813 Bacillus subtilis 1423 -11531985 7000694124 yvrA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to iron transport system) (le:649) (re:1977) (di:complement) BSUB0018 Z99121 g2635829 Bacillus subtilis 1423 -11531985 7500964875 yvrA putative metal binding protein:yvrA (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:25760) (re:27088) (di:direct) BS43KBDNA AJ223978 g2832813 Bacillus subtilis 1423 -11531985

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812557	6099	28255	285	94

Description

6500728128 hypothetical protein:similar to iron permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvrB yvrB Bacillus subtilis 1423 -11531986 7000694121 yvrB iron permease homolog yvrB (db:pir2.dat) F70046 F70046 Bacillus subtilis 1423 -11531986 6000691560 yvrB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to iron permease) (le:204527) (re:205588) (di:complement) BSUB0017 Z99120 g2635814 Bacillus subtilis 1423 -11531986 7000694122 yvrB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to iron permease) (le:1977) (re:3038) (di:complement) BSUB0018 Z99121 g2635830 Bacillus subtilis 1423 -11531986 7500964874 yvrB putative hemin permease:yvrB (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:24699) (re:25760) (di:direct) BS43KBDNA AJ223978 g2832812 Bacillus subtilis 1423 -11531986

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812561	6100	28256	615	205

Description

6500728129 hypothetical protein:similar to iron-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvrC yvrC Bacillus subtilis 1423 -11531987 7000694133 yvrC iron-binding protein homolog yvrC (db:pir2.dat) G70046 G70046 Bacillus subtilis 1423 -11531987 6000691562 yvrC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to iron-binding protein) (le:205551) (re:206495) (di:complement) BSUB0017 Z99120 g2635815 Bacillus subtilis 1423 -11531987 7000694134 yvrC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to iron-binding protein) (le:3001) (re:3945) (di:complement) BSUB0018 Z99121 g2635831 Bacillus subtilis 1423 -11531987 7500964878 yvrC putative metal binding protein:yvrC (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:23792) (re:24736) (di:direct) BS43KBDNA AJ223978 g2832811 Bacillus subtilis 1423 -11531987

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812562	6101	28257	1131	376

Description

6500728130 hypothetical protein:similar to ketoacyl-carrier protein reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvrD yvrD Bacillus subtilis 1423 -11531988 7000694137 yvrD ketoacyl-carrier protein reductase homolog yvrD (cl:ribitol dehydrogenase:short-chain alcohol dehydrogenase homology) (db:pir2.dat) H70046 H70046 Bacillus subtilis 1423 -11531988 6000691564 yvrD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to ketoacyl-carrier protein reductase) (le:206893) (re:207684) (di:direct) BSUB0017 Z99120 g2635816 Bacillus subtilis 1423 -11531988 7000694138 yvrD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to ketoacyl-carrier protein reductase) (le:4343) (re:5134) (di:direct) BSUB0018 Z99121 g2635832 Bacillus subtilis 1423 -11531988 7500953786 yvrD putative ketoreductase:yvrD (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:22603) (re:23394) (di:complement) BS43KBDNA AJ223978 g2832810 Bacillus subtilis 1423 -11531988

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812563	6102	28258	435	144

Description

6500728131 hypothetical protein:similar to rna polymerase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvrE yvrE Bacillus subtilis 1423 -11531989 7500952861 yvre (de:hypothetical 33.2 kd protein in gerac-fhuc intergenic region) (db:swissprot) YVRE\_BACSU 034940 BACILLUS SUBTILIS 1423 -11531989 7000694561 yvre rna polymerase homolog yvre (cl:senescence marker protein-30) (db:pir2.dat) A70047 A70047 Bacillus subtilis 1423 -11531989 7000694562 yvre (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to rna polymerase) (le:207722) (re:208600) (di:complement) BSUB0017 Z99120 g2635817 Bacillus subtilis 1423 -11531989 6000691566 yvre (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to rna polymerase) (le:5172) (re:6050) (di:complement) BSUB0018 Z99121 g2635833 Bacillus subtilis 1423 -11531989 7500952864 yvre putative dna directed rna polymerase:yvre (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:21687) (re:22565) (di:direct) BS43KBDNA AJ223978 g2832808 Bacillus subtilis 1423 -11531989

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812567	6103	28259	681	226

Description

GTC ORF with score 132 to: (or:Boreogadus saida) (db:genpept-vrt)  
 (de:boreogadus saida antifreeze glycopeptide afgp polyprotein precursorgene,  
 complete cds.) (nt:cleavage of polyprotein at conserved spacers r or)  
 (le:209:281) (re:211:1801) (di:directjoin)

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812572	6104	28260	474	157

Description

6500728132 hypothetical protein:similar to two-component sensor histidine  
 kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis)  
 yvrG yvrG Bacillus subtilis 1423 -11531990 7000694885 yvrg two-component  
 sensor histidine kinase homolog yvrg (db:pir2.dat) B70047 B70047 Bacillus  
 subtilis 1423 -11531990 6000691568 yvrg (fn:unknown) (db:genpept-bct1)  
 (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to  
 3414420.) (nt:similar to two-component sensor histidine kinase) (le:208672)  
 (re:210393) (di:complement) BSUB0017 Z99120 g2635818 Bacillus subtilis 1423  
 -11531990 7000694886 yvrg (fn:unknown) (db:genpept-bct1) (de:bacillus  
 subtilis complete genome (section 18 of 21): from 3399551to 3609060.)  
 (nt:similar to two-component sensor histidine kinase) (le:6122) (re:7843)  
 (di:complement) BSUB0018 Z99121 g2635834 Bacillus subtilis 1423 -11531990  
 7500965422 yvrg putative sensory protein kinase:yvrg (db:genpept-bct2)  
 (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:19894)  
 (re:21615) (di:direct) BS43KBDNA AJ223978 g2832807 Bacillus subtilis 1423  
 -11531990

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812602	6105	28261	1500	499

Description

6500728133 hypothetical protein:similar to two-component response regulator (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvrH Bacillus subtilis 1423 -11531991 7000694856 yvrh two-component response regulator yvrg homolog yvrh) (cl:response regulator homology) (db:pir2.dat) C70047 C70047 Bacillus subtilis 1423 -11531991 6000691570 yvrh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to two-component response regulator (yvrg)) (le:210411) (re:211520) (di:complement) BSUB0017 Z99120 g2635819 Bacillus subtilis 1423 -11531991 7000694857 yvrh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to two-component response regulator (yvrg)) (le:7861) (re:8970) (di:complement) BSUB0018 Z99121 g2635835 Bacillus subtilis 1423 -11531991 7500965403 yvrh putative dna binding response regulator:yvrh (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:18767) (re:19876) (di:direct) BS43KBDNA AJ223978 g2832806 Bacillus subtilis 1423 -11531991

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812606	6106	28262	465	154

Description

6500728134 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvrI yvrI Bacillus subtilis 1423 -11531992 7000694032 yvri hypothetical protein yvri (db:pir2.dat) D70047 D70047 Bacillus subtilis 1423 -11531992 6000691572 yvri (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:211524) (re:212099) (di:complement) BSUB0017 Z99120 g2635820 Bacillus subtilis 1423 -11531992 7500964818 yvri (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:8974) (re:9549) (di:complement) BSUB0018 Z99121 g2635836 Bacillus subtilis 1423 -11531992

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812618	6107	28263	966	321

Description

6500728135 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvrK yvrK Bacillus subtilis 1423 -11531993 7000692844 yvrk conserved hypothetical protein yvrk (cl:conserved hypothetical protein yoan) (db:pir2.dat) E70047 E70047 Bacillus subtilis 1423 -11531993 6000691574 yvrk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins) (le:212528) (re:213685) (di:direct) BSUB0017 Z99120 g2635821 Bacillus subtilis 1423 -11531993 7000692845 yvrk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:9978) (re:11135) (di:direct) BSUB0018 Z99121 g2635837 Bacillus subtilis 1423 -11531993 7500955955 yvrk yvrk protein (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:16602) (re:17759) (di:complement) BS43KBDNA AJ223978 g2832803 Bacillus subtilis 1423 -11531993

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812628	6108	28264	1086	361

Description

6500728136 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvrL yvrL Bacillus subtilis 1423 -11531994 7000694033 yvrL hypothetical protein yvrL (db:pir2.dat) F70047 F70047 Bacillus subtilis 1423 -11531994 6000691576 yvrL (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:213746) (re:214156) (di:direct) BSUB0017 Z99120 g2635822 Bacillus subtilis 1423 -11531994 7000694034 yvrL (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:11196) (re:11606) (di:direct) BSUB0018 Z99121 g2635838 Bacillus subtilis 1423 -11531994 7500964819 yvrL yvrL protein (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:16131) (re:16541) (di:complement) BS43KBDNA AJ223978 g2832802 Bacillus subtilis 1423 -11531994

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812631	6109	28265	1137	378

Description

6500728137 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvrM yvrM Bacillus subtilis 1423 -11531995 7000692846 yvrM conserved hypothetical protein yvrM (db:pir2.dat) G70047 G70047 Bacillus subtilis 1423 -11531995 6000691578 yvrM (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins) (le:214190) (re:214951) (di:complement) BSUB0017 Z99120 g2635823 Bacillus subtilis 1423 -11531995 7500963892 yvrM (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:11640) (re:12401) (di:complement) BSUB0018 Z99121 g2635839 Bacillus subtilis 1423 -11531995

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812659	6110	28266	594	197

Description

6500728138 yzib:yvrn hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvrN yvrN Bacillus subtilis 1423 -11531996 7000692847 yvrn conserved hypothetical protein yvrn (db:pir2.dat) H70047 H70047 Bacillus subtilis 1423 -11531996 6000691580 yvrn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate gene name: yzib; similar to hypothetical) (le:214984) (re:215439) (di:complement) BSUB0017 Z99120 g2635824 Bacillus subtilis 1423 -11531996 7500963893 yvrn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: yzib; similar to hypothetical) (le:12434) (re:12889) (di:complement) BSUB0018 Z99121 g2635840 Bacillus subtilis 1423 -11531996



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812661	6111	28267	636	211

Description

6500728139 hypothetical protein:similar to amino acid abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvrO yvrO Bacillus subtilis 1423 -11531997 7000692187 yvro amino acid abc transporter atp-binding pr homolog yvro (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) A70048 A70048 Bacillus subtilis 1423 -11531997 6000691582 yvro (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to amino acid abc transporter (atp-binding) (le:215544) (re:216101) (di:complement) BSUB0017 Z99120 g2635825 Bacillus subtilis 1423 -11531997 7500955273 yvro (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to amino acid abc transporter (atp-binding) (le:12994) (re:13551) (di:complement) BSUB0018 Z99121 g2635841 Bacillus subtilis 1423 -11531997

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812666	6112	28268	222	73

Description

6500728140 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvrP yvrP Bacillus subtilis 1423 -11531998 7000692848 yvrp conserved hypothetical protein yvrp (db:pir2.dat) B70048 B70048 Bacillus subtilis 1423 -11531998 6000691584 yvrp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to hypothetical proteins from b. subtilis) (le:216085) (re:217278) (di:complement) BSUB0017 Z99120 g2635826 Bacillus subtilis 1423 -11531998 7000692849 yvrp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins from b. subtilis) (le:13535) (re:14728) (di:complement) BSUB0018 Z99121 g2635842 Bacillus subtilis 1423 -11531998 7500963894 yvrp yvrp protein (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:13009) (re:14202) (di:direct) BS43KBDNA AJ223978 g2832799 Bacillus subtilis 1423 -11531998

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812667	6113	28269	1611	536

#### Description

6500728141 hypothetical protein:similar to abc transporter:amino acid permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvsh yvsh Bacillus subtilis 1423 -11531999 7000692074 yvsh abc transporter amino acid permease homolog yvsh (cl:l-lysine transport protein) (db:pir2.dat) D70048 D70048 Bacillus subtilis 1423 -11531999 7000692075 yvsh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to abc transporter (amino acid permease)) (le:19168) (re:20577) (di:complement) BSUB0018 Z99121 g2635847 Bacillus subtilis 1423 -11531999 7500963316 yvsh putative arginine ornithine antiporter:yvsh (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:7160) (re:8569) (di:direct) BS43KBDNA AJ223978 g2832794 Bacillus subtilis 1423 -11531999

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812680	6114	28270	348	115

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812683	6115	28271	183	60

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812695	6116	28272	195	64

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812696	6117	28273	1323	440

Description

6500728142 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvsG yvsG Bacillus subtilis 1423 -11532000 7000692850 yvsG conserved hypothetical protein yvsG (db:pir2.dat) C70048 C70048 Bacillus subtilis 1423 -11532000 7000692851 yvsG (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:21284) (re:21766) (di:direct) BSUB0018 Z99121 g2635848 Bacillus subtilis 1423 -11532000 7500963895 yvsG yvsG protein (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:5971) (re:6453) (di:complement) BS43KBDNA AJ223978 g2832793 Bacillus subtilis 1423 -11532000

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812698	6118	28274	501	166

Description

6500728143 yvsf:yvgj hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvgJ yvgJ Bacillus subtilis 1423 -11532001 7000692828 yvgj conserved hypothetical protein yvgj (db:pir2.dat) G70039 G70039 Bacillus subtilis 1423 -11532001 7000692829 yvgj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: yvsf; similar to hypothetical) (le:21866) (re:23719) (di:direct) BSUB0018 Z99121 g2635849 Bacillus subtilis 1423 -11532001 7500963885 yvgj putative molybdate binding protein:yvgj (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:4018) (re:5871) (di:complement) BS43KBDNA AJ223978 g2832792 Bacillus subtilis 1423 -11532001

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812705	6119	28275	549	182

Description

6500728144 yvse:yvgk hypothetical protein:similar to molybdenum-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvgK yvgK Bacillus subtilis 1423 -11532002 7000694225 yvgk molybdenum-binding protein homolog yvgk (db:pir2.dat) H70039 H70039 Bacillus subtilis 1423 -11532002 7000694226 yvgk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: yvse; similar to) (le:23747) (re:24673) (di:complement) BSUB0018 Z99121 g2635850 Bacillus subtilis 1423 -11532002 7500964948 yvgk yvgk protein (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:3064) (re:3990) (di:direct) BS43KBDNA AJ223978 g2832791 Bacillus subtilis 1423 -11532002

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812713	6120	28276	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812715	6121	28277	330	110

Description

6500728145 yvsd:yvgl hypothetical protein:similar to molybdate-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvgL yvgL Bacillus subtilis 1423 -11532003 7000694221 yvgl molybdate-binding protein homolog yvgl (cl:molybdate-binding periplasmic protein) (db:pir2.dat) A70040 A70040 Bacillus subtilis 1423 -11532003 7000694222 yvgl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: yvsd; similar to) (le:24784) (re:25566) (di:direct) BSUB0018 Z99121 g2635851 Bacillus subtilis 1423 -11532003 7500964946 yvgl putative molybdate binding protein:yvgl (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:2171) (re:2953) (di:complement) BS43KBDNA AJ223978 g2832790 Bacillus subtilis 1423 -11532003

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812716	6122	28278	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812728	6123	28279	423	141

Description

6500728146 yvsc:yvgm hypothetical protein:similar to molybdenum transport permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvgM yvgM Bacillus subtilis 1423 -11532004 7000694223 yvgm molybdenum transport permease homolog yvgm (cl:maltose transport protein malg) (db:pir2.dat) B70040 B70040 Bacillus subtilis 1423 -11532004 7000694224 yvgm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: yvsc; similar to molybdenum) (le:25670) (re:26230) (di:direct) BSUB0018 Z99121 g2635852 Bacillus subtilis 1423 -11532004 7500964947 yvgm putative molybdate transport protein:yvgm (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:1507) (re:2067) (di:complement) BS43KBDNA AJ223978 g2832789 Bacillus subtilis 1423 -11532004

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812735	6124	28280	1167	388

Description

6500728147 yvsb:yvgn hypothetical protein:similar to plant-metabolite dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvgN yvgN Bacillus subtilis 1423 -11532005 7000694428 yvgn plant-metabolite dehydrogenase homolog yvgn (cl:aldehyde reductase) (db:pir2.dat) C70040 C70040 Bacillus subtilis 1423 -11532005 7000694429 yvgn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: yvsb; similar to) (le:26261) (re:27091) (di:complement) BSUB0018 Z99121 g2635853 Bacillus subtilis 1423 -11532005 7500953794 yvgn putative reductase protein:yvgn (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:646) (re:1476) (di:direct) BS43KBDNA AJ223978 g2832788 Bacillus subtilis 1423 -11532005

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812741	6125	28281	336	111

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812746	6126	28282	630	209

Description

6500728148 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvgO yvgO Bacillus subtilis 1423 -11532006 7000694014 yvgo hypothetical protein yvgo (db:pir2.dat) D70040 D70040 Bacillus subtilis 1423 -11532006 7500964806 yvgo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:27314) (re:27799) (di:direct) BSUB0018 Z99121 g2635854 Bacillus subtilis 1423 -11532006

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812749	6127	28283	477	158

Description

6500728149 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvgP yvgP Bacillus subtilis 1423 -11532007 7000692830 yvgp conserved hypothetical protein yvgp (cl:hypothetical protein yvgp) (db:pir2.dat) E70040 E70040 Bacillus subtilis 1423 -11532007 7500955906 yvgp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:27843) (re:29855) (di:complement) BSUB0018 Z99121 g2635855 Bacillus subtilis 1423 -11532007

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812771	6128	28284	1737	578

Description

6500728150 hypothetical protein:similar to sulfite reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvgQ yvgQ Bacillus subtilis 1423 -11532008 7000694657 yvgq sulfite reductase homolog yvgq (cl:sulfite reductase (ferredoxin)) (db:pir2.dat) F70040 F70040 Bacillus subtilis 1423 -11532008 7500953900 yvgq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to sulfite reductase) (le:30110) (re:31825) (di:complement) BSUB0018 Z99121 g2635856 Bacillus subtilis 1423 -11532008

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812795	6129	28285	798	265

Description

6500728151 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvgS yvgS Bacillus subtilis 1423 -11532009 7000694015 yvgs hypothetical protein yvgs (db:pir2.dat) H70040 H70040 Bacillus subtilis 1423 -11532009 7500964807 yvgs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:33839) (re:36163) (di:complement) BSUB0018 Z99121 g2635858 Bacillus subtilis 1423 -11532009

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501812796	6130	28286	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812804	6131	28287	1488	495

Description

6500728152 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvgT yvgT Bacillus subtilis 1423 -11532010 7000692831 yvgT conserved hypothetical protein yvgT (db:pir2.dat) A70041 A70041 Bacillus subtilis 1423 -11532010 7500963886 yvgT (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:36361) (re:36969) (di:complement) BSUB0018 Z99121 g2635859 Bacillus subtilis 1423 -11532010

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812836	6132	28288	318	105

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812837	6133	28289	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812855	6134	28290	186	61

Description

6500728153 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvgU yvgU Bacillus subtilis 1423 -11532011 7000692832 yvgU probable protein-disulfide oxidoreductase:yvgU (cl:protein-disulfide oxidoreductase dsbb) (ec:1.8.4.-) (db:pir2.dat) B70041 B70041 Bacillus subtilis 1423 -11532011 7500955849 yvgU (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins from b. subtilis) (le:37156) (re:37572) (di:complement) BSUB0018 Z99121 g2635860 Bacillus subtilis 1423 -11532011

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812856	6135	28291	417	138

Description

6500728154 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvgV yvgV Bacillus subtilis 1423 -11532012 7000692833 yvgv conserved hypothetical protein yvgv (db:pir2.dat) C70041 C70041 Bacillus subtilis 1423 -11532012 7500963887 yvgv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:37577) (re:38245) (di:complement) BSUB0018 Z99121 g2635861 Bacillus subtilis 1423 -11532012

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812857	6136	28292	189	62

Description

6500728155 hypothetical protein:similar to heavy metal-transporting atpase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvgW yvgW Bacillus subtilis 1423 -11532013 7000693086 yvgw heavy metal-transporting atpase homolog yvgw (cl:enterococcus copper-transporting atpase copa:atpase nucleotide-binding domain homology:atpase transduction domain homology:heavy-metal-associated homology) (db:pir2.dat) D70041 D70041 Bacillus subtilis 1423 -11532013 7500964049 yvgw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to heavy metal-transporting atpase) (le:38365) (re:40473) (di:complement) BSUB0018 Z99121 g2635862 Bacillus subtilis 1423 -11532013

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812860	6137	28293	342	113

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812863	6138	28294	255	84

Description

6500728156 hypothetical protein:similar to heavy metal-transporting atpase (gtcfc:14.1) (ec:3.6.1.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvgX yvgX Bacillus subtilis 1423 -11532014 7000693087 yvgx probable copper-transporting atpase:yvgx (cl:bacillus probable copper-transporting atpase yvgx:atpase nucleotide-binding domain homology:atpase transduction domain homology:heavy-metal-associated homology) (ec:3.6.1.-) (db:pir1.dat) E70041 E70041 Bacillus subtilis 1423 -11532014 7500954350 yvgx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to heavy metal-transporting atpase) (le:40633) (re:43044) (di:complement) BSUB0018 Z99121 g2635863 Bacillus subtilis 1423 -11532014

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812873	6139	28295	270	90

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812878	6140	28296	1047	348

Description

6500728157 hypothetical protein:similar to mercuric transport protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvgY yvgY Bacillus subtilis 1423 -11532015 7000694202 yvgY probable mercuric ion-binding protein yvgY:periplasmic mercuric ion-binding protein merp homolog (cl:mercuric resistance operon regulatory protein:heavy-metal-associated homology) (db:pir1.dat) F70041 F70041 Bacillus subtilis 1423 -11532015 7500964929 yvgY (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to mercuric transport protein) (le:43125) (re:43334) (di:complement) BSUB0018 Z99121 g2635864 Bacillus subtilis 1423 -11532015

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812880	6141	28297	246	81

Description

6500728158 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvgZ yvgZ Bacillus subtilis 1423 -11532016 7000692834 yvgz conserved hypothetical protein yvgz (db:pir2.dat) G70041 G70041 Bacillus subtilis 1423 -11532016 7500963888 yvgz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:43408) (re:43713) (di:complement) BSUB0018 Z99121 g2635865 Bacillus subtilis 1423 -11532016

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812882	6142	28298	594	197

Description

GTC ORF with score 411 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1008.) (nt:similar to saccharomyces cerevisiae vacuolar) (le:<1) (re:1524) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812892	6143	28299	636	211

Description

6500728159 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvaA yvaA Bacillus subtilis 1423 -11532017 7502851750 yvaa (de:hypothetical oxidoreductase in fhud-opubd intergenic region) (db:swissprot) YVAA\_BACSU 032223 BACILLUS SUBTILIS 1423 -11532017 7000692801 yvaa conserved hypothetical protein yvaa (cl:conserved hypothetical protein b1624) (db:pir2.dat) G70026 G70026 Bacillus subtilis 1423 -11532017 7500963866 yvaa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:43841) (re:44917) (di:direct) BSUB0018 Z99121 g2635866 Bacillus subtilis 1423 -11532017

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812898	6144	28300	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812905	6145	28301	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812907	6146	28302	777	259

Description

6500728160 hypothetical protein:similar to nadph dehydrogenase:quinone (gtcfc:9.12) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvaB yvaB Bacillus subtilis 1423 -11532018 7000694298 yvab nad p h dehydrogenase quinone homolog yvab (cl:acyl carrier protein phosphodiesterase) (db:pir2.dat) H70026 H70026 Bacillus subtilis 1423 -11532018 7500965007 yvab (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to nad(p)h dehydrogenase (quinone)) (le:44954) (re:45589) (di:complement) BSUB0018 Z99121 g2635867 Bacillus subtilis 1423 -11532018

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812941	6147	28303	597	198

Description

6500728161 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvaC yvaC Bacillus subtilis 1423 -11532019 7000692802 yvac conserved hypothetical protein yvac (db:pir2.dat) A70027 A70027 Bacillus subtilis 1423 -11532019 7500963867 yvac (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:45749) (re:47644) (di:complement) BSUB0018 Z99121 g2635868 Bacillus subtilis 1423 -11532019

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812946	6148	28304	1428	476

Description

6500728162 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvaD yvaD Bacillus subtilis 1423 -11532020 7000693993 yvad hypothetical protein yvad (db:pir2.dat) B70027 B70027 Bacillus subtilis 1423 -11532020 7500964785 yvad (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:47807) (re:48208) (di:complement) BSUB0018 Z99121 g2635869 Bacillus subtilis 1423 -11532020

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812964	6149	28305	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812984	6150	28306	318	105

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501812991	6151	28307	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813004	6152	28308	1809	603

Description

6500728163 hypothetical protein:similar to multidrug-efflux transporter (gtcfc:12.6) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvaE yvaE Bacillus subtilis 1423 -11532021 7000694258 yvae multidrug-efflux transporter homolog yvae (cl:suge protein) (db:pir2.dat) C70027 C70027 Bacillus subtilis 1423 -11532021 7500964978 yvae (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to multidrug-efflux transporter) (le:48205) (re:48564) (di:complement) BSUB0018 Z99121 g2635870 Bacillus subtilis 1423 -11532021

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813032	6153	28309	666	221

Description

6500728164 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvaF yvaF Bacillus subtilis 1423 -11532022 7000693994 yvaf hypothetical protein yvaf (db:pir2.dat) D70027 D70027 Bacillus subtilis 1423 -11532022 7500964786 yvaf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:48561) (re:49133) (di:complement) BSUB0018 Z99121 g2635871 Bacillus subtilis 1423 -11532022

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813033	6154	28310	399	132
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813034	6155	28311	273	90
<u>Description</u>				

6500728165 hypothetical protein:similar to 3-oxoacyl-acyl-carrier protein reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvaG yvaG Bacillus subtilis 1423 -11532023 7000692057 yvag 3-oxoacyl-acyl-carrier protein reductase homolog yvag (cl:ribitol dehydrogenase:short-chain alcohol dehydrogenase homology) (db:pir2.dat) E70027 E70027 Bacillus subtilis 1423 -11532023 7500953785 yvag (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to 3-oxoacyl-acyl-carrier protein) (le:49244) (re:50038) (di:complement) BSUB0018 Z99121 g2635872 Bacillus subtilis 1423 -11532023

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813038	6156	28312	768	255
<u>Description</u>				

6500728166 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvaI yvaI Bacillus subtilis 1423 -11532024 7500891743 smpb (de:small protein b homolog) (db:swissprot) SMPB\_BACSU O32230 BACILLUS SUBTILIS 1423 -11532024 7000692803 yvai conserved hypothetical protein yvai (cl:small protein smpb) (db:pir2.dat) F70027 F70027 Bacillus subtilis 1423 -11532024 7500891745 yvai (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:50760) (re:51230) (di:complement) BSUB0018 Z99121 g2635873 Bacillus subtilis 1423 -11532024

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813043	6157	28313	1848	615

Description

6500728167 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvaJ yvaJ Bacillus subtilis 1423 -11532025 7000692804 yvaj conserved hypothetical protein yvaj (cl:virulence-associated protein vacb homolog) (db:pir2.dat) G70027 G70027 Bacillus subtilis 1423 -11532025 7500963868 yvaj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:51375) (re:53714) (di:complement) BSUB0018 Z99121 g2635874 Bacillus subtilis 1423 -11532025

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813056	6158	28314	747	248

Description

6500728168 hypothetical protein:similar to carboxylesterase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvaK yvaK Bacillus subtilis 1423 -11532026 7000692324 yvak carboxylesterase homolog yvak (db:pir2.dat) H70027 H70027 Bacillus subtilis 1423 -11532026 7500963494 yvak (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to carboxylesterase) (le:53733) (re:54479) (di:complement) BSUB0018 Z99121 g2635875 Bacillus subtilis 1423 -11532026

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813061	6159	28315	1647	548

Description

6500728169 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvaL yvaL Bacillus subtilis 1423 -11532027 7000693995 yval hypothetical protein yval (db:pir2.dat) A70028 A70028 Bacillus subtilis 1423 -11532027 7500964787 yval (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:54605) (re:54835) (di:complement) BSUB0018 Z99121 g2635876 Bacillus subtilis 1423 -11532027

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813095	6160	28316	1398	465

Description

6500728170 hypothetical protein:similar to hydrolase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvaM yvaM Bacillus subtilis 1423 -11532028 7000693114 yvam hydrolase homolog yvam (db:pir2.dat) B70028 B70028 Bacillus subtilis 1423 -11532028 7500964059 yvam (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hydrolase) (le:54984) (re:55754) (di:direct) BSUB0018 Z99121 g2635877 Bacillus subtilis 1423 -11532028

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813105	6161	28317	747	248

Description

6500728171 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvzC yvzC Bacillus subtilis 1423 -11532029 7000694037 yvzc hypothetical protein yvzc (db:pir2.dat) G70049 G70049 Bacillus subtilis 1423 -11532029 7500964822 yvzc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:55794) (re:56027) (di:complement) BSUB0018 Z99121 g2635878 Bacillus subtilis 1423 -11532029

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813121	6162	28318	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813122	6163	28319	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813131	6164	28320	588	196

Description

6500728172 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvaN yvaN Bacillus subtilis 1423 -11532030 7000692805 yvan conserved hypothetical protein yvan (db:pir2.dat) C70028 Bacillus subtilis 1423 -11532030 7000692806 yvan yvan (db:genpept-bct1) (de:bacillus subtilis spab, spat, spac, subtilin (spas), spai, spaf,spae, spag, spar spak and yvan genes, complete cds.) (nt:hypothetical) (le:13424) (re:13831) (di:complement) BSU09819 U09819 g2702241 Bacillus subtilis 1423 -11532030 7500963869 yvan (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:56179) (re:56586) (di:direct) BSUB0018 Z99121 g2635879 Bacillus subtilis 1423 -11532030

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813133	6165	28321	387	128

Description

6500728173 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvaO yvaO Bacillus subtilis 1423 -11532031 7000692807 yvao conserved hypothetical protein yvao (db:pir2.dat) D70028 D70028 Bacillus subtilis 1423 -11532031 7500963870 yvao (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:56616) (re:57035) (di:direct) BSUB0018 Z99121 g2635880 Bacillus subtilis 1423 -11532031

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813149	6166	28322	198	65

Description

6500728174 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvaP yvaP Bacillus subtilis 1423 -11532032 7000692808 yvap conserved hypothetical protein yvap (db:pir2.dat) E70028 E70028 Bacillus subtilis 1423 -11532032 7500963871 yvap (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:56878) (re:57588) (di:direct) BSUB0018 Z99121 g2635881 Bacillus subtilis 1423 -11532032



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813151	6167	28323	1014	337

Description

6500728175 hypothetical protein:similar to transmembrane receptor taxis protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvaQ yvaQ Bacillus subtilis 1423 -11532033 7000694812 yvaq transmembrane receptor taxis protein homolog yvaq (db:pir2.dat) F70028 F70028 Bacillus subtilis 1423 -11532033 7500965366 yvaq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to transmembrane receptor taxis protein) (le:57579) (re:59279) (di:direct) BSUB0018 Z99121 g2635882 Bacillus subtilis 1423 -11532033

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813154	6168	28324	708	235

Description

6500728176 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvaV yvaV Bacillus subtilis 1423 -11532034 7000692809 yvav conserved hypothetical protein yvav (db:pir2.dat) G70028 G70028 Bacillus subtilis 1423 -11532034 7000692810 unknown (db:genpept-bct1) (de:bacillus subtilis choline transport system including atpase(opuba), transmembrane protein (opubb), choline binding proteinprecursor (opubc) and transmembrane protein (opubd) genes, completecds; and unknown gene.) (nt:orf-1) (le:64... AF008930 AF008930 g2911702 Bacillus subtilis 1423 -11532034 7500963872 yvav (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:63038) (re:63580) (di:direct) BSUB0018 Z99121 g2635887 Bacillus subtilis 1423 -11532034

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813164	6169	28325	450	149

Description

6500728177 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvaW yvaW Bacillus subtilis 1423 -11532035 7000692811 yvaw conserved hypothetical protein yvaw (db:pir2.dat) H70028 H70028 Bacillus subtilis 1423 -11532035 5500687064 orfa (sr:bacillus subtilis (strain:jh642) dna) (db:genpept-bct1) (de:bacillus subtilis dna for orfa, orfb, orfc, complete cds.) (le:747) (re:1223) (di:direct) AB006738 AB006738 g2344761 Bacillus subtilis 1423 -11532035 7500963873 yvaw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins from b. subtilis) (le:63802) (re:64278) (di:direct) BSUB0018 Z99121 g2635888 Bacillus subtilis 1423 -11532035

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813173	6170	28326	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813206	6171	28327	1344	448

Description

6500728178 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvaX yvaX Bacillus subtilis 1423 -11532036 7000693996 yvax hypothetical protein yvax (db:pir2.dat) A70029 A70029 Bacillus subtilis 1423 -11532036 5500687065 orfb (sr:bacillus subtilis (strain:jh642) dna) (db:genpept-bct1) (de:bacillus subtilis dna for orfa, orfb, orfc, complete cds.) (le:1220) (re:2191) (di:direct) AB006738 AB006738 g2344762 Bacillus subtilis 1423 -11532036 7500964788 yvax (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:64275) (re:65246) (di:direct) BSUB0018 Z99121 g2635889 Bacillus subtilis 1423 -11532036

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813217	6172	28328	636	211

Description

6500728179 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvaY yvaY Bacillus subtilis 1423 -11532037 7000692812 yvay conserved hypothetical protein yvay (db:pir2.dat) B70029 B70029 Bacillus subtilis 1423 -11532037 5500687066 orfc (sr:bacillus subtilis (strain:jh642) dna) (db:genpept-bct1) (de:bacillus subtilis dna for orfa, orfb, orfc, complete cds.) (le:2234) (re:2845) (di:direct) AB006738 AB006738 g2344763 Bacillus subtilis 1423 -11532037 7500963874 yvay (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins from b. subtilis) (le:65289) (re:65900) (di:direct) BSUB0018 Z99121 g2635890 Bacillus subtilis 1423 -11532037

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813225	6173	28329	363	120

Description

6500728180 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvaZ yvaZ Bacillus subtilis 1423 -11532038  
7000693997 yvaz hypothetical protein yvaz (db:pir2.dat) C70029 C70029 Bacillus subtilis 1423 -11532038 7500964789 yvaz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:65947) (re:66570) (di:complement) BSUB0018 Z99121 g2635891 Bacillus subtilis 1423 -11532038

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813226	6174	28330	216	71

Description

6500728181 hypothetical protein:similar to transcriptional regulator:arsr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvbA yvbA Bacillus subtilis 1423 -11532039 7000694724 yvba transcription regulator arsR family homolog yvba (cl:arsenical resistance operon repressor) (db:pir2.dat) D70029 D70029 Bacillus subtilis 1423 -11532039 7500965299 yvba (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to transcriptional regulator (arsr family)) (le:66567) (re:66839) (di:complement) BSUB0018 Z99121 g2635892 Bacillus subtilis 1423 -11532039

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813241	6175	28331	1092	363

Description

6500728182 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvbF yvbF Bacillus subtilis 1423 -11532040 7000692813 yvbf conserved hypothetical protein yvbf (db:pir2.dat) E70029 E70029 Bacillus subtilis 1423 -11532040 4000714290 orf-1 (db:genpept-bct1) (de:bacillus subtilis osmoprotectant transport system opuc includingatpase (opuca), transmembrane protein (opuch), osmoprotectantbinding protein precursor (opucc) and transmembrane protein (opucd)genes, complete cds.) (le:39) (re:596)... AF009352 AF009352 g2271393 Bacillus subtilis 1423 -11532040 7500963875 yvbf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins from b. subtilis) (le:70779) (re:71336) (di:direct) BSUB0018 Z99121 g2635897 Bacillus subtilis 1423 -11532040

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813255	6176	28332	1317	438

Description

GTC ORF with score 1623 to: (sr:schizosaccharomyces pombe (strain 972 h-) dna) (db:genpept-pln1) (de:schizosaccharomyces pombe dna polymerase delta (pold) gene,complete cds.) (nt:putative) (le:341:622) (re:569:3653) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813257	6177	28333	360	119

Description

6500728183 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvbG yvbG Bacillus subtilis 1423 -11532041 7502851751 yvbG (de:hypothetical 22.6 kd protein in opuca-eno intergenic region) (db:swissprot) YVBG\_BACSU O32244 BACILLUS SUBTILIS 1423 -11532041 7000692814 yvbG conserved hypothetical protein yvbG (cl:conserved hypothetical protein mjl677) (db:pir2.dat) F70029 F70029 Bacillus subtilis 1423 -11532041 7500963876 yvbG (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:71354) (re:71989) (di:complement) BSUB0018 Z99121 g2635898 Bacillus subtilis 1423 -11532041

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813280	6178	28334	1110	369

Description

6500728184 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvbH yvbH Bacillus subtilis 1423 -11532042 7000693998 yvbH hypothetical protein yvbH (db:pir2.dat) G70029 G70029 Bacillus subtilis 1423 -11532042 7500964790 yvbH (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:72139) (re:72753) (di:direct) BSUB0018 Z99121 g2635899 Bacillus subtilis 1423 -11532042

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813290	6179	28335	1308	436

Description

6500728185 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvbI yvbI Bacillus subtilis 1423 -11532043  
7000693999 yvbi hypothetical protein yvbi (db:pir2.dat) H70029 H70029 Bacillus subtilis 1423 -11532043 7500964791 yvbi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:72885) (re:73583) (di:direct) BSUB0018 Z99121 g2635900 Bacillus subtilis 1423 -11532043

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813295	6180	28336	447	148

Description

6500728186 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvbJ yvbJ Bacillus subtilis 1423 -11532044  
7000694000 yvbJ hypothetical protein yvbJ (db:pir2.dat) A70030 A70030 Bacillus subtilis 1423 -11532044 7500964792 yvbJ (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:73619) (re:75436) (di:complement) BSUB0018 Z99121 g2635901 Bacillus subtilis 1423 -11532044

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813300	6181	28337	519	172

Description

6500728187 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvbK yvbK Bacillus subtilis 1423 -11532045 7000692815 yvbK conserved hypothetical protein yvbK (db:pir2.dat) B70030 B70030 Bacillus subtilis 1423 -11532045 7500963877 yvbK (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins from b. subtilis) (le:75556) (re:76023) (di:direct) BSUB0018 Z99121 g2635902 Bacillus subtilis 1423 -11532045

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813301	6182	28338	714	238

Description

6500728188 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvbQ yvbQ Bacillus subtilis 1423 -11532046  
7000694001 yvbq hypothetical protein yvbq (db:pir2.dat) C70030 C70030 Bacillus subtilis 1423 -11532046 7500964793 yvbq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:82265) (re:83287) (di:complement) BSUB0018 Z99121 g2635908 Bacillus subtilis 1423 -11532046

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813313	6183	28339	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813324	6184	28340	462	153

Description

6500728189 hypothetical protein:similar to alkanal monooxygenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvbT yvbT Bacillus subtilis 1423 -11532047 7000692177 yvbt alkanal monooxygenase homolog yvbt (cl:ynbw protein) (db:pir2.dat) D70030 D70030 Bacillus subtilis 1423 -11532047 7500955792 yvbt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to alkanal monooxygenase) (le:86320) (re:87330) (di:complement) BSUB0018 Z99121 g2635911 Bacillus subtilis 1423 -11532047

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813330	6185	28341	360	119

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813341	6186	28342	1047	349

#### Description

6500728190 hypothetical protein:similar to transcriptional regulator:lysr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvbU yvbU Bacillus subtilis 1423 -11532048 7000694761 yvbU transcription regulator lysr family homolog yvbU (db:pir2.dat) E70030 E70030 Bacillus subtilis 1423 -11532048 7500965331 yvbU (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to transcriptional regulator (lysr family)) (le:87487) (re:88365) (di:complement) BSUB0018 Z99121 g2635912 Bacillus subtilis 1423 -11532048

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813342	6187	28343	480	159

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813353	6188	28344	1491	497

#### Description

6500728191 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvbV yvbV Bacillus subtilis 1423 -11532049 7000692816 yvbV conserved hypothetical protein yvbV (db:pir2.dat) F70030 F70030 Bacillus subtilis 1423 -11532049 7500963878 yvbV (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:88465) (re:89382) (di:direct) BSUB0018 Z99121 g2635913 Bacillus subtilis 1423 -11532049

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813356	6189	28345	186	61

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813364	6190	28346	1503	501

Description

6500728192 hypothetical protein:similar to amino acid permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvbW yvbW Bacillus subtilis 1423 -11532050 7000692198 yvbW amino acid permease homolog yvbW (cl:arginine permease) (db:pir2.dat) G70030 G70030 Bacillus subtilis 1423 -11532050 7500963405 yvbW (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to amino acid permease) (le:89423) (re:90766) (di:complement) BSUB0018 Z99121 g2635914 Bacillus subtilis 1423 -11532050

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813374	6191	28347	1527	508

Description

6500728193 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvbX yvbX Bacillus subtilis 1423 -11532051 7000692817 yvbX conserved hypothetical protein yvbX (cl:hypothetical protein yaah) (db:pir2.dat) H70030 H70030 Bacillus subtilis 1423 -11532051 7500963879 yvbX (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:91168) (re:92202) (di:complement) BSUB0018 Z99121 g2635915 Bacillus subtilis 1423 -11532051

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813376	6192	28348	525	174

Description

6500728194 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvbY yvbY Bacillus subtilis 1423 -11532052 7000692818 yvbY conserved hypothetical protein yvbY (cl:ykgg protein) (db:pir2.dat) A70031 A70031 Bacillus subtilis 1423 -11532052 7500955834 yvbY (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:92310) (re:93032) (di:complement) BSUB0018 Z99121 g2635916 Bacillus subtilis 1423 -11532052



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813387	6193	28349	231	76

Description

6500728195 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvfw yvfw Bacillus subtilis 1423 -11532053 7000692827 yvfw conserved hypothetical protein yvfw (cl:conserved hypothetical iron-sulfur protein hp0138) (db:pir2.dat) F70039 F70039 Bacillus subtilis 1423 -11532053 7500963884 yvfw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:93032) (re:94471) (di:complement) BSUB0018 Z99121 g2635917 Bacillus subtilis 1423 -11532053

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813388	6194	28350	396	131

Description

GTC ORF with score 206 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f56f10.) (nt:similar to human cysteine dioxygenase (pir:s34292);) (le:10544:10681:10890) (re:10633:10784:11041) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813422	6195	28351	186	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813439	6196	28352	1248	416

Description

6500728196 hypothetical protein:similar to glycolate oxidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvfv yvfv Bacillus subtilis 1423 -11532054 7000693067 yvfv glycolate oxidase homolog yvfv (cl:conserved hypothetical protein hp0139) (db:pir2.dat) E70039 E70039 Bacillus subtilis 1423 -11532054 1500694068 yvfv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to glycolate oxidase) (le:94498) (re:95214) (di:complement) BSUB0018 Z99121 g2635918 Bacillus subtilis 1423 -11532054 7500964037 yvfv hypothetical protein (db:genpept-bct1) (de:bacillus subtilis genomic dna fragment (88 kb).) (nt:similar to trembl:ecglcc\_4 escherichia coli) (le:86457) (re:87173) (di:direct) BSZ94043 Z94043 g1945722 Bacillus subtilis 1423 -11532054

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813440	6197	28353	327	108

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813443	6198	28354	513	170

Description

6500728197 hypothetical protein:similar to two-component response regulator (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvfU yvfU Bacillus subtilis 1423 -11532055 7000694851 yvfU two-component response regulator yvft homolog yvfU) (cl:regulatory protein coma:response regulator homology) (db:pir2.dat) D70039 D70039 Bacillus subtilis 1423 -11532055 1500694067 yvfU (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to two-component response regulator (yvft)) (le:95389) (re:95991) (di:complement) BSUB0018 Z99121 g2635919 Bacillus subtilis 1423 -11532055 7500965400 yvfU hypothetical protein (db:genpept-bct1) (de:bacillus subtilis genomic dna fragment (88 kb).) (nt:probable two component regulatory system:) (le:85680) (re:86282) (di:direct) BSZ94043 Z94043 g1945721 Bacillus subtilis 1423 -11532055

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813445	6199	28355	1095	364

Description

6500728198 hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvft yvft Bacillus subtilis 1423 -11532056 7000694880 yvft two-component sensor histidine kinase homolog yvft (db:pir2.dat) C70039 C70039 Bacillus subtilis 1423 -11532056 7500965419 yvft (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to two-component sensor histidine kinase) (le:96008) (re:96994) (di:complement) BSUB0018 Z99121 g2635920 Bacillus subtilis 1423 -11532056

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813448	6200	28356	1239	412

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813451	6201	28357	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813452	6202	28358	1233	411

Description

6500728199 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvfs yvfs Bacillus subtilis 1423 -11532057  
7000694013 yvfs hypothetical protein yvfs (db:pir2.dat) B70039 B70039 Bacillus subtilis 1423 -11532057 1500694065 yvfs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:97127) (re:97864) (di:complement) BSUB0018 Z99121 g2635921 Bacillus subtilis 1423 -11532057 7500964805 yvfs hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:probable permease) (le:83807) (re:84544) (di:direct) BSZ94043 Z94043 g1945719 Bacillus subtilis 1423 -11532057

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813467	6203	28359	570	190

Description

GTC ORF with score 110 to: (sr:human) (db:genpept-pri3) (de:homo sapiens lysosomal pepstatin insensitive protease (cln2) gene,complete cds.) (nt:deficient in late-infantile neuronal ceroid) (le:1329:1462:1814:2938) (re:1345:1533:1953:3088) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813470	6204	28360	273	90

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813494	6205	28361	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813502	6206	28362	1191	396

Description

6500728200 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvfr yvfr Bacillus subtilis 1423 -11532058 7000692106 yvfr abc transporter atp-binding protein homolog yvfr (cl:atp-binding cassette homology) (db:pir2.dat) A70039 A70039 Bacillus subtilis 1423 -11532058 1500694064 yvfr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to abc transporter (atp-binding protein)) (le:97865) (re:98770) (di:complement) BSUB0018 Z99121 g2635922 Bacillus subtilis 1423 -11532058 7500963347 yvfr hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:probable abc transporter) (le:82901) (re:83806) (di:direct) BSZ94043 Z94043 g1945718 Bacillus subtilis 1423 -11532058

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813516	6207	28363	606	201

Description

6500728201 hypothetical protein:similar to hydrolase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvfQ yvfQ Bacillus subtilis 1423 -11532059 7000693115 yvfq probable hydrolase yvfq (cl:bacillus subtilis probable hydrolase yvfq) (db:pir2.dat) H70038 H70038 Bacillus subtilis 1423 -11532059 1500694063 yvfq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hydrolase) (le:99054) (re:99863) (di:direct) BSUB0018 Z99121 g2635923 Bacillus subtilis 1423 -11532059 7500964060 yvfq hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to trembl:sscpnc\_22 synechocystis sp. cpn60) (le:81808) (re:82617) (di:complement) BSZ94043 Z94043 g1945717 Bacillus subtilis 1423 -11532059

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813517	6208	28364	522	173

Description

GTC ORF with score 146 to: (or:Phaseolus vulgaris) (sr:kidney bean) (db:genpept-pln1) (de:phaseolus vulgaris hydroxyproline-rich glycoprotein precursor gene,complete cds and promoter region.) (nt:extensin; cell wall protein) (le:949) (re:2691) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813527	6209	28365	468	155

Description

GTC ORF with score 120 to: (db:genpept-inv) (de:brugia malayi glia maturation factor bmgmf (bmgmf), complete cds.) (nt:mammalian glia maturation factor homolog; confirmed) (le:371:601:903:1051:1355) (re:373:697:952:1183:1435) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813531	6210	28366	252	83

Description

6500728202 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvfp yvfp Bacillus subtilis 1423 -11532060 7000692826 yvfp conserved hypothetical protein yvfp (db:pir2.dat) G70038 G70038 Bacillus subtilis 1423 -11532060 1500694062 yvfp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins from b. subtilis) (le:99899) (re:101110) (di:direct) BSUB0018 Z99121 g2635924 Bacillus subtilis 1423 -11532060 7500963883 yvfp hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to icfg\_syny3 icfg protein) (le:80561) (re:81772) (di:complement) BSZ94043 Z94043 g1945716 Bacillus subtilis 1423 -11532060

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813537	6211	28367	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813538	6212	28368	531	176

Description

6500728203 hypothetical protein:similar to arabinogalactan endo-1:4-beta-galactosidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvfo yvfo Bacillus subtilis 1423 -11532061 7000692223 yvfo arabinogalactan endo-1:4-beta-galactosidas homolog yvfo (db:pir2.dat) F70038 F70038 Bacillus subtilis 1423 -11532061 7500963426 yvfo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to arabinogalactan) (le:101164) (re:102441) (di:complement) BSUB0018 Z99121 g2635925 Bacillus subtilis 1423 -11532061

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813543	6213	28369	687	228

Description

6500728204 hypothetical protein:similar to maltodextrin transport system permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvfm yvfm Bacillus subtilis 1423 -11532062 7000694191 yvfm maltodextrin transport system permease homolog yvfm (cl:maltose transport protein malg) (db:pir2.dat) E70038 E70038 Bacillus subtilis 1423 -11532062 1500694059 yvfm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to maltodextrin transport system permease) (le:104615) (re:105466) (di:complement) BSUB0018 Z99121 g2635927 Bacillus subtilis 1423 -11532062 7500964918 yvfm hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to mald\_strpn maltodextrin transport system) (le:76205) (re:77056) (di:direct) BSZ94043 Z94043 g1945713 Bacillus subtilis 1423 -11532062

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813550	6214	28370	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813557	6215	28371	468	156

Description

6500728205 hypothetical protein:similar to maltodextrin transport system permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvfl yvfl Bacillus subtilis 1423 -11532063 7000694190 yvfl maltodextrin transport system permease homolog yvfl (cl:inner membrane protein malf) (db:pir2.dat) D70038 D70038 Bacillus subtilis 1423 -11532063 7500964917 yvfl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to maltodextrin transport system permease) (le:105470) (re:106726) (di:complement) BSUB0018 Z99121 g2635928 Bacillus subtilis 1423 -11532063

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813567	6216	28372	645	215

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813571	6217	28373	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813585	6218	28374	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813591	6219	28375	1086	361

Description

6500728206 hypothetical protein:similar to maltose/maltodextrin-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvfK yvfK Bacillus subtilis 1423 -11532064 7000694194 yvfK maltose/maltodextrin-binding protein homolog yvfK (db:pir2.dat) C70038 C70038 Bacillus subtilis 1423 -11532064 1500694057 yvfK (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to maltose/maltodextrin-binding protein) (le:106766) (re:108031) (di:complement) BSUB0018 Z99121 g2635929 Bacillus subtilis 1423 -11532064 7500964921 yvfK hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to malx\_strpn maltose/maltodextrin-binding) (le:73640) (re:74905) (di:direct) BSZ94043 Z94043 g1945711 Bacillus subtilis 1423 -11532064

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813593	6220	28376	480	159

Description

6500728207 hypothetical protein:similar to transcriptional regulator:gntr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvfI yvfI Bacillus subtilis 1423 -11532065 7000694741 yvfI transcription regulator gntr family homolog yvfI (db:pir2.dat) B70038 B70038 Bacillus subtilis 1423 -11532065 7500965313 yvfI (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to transcriptional regulator (gntr family)) (le:109344) (re:109871) (di:complement) BSUB0018 Z99121 g2635931 Bacillus subtilis 1423 -11532065

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813606	6221	28377	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813607	6222	28378	465	154

Description

6500728208 hypothetical protein:similar to l-lactate permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvfH yvfH Bacillus subtilis 1423 -11532066 7500952847 yvfH (de:putative l-lactate permease yvfH) (db:swissprot) YVFH\_BACSU P71067 BACILLUS SUBTILIS 1423 -11532066 7000694151 yvfH l-lactate permease homolog yvfH (cl:l-lactate permease) (db:pir2.dat) A70038 A70038 Bacillus subtilis 1423 -11532066 7500952849 yvfH (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to l-lactate permease) (le:110293) (re:111984) (di:direct) BSUB0018 Z99121 g2635932 Bacillus subtilis 1423 -11532066 1500694054 yvfH hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to lldp\_ecoli l-lactate permease) (le:69687) (re:71378) (di:complement) BSZ94043 Z94043 g1945708 Bacillus subtilis 1423 -11532066

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813624	6223	28379	639	212

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813646	6224	28380	1371	456

Description

6500728209 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvfG yvfG Bacillus subtilis 1423 -11532067 7000694012 yvfG hypothetical protein yvfG (db:pir2.dat) H70037 H70037 Bacillus subtilis 1423 -11532067 220268 yvfG (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:113400) (re:113618) (di:direct) BSUB0018 Z99121 g2635934 Bacillus subtilis 1423 -11532067 1500689798 yvfG hypothetical protein (db:genpept-bct1) (de:b.subtilis pnba, sigl, yve(j,k,l,m,n,o,p,q,r,s,t) andyvf(a,b,c,d,e,f,g,h) genes.) (le:18128) (re:18346) (di:complement) BSYVEFGNS Z71928 g1495295 Bacillus subtilis 1423 -11532067 7500964804 yvfG hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (le:68053) (re:68271) (di:complement) BSZ94043 Z94043 g1945706 Bacillus subtilis 1423 -11532067



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813666	6225	28381	264	87

Description

6500728210 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvfF yvfF Bacillus subtilis 1423 -11532068 7000692825 yvff conserved hypothetical protein yvff (cl:hypothetical protein yxab) (db:pir2.dat) G70037 G70037 Bacillus subtilis 1423 -11532068 220267 yvff (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins from b. subtilis) (le:113628) (re:114596) (di:complement) BSUB0018 Z99121 g2635935 Bacillus subtilis 1423 -11532068 1500689797 yvff hypothetical protein (db:genpept-bct1) (de:b.subtilis pnba, sigl, yve(j,k,l,m,n,o,p,q,r,s,t) andyvf(a,b,c,d,e,f,g,h) genes.) (le:17150) (re:18118) (di:direct) BSYVEFGNS Z71928 g1495294 Bacillus subtilis 1423 -11532068 7500955857 yvff hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to tremblst40830\_13 epsl streptococcus) (le:67075) (re:68043) (di:direct) BSZ94043 Z94043 g1945705 Bacillus subtilis 1423 -11532068

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813667	6226	28382	702	233

Description

6500728211 hypothetical protein:similar to spore coat polysaccharide biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvfE yvfE Bacillus subtilis 1423 -11532069 7000694603 yvfe spore coat polysaccharide biosynthesis homolog yvfe (cl:erythromycin resistance protein) (db:pir2.dat) F70037 F70037 Bacillus subtilis 1423 -11532069 220266 yvfe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to spore coat polysaccharide biosynthesis) (le:114834) (re:115739) (di:complement) BSUB0018 Z99121 g2635936 Bacillus subtilis 1423 -11532069 1500689796 yvfe hypothetical protein (db:genpept-bct1) (de:b.subtilis pnba, sigl, yve(j,k,l,m,n,o,p,q,r,s,t) andyvf(a,b,c,d,e,f,g,h) genes.) (nt:similar to spsc of b.subtilis) (le:16007) (re:16912) (di:direct) BSYVEFGNS Z71928 g1495293 Bacillus subtilis 1423 -11532069 7500965200 yvfe hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to pir:s28471 probable perosamine) (le:65932) (re:66837) (di:direct) BSZ94043 Z94043 g1945704 Bacillus subtilis 1423 -11532069

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813668	6227	28383	612	204

Description

GTC ORF with score 134 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid t05h4.) (nt:similar to the beta transducin family; coded for by) (le:21327:21799:22163) (re:21751:22118:22341) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813672	6228	28384	477	158

Description

6500728212 hypothetical protein:similar to serine o-acetyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvfd yvfd Bacillus subtilis 1423 -11532070 7000694578 yvfd serine o-acetyltransferase homolog yvfd (db:pir2.dat) E70037 E70037 Bacillus subtilis 1423 -11532070 220265 yvfd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to serine o-acetyltransferase) (le:115744) (re:116394) (di:complement) BSUB0018 Z99121 g2635937 Bacillus subtilis 1423 -11532070 1500689795 yvfd hypothetical protein (db:genpept-bct1) (de:b.subtilis pnba, sigl, yve(j,k,l,m,n,o,p,q,r,s,t) andyvf(a,b,c,d,e,f,g,h) genes.) (nt:similar to capg of s.aureus) (le:15352) (re:16002) (di:direct) BSYVEFGNS Z71928 g1495292 Bacillus subtilis 1423 -11532070 7500965177 yvfd hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to trembl:ec05248\_1 neud escherichia coli) (le:65277) (re:65927) (di:direct) BSZ94043 Z94043 g1945703 Bacillus subtilis 1423 -11532070

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813675	6229	28385	558	185

Description

6500728213 hypothetical protein:similar to capsular polysaccharide biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvfc yvfc Bacillus subtilis 1423 -11532071 7000692315 yvfc capsular polysaccharide biosynthesis homolog yvfc (db:pir2.dat) D70037 D70037 Bacillus subtilis 1423 -11532071 220264 yvfc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to capsular polysaccharide biosynthesis) (le:116391) (re:116999) (di:complement) BSUB0018 Z99121 g2635938 Bacillus subtilis 1423 -11532071 1500689794 yvfc hypothetical protein (db:genpept-bct1) (de:b.subtilis pnba, sigl, yve(j,k,l,m,n,o,p,q,r,s,t) andyvf(a,b,c,d,e,f,g,h) genes.) (nt:similar to exoy of r.meliloti) (le:14747) (re:15355) (di:direct) BSYVEFGNS Z71928 g1495291 Bacillus subtilis 1423 -11532071 7500963483 yvfc hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to trembl:chrhbfpg\_2 rfbp campylobacter) (le:64672) (re:65280) (di:direct) BSZ94043 Z94043 g1945702 Bacillus subtilis 1423 -11532071

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813687	6230	28386	507	168

Description

6500728214 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvfb yvfb Bacillus subtilis 1423 -11532072 7000694011 yvfb hypothetical protein yvfb (db:pir2.dat) C70037 C70037 Bacillus subtilis 1423 -11532072 220263 yvfb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:116996) (re:118033) (di:complement) BSUB0018 Z99121 g2635939 Bacillus subtilis 1423 -11532072 7500964803 yvfb hypothetical protein (db:genpept-bct1) (de:b.subtilis pnba, sigl, yve(j,k,l,m,n,o,p,q,r,s,t) andyvf(a,b,c,d,e,f,g,h) genes.) (le:13713) (re:14750) (di:direct) BSYVEFGNS Z71928 g1495290 Bacillus subtilis 1423 -11532072

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813691	6231	28387	828	275

Description

6500728215 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvfa yvfa Bacillus subtilis 1423 -11532073  
7000694010 yvfa hypothetical protein yvfa (db:pir2.dat) B70037 B70037  
Bacillus subtilis 1423 -11532073 220262 yvfa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:118183) (re:118512) (di:complement) BSUB0018 Z99121 g2635940  
Bacillus subtilis 1423 -11532073 1500689793 yvfa hypothetical protein (db:genpept-bct1) (de:b.subtilis pnba, sigl, yve(j,k,l,m,n,o,p,q,r,s,t) andyvf(a,b,c,d,e,f,g,h) genes.) (le:13234) (re:13563) (di:direct) BSYVEFGNS Z71928 g1495289 Bacillus subtilis 1423 -11532073 7500964802 yvfa hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (le:63159) (re:63488) (di:direct) BSZ94043 Z94043 g1945700  
Bacillus subtilis 1423 -11532073

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813695	6232	28388	357	118

Description

6500728216 hypothetical protein:similar to capsular polysaccharide biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yveT yveT Bacillus subtilis 1423 -11532074 7000692314 yvet capsular polysaccharide biosynthesis homolog yvet (db:pir2.dat) A70037 A70037 Bacillus subtilis 1423 -11532074 220261 yvet (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to capsular polysaccharide biosynthesis) (le:118509) (re:119543) (di:complement) BSUB0018 Z99121 g2635941 Bacillus subtilis 1423 -11532074 1500689792 yvet hypothetical protein (db:genpept-bct1) (de:b.subtilis pnba, sigl, yve(j,k,l,m,n,o,p,q,r,s,t) andyvf(a,b,c,d,e,f,g,h) genes.) (nt:similar to ggab of b.subtilis) (le:12203) (re:13237) (di:direct) BSYVEFGNS Z71928 g1495288 Bacillus subtilis 1423 -11532074 7500963482 yvet hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to tremblst40830\_10 epsi streptococcus) (le:62128) (re:63162) (di:direct) BSZ94043 Z94043 g1945699 Bacillus subtilis 1423 -11532074

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813699	6233	28389	1218	405

Description

6500728217 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yves yveS Bacillus subtilis 1423 -11532075 7000692824 yves conserved hypothetical protein yves (cl:hypothetical protein yxab) (db:pir2.dat) H70036 H70036 Bacillus subtilis 1423 -11532075 220260 yves (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:119540) (re:120616) (di:complement) BSUB0018 Z99121 g2635942 Bacillus subtilis 1423 -11532075 1500689791 yves hypothetical protein (db:genpept-bct1) (de:b.subtilis pnba, sigl, yve(j,k,l,m,n,o,p,q,r,s,t) andyvf(a,b,c,d,e,f,g,h) genes.) (le:11130) (re:12206) (di:direct) BSYVEFGNS Z71928 g1495287 Bacillus subtilis 1423 -11532075 7500955856 yves hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to tremblst40830\_13 epsl streptococcus) (le:61055) (re:62131) (di:direct) BSZ94043 Z94043 g1945698 Bacillus subtilis 1423 -11532075

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813703	6234	28390	300	99

Description

6500728218 hypothetical protein:similar to spore coat polysaccharide biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yveR yveR Bacillus subtilis 1423 -11532076 7000694602 yver spore coat polysaccharide biosynthesis homolog yver (db:pir2.dat) G70036 G70036 Bacillus subtilis 1423 -11532076 220259 yver (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to spore coat polysaccharide biosynthesis) (le:120621) (re:121655) (di:complement) BSUB0018 Z99121 g2635943 Bacillus subtilis 1423 -11532076 1500689790 yver hypothetical protein (db:genpept-bct1) (de:b.subtilis pnba, sigl, yve(j,k,l,m,n,o,p,q,r,s,t) andyvf(a,b,c,d,e,f,g,h) genes.) (nt:similar to exoo r.meliloti) (le:10091) (re:11125) (di:direct) BSYVEFGNS Z71928 g1495286 Bacillus subtilis 1423 -11532076 7500965199 yver hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to tremblst40830\_10 epsi streptococcus) (le:60016) (re:61050) (di:direct) BSZ94043 Z94043 g1945697 Bacillus subtilis 1423 -11532076

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813711	6235	28391	1518	506

Description

6500728219 hypothetical protein:similar to capsular polysaccharide biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yveQ yveQ Bacillus subtilis 1423 -11532077 7000692313 yveq capsular polysaccharide biosynthesis homolog yveq (db:pir2.dat) F70036 F70036 Bacillus subtilis 1423 -11532077 220258 yveq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to capsular polysaccharide biosynthesis) (le:121680) (re:122783) (di:complement) BSUB0018 Z99121 g2635944 Bacillus subtilis 1423 -11532077 1500689789 yveq hypothetical protein (db:genpept-bct1) (de:b.subtilis pnba, sigl, yve(j,k,l,m,n,o,p,q,r,s,t) andyvf(a,b,c,d,e,f,g,h) genes.) (le:8963) (re:10066) (di:direct) BSYVEFGNS Z71928 g1495285 Bacillus subtilis 1423 -11532077 7500963481 yveq hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to tremblst40830\_11 epsj streptococcus) (le:58888) (re:59991) (di:direct) BSZ94043 Z94043 g1945696 Bacillus subtilis 1423 -11532077

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813720	6236	28392	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813721	6237	28393	183	60

Description

6500728220 hypothetical protein:similar to capsular polysaccharide biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yveP yveP Bacillus subtilis 1423 -11532078 7000692312 yvep capsular polysaccharide biosynthesis homolog yvep (db:pir2.dat) E70036 E70036 Bacillus subtilis 1423 -11532078 220257 yvep (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to capsular polysaccharide biosynthesis) (le:122780) (re:123934) (di:complement) BSUB0018 Z99121 g2635945 Bacillus subtilis 1423 -11532078 1500689788 yvep hypothetical protein (db:genpept-bct1) (de:b.subtilis pnba, sigl, yve(j,k,l,m,n,o,p,q,r,s,t) andyvf(a,b,c,d,e,f,g,h) genes.) (nt:similar to vipc of s.typhi) (le:7812) (re:8966) (di:direct) BSYVEFGNS Z71928 g1495284 Bacillus subtilis 1423 -11532078 7500963480 yvep hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to vipc\_salti vi polysaccharide) (le:57737) (re:58891) (di:direct) BSZ94043 Z94043 g1945695 Bacillus subtilis 1423 -11532078

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813731	6238	28394	201	66

Description

6500728221 hypothetical protein:similar to exopolysaccharide biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yveO yveO Bacillus subtilis 1423 -11532079 7000692976 yveo exopolysaccharide biosynthesis homolog yveo (db:pir2.dat) D70036 D70036 Bacillus subtilis 1423 -11532079 220256 yveo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to exopolysaccharide biosynthesis) (le:123927) (re:124763) (di:complement) BSUB0018 Z99121 g2635946 Bacillus subtilis 1423 -11532079 1500689787 yveo hypothetical protein (db:genpept-bct1) (de:b.subtilis pnba, sigl, yve(j,k,l,m,n,o,p,q,r,s,t) andyvf(a,b,c,d,e,f,g,h) genes.) (nt:similar to spsa of b.subtilis) (le:6983) (re:7819) (di:direct) BSYVEFGNS Z71928 g1495283 Bacillus subtilis 1423 -11532079 7500963976 yveo hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to trembl:eckfaaf\_3 putative) (le:56908) (re:57744) (di:direct) BSZ94043 Z94043 g1945694 Bacillus subtilis 1423 -11532079

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813736	6239	28395	234	77

Description

6500728222 hypothetical protein:similar to capsular polysaccharide biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yveN yveN Bacillus subtilis 1423 -11532080 7000692311 yven capsular polysaccharide biosynthesis homolog yven (db:pir2.dat) C70036 C70036 Bacillus subtilis 1423 -11532080 220255 yven (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to capsular polysaccharide biosynthesis) (le:124760) (re:125905) (di:complement) BSUB0018 Z99121 g2635947 Bacillus subtilis 1423 -11532080 1500689786 yven hypothetical protein (db:genpept-bct1) (de:b.subtilis pnba, sigl, yve(j,k,l,m,n,o,p,q,r,s,t) andyvf(a,b,c,d,e,f,g,h) genes.) (nt:similar to rfag of e.coli) (le:5841) (re:6986) (di:direct) BSYVEFGNS Z71928 g1495282 Bacillus subtilis 1423 -11532080 7500963479 yven hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to rfag\_ecoli lipopolysaccharide core) (le:55766) (re:56911) (di:direct) BSZ94043 Z94043 g1945693 Bacillus subtilis 1423 -11532080

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813737	6240	28396	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813746	6241	28397	1386	461

Description

6500728223 hypothetical protein:similar to capsular polysaccharide biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yveM yveM Bacillus subtilis 1423 -11532081 7000692310 yvem capsular polysaccharide biosynthesis homolog yvem (cl:trsg protein) (db:pir2.dat) B70036 B70036 Bacillus subtilis 1423 -11532081 220254 yvem (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to capsular polysaccharide biosynthesis) (le:125917) (re:127713) (di:complement) BSUB0018 Z99121 g2635948 Bacillus subtilis 1423 -11532081 1500689785 yvem hypothetical protein (db:genpept-bct1) (de:b.subtilis pnba, sigl, yve(j,k,l,m,n,o,p,q,r,s,t) andyvf(a,b,c,d,e,f,g,h) genes.) (nt:similar to capd of s.aureus) (le:4033) (re:5829) (di:direct) BSYVEFGNS Z71928 g1495281 Bacillus subtilis 1423 -11532081 7500963478 yvem hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to capd\_staau capd protein) (le:53958) (re:55754) (di:direct) BSZ94043 Z94043 g1945692 Bacillus subtilis 1423 -11532081

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813747	6242	28398	450	149

Description

6500728224 hypothetical protein:similar to capsular polysaccharide biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yveL yveL Bacillus subtilis 1423 -11532082 7000692309 yvel capsular polysaccharide biosynthesis homolog yvel (cl:capsular polysaccharide biosynthesis protein cpse) (db:pir2.dat) A70036 A70036 Bacillus subtilis 1423 -11532082 220253 yvel (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to capsular polysaccharide biosynthesis) (le:127972) (re:128655) (di:complement) BSUB0018 Z99121 g2635949 Bacillus subtilis 1423 -11532082 1500689784 yvel hypothetical protein (db:genpept-bct1) (de:b.subtilis pnba, sigl, yve(j,k,l,m,n,o,p,q,r,s,t) andyvf(a,b,c,d,e,f,g,h) genes.) (nt:similar to capb of s.aureus) (le:3091) (re:3774) (di:direct) BSYVEFGNS Z71928 g1495280 Bacillus subtilis 1423 -11532082 7500963477 yvel hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to capb\_staau capb protein) (le:53016) (re:53699) (di:direct) BSZ94043 Z94043 g1945691 Bacillus subtilis 1423 -11532082



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813752	6243	28399	1152	384

Description

6500728225 hypothetical protein:similar to capsular polysaccharide biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yveK yveK Bacillus subtilis 1423 -11532083 7000692308 yvek capsular polysaccharide biosynthesis homolog yvek (cl:streptococcus agalactiae cpsb protein) (db:pir2.dat) H70035 H70035 Bacillus subtilis 1423 -11532083 220252 yvek (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to capsular polysaccharide biosynthesis) (le:128661) (re:129365) (di:complement) BSUB0018 Z99121 g2635950 Bacillus subtilis 1423 -11532083 1500689783 yvek hypothetical protein (db:genpept-bct1) (de:b.subtilis pnba, sigl, yve(j,k,l,m,n,o,p,q,r,s,t) andyvf(a,b,c,d,e,f,g,h) genes.) (nt:similar to capa of s.aureus) (le:2381) (re:3085) (di:direct) BSYVEFGNS Z71928 g1495279 Bacillus subtilis 1423 -11532083 7500963476 yvek hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to capa\_staaу capa protein) (le:52306) (re:53010) (di:direct) BSZ94043 Z94043 g1945690 Bacillus subtilis 1423 -11532083

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813757	6244	28400	405	134

Description

6500728226 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yveG yveG Bacillus subtilis 1423 -11532084 7000694009 yveg hypothetical protein yveg (db:pir2.dat) G70035 G70035 Bacillus subtilis 1423 -11532084 1500694051 yveg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:132343) (re:132630) (di:complement) BSUB0018 Z99121 g2635954 Bacillus subtilis 1423 -11532084 7500964801 yveg hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (le:49041) (re:49328) (di:direct) BSZ94043 Z94043 g1945686 Bacillus subtilis 1423 -11532084

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813768	6245	28401	1683	560

Description

6500728227 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yveF yveF Bacillus subtilis 1423 -11532085  
7000694008 yvef hypothetical protein yvef (db:pir2.dat) F70035 F70035 Bacillus subtilis 1423 -11532085 1500694050 yvef (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:132706) (re:132798) (di:complement) BSUB0018 Z99121 g2635955 Bacillus subtilis 1423 -11532085 7500964800 yvef hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (le:48873) (re:48965) (di:direct) BSZ94043 Z94043 g1945685 Bacillus subtilis 1423 -11532085

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813769	6246	28402	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813773	6247	28403	726	241

Description

6500728228 hypothetical protein:similar to levanase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yveB yveB Bacillus subtilis 1423 -11532086 7000694162 yveb levanase homolog yveb (cl:penicillium purporogenun inulinase) (db:pir2.dat) E70035 E70035 Bacillus subtilis 1423 -11532086 1500694047 yveb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to levanase) (le:137017) (re:138567) (di:direct) BSUB0018 Z99121 g2635959 Bacillus subtilis 1423 -11532086 7500964894 yveb hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to sacc\_bacsu levanase precursor) (le:43104) (re:44654) (di:complement) BSZ94043 Z94043 g1945681 Bacillus subtilis 1423 -11532086

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813790	6248	28404	342	113

Description

6500728229 hypothetical protein:similar to permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yveA yveA Bacillus subtilis 1423 -11532087 7000694363 yvea permease homolog yvea (db:pir2.dat) D70035 D70035 Bacillus subtilis 1423 -11532087 1500694046 yvea (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to permease) (le:138675) (re:140237) (di:direct) BSUB0018 Z99121 g2635960 Bacillus subtilis 1423 -11532087 7500965049 yvea hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:probable permease) (le:41434) (re:42996) (di:complement) BSZ94043 Z94043 g1945680 Bacillus subtilis 1423 -11532087

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813791	6249	28405	1422	474

Description

GTC ORF with score 321 to: (fn:oxidoreductase; production of hydrogen-peroxide) (db:genpept-pln2) (ec:1.1.3.7) (de:pleurotus eryngii aryl-alcohol oxidase precursor (aao) gene,complete cds.) (nt:veratryl-alcohol oxidase; flavoprotein; catalytic) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813799	6250	28406	309	103

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813805	6251	28407	573	190

Description

6500728230 hypothetical protein:similar to transcriptional regulator:tetr/acrr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvdt yvdt Bacillus subtilis 1423 -11532088 7000694787 yvdt transcription regulator tetr/acrr family homolog yvdt (db:pir2.dat) C70035 C70035 Bacillus subtilis 1423 -11532088 1500694045 yvdt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to transcriptional regulator (tetr/acrr) (le:140332) (re:140916) (di:direct) BSUB0018 Z99121 g2635961 Bacillus subtilis 1423 -11532088 7500965348 yvdt hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:probable transcriptional regulator (terr family)) (le:40755) (re:41339) (di:complement) BSZ94043 Z94043 g1945679 Bacillus subtilis 1423 -11532088

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813826	6252	28408	207	68
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813829	6253	28409	900	299
<u>Description</u>				

6500728231 hypothetical protein:similar to chaperonin (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvdS yvdS Bacillus subtilis 1423 -11532089 7000692358 yvds chaperonin homolog yvds (cl:suge protein) (db:pir2.dat) B70035 B70035 Bacillus subtilis 1423 -11532089 7500963522 yvds (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to chaperonin) (le:140998) (re:141333) (di:direct) BSUB0018 Z99121 g2635962 Bacillus subtilis 1423 -11532089

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813837	6254	28410	198	65
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813838	6255	28411	1053	350
<u>Description</u>				

6500728232 hypothetical protein:similar to chaperonin (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvdr yvdr Bacillus subtilis 1423 -11532090 7000692357 yvdr chaperonin homolog yvdr (cl:suge protein) (db:pir2.dat) A70035 A70035 Bacillus subtilis 1423 -11532090 1500694043 yvdr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to chaperonin) (le:141333) (re:141653) (di:direct) BSUB0018 Z99121 g2635963 Bacillus subtilis 1423 -11532090 7500963521 yvdr hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to suge\_provu suge protein) (le:40018) (re:40338) (di:complement) BSZ94043 Z94043 g1945677 Bacillus subtilis 1423 -11532090

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813841	6256	28412	669	222

Description

GTC ORF with score 136 to: (fn:gel formation, gastric epithelial protection) (sr:pig) (db:genpept-mam) (de:sus scrofa yorkshire/chester white/hampshire clone pgm-ss-2agastric mucin mrna, partial cds.) (nt:bases 1-105 encode a cysteine rich, non-repeat)...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813847	6257	28413	384	127

Description

6500728233 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvdQ yvdQ Bacillus subtilis 1423 -11532091  
7000694007 yvdq hypothetical protein yvdq (db:pir2.dat) H70034 H70034 Bacillus subtilis 1423 -11532091 1500694042 yvdq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:141689) (re:142201) (di:complement) BSUB0018 Z99121 g2635964 Bacillus subtilis 1423 -11532091 7500964799 yvdq hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (le:39470) (re:39982) (di:direct) BSZ94043 Z94043 g1945676 Bacillus subtilis 1423 -11532091

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813862	6258	28414	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813875	6259	28415	576	192

Description

6500728234 hypothetical protein:similar to reticuline oxidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvdP yvdP Bacillus subtilis 1423 -11532092 7000694506 yvdP reticuline oxidase homolog yvdP (db:pir2.dat) G70034 G70034 Bacillus subtilis 1423 -11532092 1500694041 yvdP (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to reticuline oxidase) (le:142453) (re:143796) (di:complement) BSUB0018 Z99121 g2635965 Bacillus subtilis 1423 -11532092 7500965144 yvdP hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to hdno\_artox 6-hydroxy-d-nicotine oxidase) (le:37875) (re:39218) (di:direct) BSZ94043 Z94043 g1945675 Bacillus subtilis 1423 -11532092

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813891	6260	28416	288	95
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813895	6261	28417	333	110
<u>Description</u>				

6500728235 hypothetical protein:similar to hypothetical proteins  
(gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvdO  
yvdO Bacillus subtilis 1423 -11532093 7000692823 yvdO conserved  
hypothetical protein yvdO (db:pir2.dat) F70034 F70034 Bacillus subtilis 1423  
-11532093 1500694040 yvdO (fn:unknown) (db:genpept-bct1) (de:bacillus  
subtilis complete genome (section 18 of 21): from 3399551to 3609060.)  
(nt:similar to hypothetical proteins) (le:144152) (re:145114) (di:direct)  
BSUB0018 Z99121 g2635966 Bacillus subtilis 1423 -11532093 7500963882 yvdO  
hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment  
(88 kb).) (nt:similar to teg\_bacme teg protein) (le:36557) (re:37519)  
(di:complement) BSZ94043 Z94043 g1945674 Bacillus subtilis 1423 -11532093

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813896	6262	28418	201	66
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813898	6263	28419	999	332
<u>Description</u>				

6500728236 hypothetical protein:similar to beta-phosphoglucomutase  
(gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvdM  
yvdM Bacillus subtilis 1423 -11532094 7500887966 yvdM (ec:5.4.2.6)  
(de:putative beta-phosphoglucomutase, (beta-pgm)) (db:swissprot) PGMB\_BACSU  
006995 BACILLUS SUBTILIS 1423 -11532094 7000692267 yvdM  
beta-phosphoglucomutase homolog yvdM (cl:hypothetical protein b2690)  
(db:pir2.dat) E70034 E70034 Bacillus subtilis 1423 -11532094 7500887968  
yvdM (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome  
(section 18 of 21): from 3399551to 3609060.) (nt:similar to  
beta-phosphoglucomutase) (le:146383) (re:147063) (di:complement) BSUB0018  
Z99121 g2635968 Bacillus subtilis 1423 -11532094 1500694038 yvdM  
hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment  
(88 kb).) (nt:putative beta-phosphoglucomutase) (le:34608) (re:35288)  
(di:direct) BSZ94043 Z94043 g1945672 Bacillus subtilis 1423 -11532094

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813905	6264	28420	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813907	6265	28421	288	95

Description

6500728237 hypothetical protein:similar to oligo-1:6-glucosidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvdL yvdL Bacillus subtilis 1423 -11532095 7000694333 yvdL oligo-1:6-glucosidase homolog yvdL (cl:alpha-glucosidase:alpha-amylase core homology) (db:pir2.dat) D70034 D70034 Bacillus subtilis 1423 -11532095 1500694037 yvdL (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to oligo-1,6-glucosidase) (le:147060) (re:148745) (di:complement) BSUB0018 Z99121 g2635969 Bacillus subtilis 1423 -11532095 7500965028 yvdL hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to o16g bacsp oligo-16-glucosidase) (le:32926) (re:34611) (di:direct) BSZ94043 Z94043 g1945671 Bacillus subtilis 1423 -11532095

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813913	6266	28422	258	85

Description

6500728238 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvdK yvdK Bacillus subtilis 1423 -11532096 7500952843 yvdK (de:hypothetical 88.3 kd protein in clpp-crh intergenic region) (db:swissprot) YVDK\_BACSU 006993 BACILLUS SUBTILIS 1423 -11532096 7000692822 yvdK conserved hypothetical protein yvdK (db:pir2.dat) C70034 C70034 Bacillus subtilis 1423 -11532096 7500952845 yvdK (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:148738) (re:151011) (di:complement) BSUB0018 Z99121 g2635970 Bacillus subtilis 1423 -11532096 1500694036 yvdK hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to trembl:ml015\_21 mycobacterium leprae) (le:30660) (re:32933) (di:direct) BSZ94043 Z94043 g1945670 Bacillus subtilis 1423 -11532096

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813918	6267	28423	495	164

Description

6500728239 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvdJ yvdJ Bacillus subtilis 1423 -11532097  
7000694006 yvdj hypothetical protein yvdj (db:pir2.dat) B70034 B70034 Bacillus subtilis 1423 -11532097 1500694035 yvdj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:150989) (re:151873) (di:complement) BSUB0018 Z99121 g2635971 Bacillus subtilis 1423 -11532097 7500964798 yvdj hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (le:29798) (re:30682) (di:direct) BSZ94043 Z94043 g1945669 Bacillus subtilis 1423 -11532097

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501813925	6268	28424	957	318

Description

6500728240 hypothetical protein:similar to maltodextrin transport system permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvdI yvdI Bacillus subtilis 1423 -11532098 7000694189 yvdi maltodextrin transport system permease homolog yvdi (cl:maltose transport protein malg) (db:pir2.dat) A70034 A70034 Bacillus subtilis 1423 -11532098 1500694034 yvdi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to maltodextrin transport system permease) (le:151879) (re:152715) (di:complement) BSUB0018 Z99121 g2635972 Bacillus subtilis 1423 -11532098 7500964916 yvdi hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to mald\_strpn maltodextrin transport system) (le:28956) (re:29792) (di:direct) BSZ94043 Z94043 g1945668 Bacillus subtilis 1423 -11532098



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813935	6269	28425	741	246

Description

6500728241 hypothetical protein:similar to maltodextrin transport system permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvdH yvdH Bacillus subtilis 1423 -11532099 7000694188 yvdh maltodextrin transport system permease homolog yvdh (cl:inner membrane protein malf) (db:pir2.dat) H70033 H70033 Bacillus subtilis 1423 -11532099 1500694033 yvdh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to maltodextrin transport system permease) (le:152716) (re:154023) (di:complement) BSUB0018 Z99121 g2635973 Bacillus subtilis 1423 -11532099 7500964915 yvdh hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to malc\_strpn maltodextrin transport system) (le:27648) (re:28955) (di:direct) BSZ94043 Z94043 g1945667 Bacillus subtilis 1423 -11532099

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813945	6270	28426	1005	334

Description

GTC ORF with score 111 to: (sr:thale cress) (db:genpept) (de:arabidopsis thaliana chromosome i bac t5a14 genomic sequence,complete sequence.) (nt:hypothetical protein) (le:27887:28158:28449:28726) (re:28076:28381:28617:28872) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813946	6271	28427	816	271

Description

6500728242 hypothetical protein:similar to maltose/maltodextrin-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvdG yvdG Bacillus subtilis 1423 -11532100 7000694193 yvdg maltose/maltodextrin-binding protein homolog yvdg (db:pir2.dat) G70033 G70033 Bacillus subtilis 1423 -11532100 1500694032 yvdg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to maltose/maltodextrin-binding protein) (le:154063) (re:155316) (di:complement) BSUB0018 Z99121 g2635974 Bacillus subtilis 1423 -11532100 7500964920 yvdg hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to malx\_strpn maltose/maltodextrin-binding) (le:26355) (re:27608) (di:direct) BSZ94043 Z94043 g1945666 Bacillus subtilis 1423 -11532100

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813953	6272	28428	351	116

Description

6500728243 hypothetical protein:similar to glucan 1:4-alpha-maltohydrolase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvdf yvdf Bacillus subtilis 1423 -11532101 7000693026 yvdf glucan 1:4-alpha-maltohydrolase homolog yvdf (cl:neopullulanase:alpha-amylase core homology) (db:pir2.dat) F70033 F70033 Bacillus subtilis 1423 -11532101 1500694031 yvdf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to glucan 1,4-alpha-maltohydrolase) (le:155412) (re:157181) (di:complement) BSUB0018 Z99121 g2635975 Bacillus subtilis 1423 -11532101 7500954264 yvdf hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:probable neopullulanase) (le:24490) (re:26259) (di:direct) BSZ94043 Z94043 g1945665 Bacillus subtilis 1423 -11532101

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813976	6273	28429	510	169

Description

6500728244 hypothetical protein:similar to transcriptional regulator:laci family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvde yvde Bacillus subtilis 1423 -11532102 7500952839 yvde (de:hypothetical transcriptional regulator in clpp-crh intergenic region) (db:swissprot) YVDE\_BACSU 006987 BACILLUS SUBTILIS 1423 -11532102 7000694748 yvde transcription regulator lacI family homolog yvde (db:pir2.dat) E70033 E70033 Bacillus subtilis 1423 -11532102 7500952841 yvde (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to transcriptional regulator (laci family)) (le:157294) (re:158244) (di:complement) BSUB0018 Z99121 g2635976 Bacillus subtilis 1423 -11532102 1500694030 yvde hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:probable transcriptional regulator (laci family)) (le:23427) (re:24377) (di:direct) BSZ94043 Z94043 g1945664 Bacillus subtilis 1423 -11532102

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813983	6274	28430	291	96

Description

6500728245 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvdD yvdD Bacillus subtilis 1423 -11532103 7000692821 yvdd conserved hypothetical protein yvdd (cl:yeast conserved hypothetical protein yj1055w) (db:pir2.dat) D70033 D70033 Bacillus subtilis 1423 -11532103 1500694029 yvdd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:158450) (re:159025) (di:complement) BSUB0018 Z99121 g2635977 Bacillus subtilis 1423 -11532103 7500963881 yvdd hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to yjf5\_yeast hypothetical 26.9 kd protein) (le:22646) (re:23221) (di:direct) BSZ94043 Z94043 g1945663 Bacillus subtilis 1423 -11532103

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501813999	6275	28431	201	66

Description

6500728246 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvdC yvdC Bacillus subtilis 1423 -11532104 7000694005 yvdc hypothetical protein yvdc (db:pir2.dat) C70033 C70033 Bacillus subtilis 1423 -11532104 7500964797 yvdc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:159142) (re:159462) (di:direct) BSUB0018 Z99121 g2635978 Bacillus subtilis 1423 -11532104

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814001	6276	28432	315	105

Description

6500728247 hypothetical protein:similar to transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvdB yvdB Bacillus subtilis 1423 -11532105 7000694818 yvdb transporter homolog yvdb (db:pir2.dat) B70033 B70033 Bacillus subtilis 1423 -11532105 1500694027 yvdb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to transporter) (le:159489) (re:161081) (di:complement) BSUB0018 Z99121 g2635979 Bacillus subtilis 1423 -11532105 7500965372 yvdb hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:probable transporter) (le:20590) (re:22182) (di:direct) BSZ94043 Z94043 g1945661 Bacillus subtilis 1423 -11532105

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814002	6277	28433	240	79

Description

6500728248 hypothetical protein:similar to carbonic anhydrase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvda yvda Bacillus subtilis 1423 -11532106 7000692320 yvda carbonic anhydrase homolog yvda (cl:methanobacterium thermoautotrophicum carbonic anhydrase) (db:pir2.dat) A70033 A70033 Bacillus subtilis 1423 -11532106 1500694026 yvda (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to carbonic anhydrase) (le:161100) (re:161693) (di:complement) BSUB0018 Z99121 g2635980 Bacillus subtilis 1423 -11532106 7500963489 yvda hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to tremblnew|u52681|mt52681\_5) (le:19978) (re:20571) (di:direct) BSZ94043 Z94043 g1945660 Bacillus subtilis 1423 -11532106

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814004	6278	28434	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814005	6279	28435	351	116

Description

6500728249 hypothetical protein:similar to glycerate dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvcT yvcT Bacillus subtilis 1423 -11532107 7000693059 yvcT glycerate dehydrogenase homolog yvcT (db:pir2.dat) H70032 H70032 Bacillus subtilis 1423 -11532107 7500964031 yvcT (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to glycerate dehydrogenase) (le:162076) (re:163053) (di:direct) BSUB0018 Z99121 g2635981 Bacillus subtilis 1423 -11532107

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814006	6280	28436	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814008	6281	28437	495	164

Description

6500728250 hypothetical protein:similar to abc transporter:permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvcS yvcS Bacillus subtilis 1423 -11532108 7000692123 yvcS abc transporter permease homolog yvcS (db:pir2.dat) G70032 G70032 Bacillus subtilis 1423 -11532108 1500694024 yvcS (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to abc transporter (permease)) (le:163091) (re:165031) (di:complement) BSUB0018 Z99121 g2635982 Bacillus subtilis 1423 -11532108 7500963362 yvcS hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:probable permease) (le:16640) (re:18580) (di:direct) BSZ94043 Z94043 g1945658 Bacillus subtilis 1423 -11532108

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814010	6282	28438	705	234

Description

6500728251 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvcr yvcr Bacillus subtilis 1423 -11532109 7000692105 yvcr abc transporter atp-binding protein homolog yvcr (cl:atp-binding cassette homology) (db:pir2.dat) F70032 F70032 Bacillus subtilis 1423 -11532109 1500694023 yvcr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to abc transporter (atp-binding protein)) (le:165006) (re:165785) (di:complement) BSUB0018 Z99121 g2635983 Bacillus subtilis 1423 -11532109 7500963346 yvcr hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:probable abc transporter) (le:15886) (re:16665) (di:direct) BSZ94043 Z94043 g1945657 Bacillus subtilis 1423 -11532109

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814011	6283	28439	771	256

Description

6500728252 hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvcQ yvcQ Bacillus subtilis 1423 -11532110 7000694879 yvcq two-component sensor histidine kinase homolog yvcq (db:pir2.dat) E70032 E70032 Bacillus subtilis 1423 -11532110 1500694022 yvcq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to two-component sensor histidine kinase) (le:165868) (re:166938) (di:complement) BSUB0018 Z99121 g2635984 Bacillus subtilis 1423 -11532110 7500965418 yvcq hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:probable two component regulatory system: sensor) (le:14733) (re:15803) (di:direct) BSZ94043 Z94043 g1945656 Bacillus subtilis 1423 -11532110

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814013	6284	28440	249	82

Description

6500728253 hypothetical protein:similar to two-component response regulator (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvcP yvcP Bacillus subtilis 1423 -11532111 7000694850 yvcP two-component response regulator yvcq homolog yvcP) (cl:ompr protein:response regulator homology) (db:pir2.dat) D70032 D70032 Bacillus subtilis 1423 -11532111 1500694021 yvcP (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to two-component response regulator (yvcq)) (le:166932) (re:167645) (di:complement) BSUB0018 Z99121 g2635985 Bacillus subtilis 1423 -11532111 7500965399 yvcP hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:probable two component regulatory system:) (le:14026) (re:14739) (di:direct) BSZ94043 Z94043 g1945655 Bacillus subtilis 1423 -11532111

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814014	6285	28441	243	80

Description

6500728254 hypothetical protein:similar to n-hydroxyarylamine o-acetyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvcN yvcN Bacillus subtilis 1423 -11532112 7000694288 yvcn n-hydroxyarylamine o-acetyltransferase homolog yvcn (db:pir2.dat) C70032 C70032 Bacillus subtilis 1423 -11532112 1500694020 yvcn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to n-hydroxyarylamine o-acetyltransferase) (le:168037) (re:168801) (di:complement) BSUB0018 Z99121 g2635986 Bacillus subtilis 1423 -11532112 7500964997 yvcn hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to ary2\_rabit arylamine) (le:12870) (re:13634) (di:direct) BSZ94043 Z94043 g1945654 Bacillus subtilis 1423 -11532112

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814018	6286	28442	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814025	6287	28443	900	300

Description

GTC ORF with score 116 to: (db:genpept-bct2) (de:streptomyces hygroscopicus putative pteridine-dependentdioxxygenase, pks modules 1,2,3 and 4, and putative regulatoryprotein genes, complete cds and putative hydroxylase gene, partialcds.) (nt:orf8) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814042	6288	28444	609	202

Description

6500728255 hypothetical protein:similar to hypothetical proteins  
(gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvcl  
yvcl Bacillus subtilis 1423 -11532113 7000692820 yvcl conserved  
hypothetical protein yvcl (db:pir2.dat) B70032 B70032 Bacillus subtilis 1423  
-11532113 1500694018 yvcl (fn:unknown) (db:genpept-bct1) (de:bacillus  
subtilis complete genome (section 18 of 21): from 3399551to 3609060.)  
(nt:similar to hypothetical proteins) (le:169083) (re:170033)  
(di:complement) BSUB0018 Z99121 g2635988 Bacillus subtilis 1423 -11532113  
7500963880 yvcl hypothetical protein (db:genpept-bct1) (de:b.subtilis  
genomic dna fragment (88 kb).) (nt:similar to y103 mycge hypothetical  
protein mg103) (le:11638) (re:12588) (di:direct) BSZ94043 Z94043 g1945652  
Bacillus subtilis 1423 -11532113

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814064	6289	28445	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814073	6290	28446	2019	673

Description

6500728256 hypothetical protein:similar to hypothetical proteins  
(gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvck  
yvck Bacillus subtilis 1423 -11532114 7000692819 yvck conserved  
hypothetical protein yvck (cl:escherichia coli ybhk protein) (db:pir2.dat)  
A70032 A70032 Bacillus subtilis 1423 -11532114 7500955835 yvck (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21):  
from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:170056)  
(re:171051) (di:complement) BSUB0018 Z99121 g2635989 Bacillus subtilis 1423  
-11532114



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814083	6291	28447	894	297

Description

6500728257 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvcJ yvcJ Bacillus subtilis 1423 -11532115 7000688626 yvcj (de:hypothetical 33.9 kd protein in crh-trxb intergenic region) (db:swissprot) YVCJ\_BACSU 006973 BACILLUS SUBTILIS 1423 -11532115 7000688627 yvcj conserved hypothetical protein yvcj (cl:bacillus subtilis conserved hypothetical protein yvcj) (db:pir2.dat) H70031 H70031 Bacillus subtilis 1423 -11532115 1500694016 yvcj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:171011) (re:171898) (di:complement) BSUB0018 Z99121 g2635990 Bacillus subtilis 1423 -11532115 7500952836 yvcj hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to hypothetical mtcy21b4) (le:9773) (re:10660) (di:direct) BSZ94043 Z94043 g1945650 Bacillus subtilis 1423 -11532115

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814087	6292	28448	291	96

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814090	6293	28449	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814105	6294	28450	675	225

Description

GTC ORF with score 117 to: (or:Homo sapiens) (sr:homo sapiens male brain cdna to mrna, clone\_lib:psport ) (db:genpept-pri2) (de:human mrna for kiaa0269 gene, complete cds.) (nt:similar to volbox carteri extensin (s22697)) (le:243) (re:1922) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814112	6295	28451	210	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814117	6296	28452	603	200

Description

6500728258 hypothetical protein:similar to mutator mutt protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvcI yvcI Bacillus subtilis 1423 -11532116 7000694270 yvci mutator mutt protein homolog yvci (cl:mutt domain homology) (db:pir2.dat) G70031 G70031 Bacillus subtilis 1423 -11532116 1500694015 yvci (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to mutator mutt protein) (le:171923) (re:172399) (di:complement) BSUB0018 Z99121 g2635991 Bacillus subtilis 1423 -11532116 7500964987 yvci hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:probable nudix hydrolase) (le:9272) (re:9748) (di:direct) BSZ94043 Z94043 g1945649 Bacillus subtilis 1423 -11532116

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814120	6297	28453	183	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814122	6298	28454	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814128	6299	28455	918	306

Description

6500728259 yzka:yvce hypothetical protein:similar to cell wall-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvcE yvcE Bacillus subtilis 1423 -11532117 7000692340 yvce cell wall-binding protein homolog yvce (db:pir2.dat) F70031 F70031 Bacillus subtilis 1423 -11532117 1500694012 yvce (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: yzka; similar to cell) (le:173873) (re:175294) (di:complement) BSUB0018 Z99121 g2635993 Bacillus subtilis 1423 -11532117 7500963508 yvce hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to p54\_entfc p54 protein precursor) (le:6377) (re:7798) (di:direct) BSZ94043 Z94043 g1945646 Bacillus subtilis 1423 -11532117

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814140	6300	28456	192	63

Description

6500728260 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvcD yvcD Bacillus subtilis 1423 -11532118  
7000694004 yvcD hypothetical protein yvcD (cl:tetratricopeptide repeat homology) (db:pir2.dat) E70031 E70031 Bacillus subtilis 1423 -11532118  
1500694011 yvcD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:175675) (re:177129) (di:complement) BSUB0018 Z99121 g2635994 Bacillus subtilis 1423 -11532118 7500964796 yvcD hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (le:4542) (re:5996) (di:direct) BSZ94043 Z94043 g1945645 Bacillus subtilis 1423 -11532118

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814141	6301	28457	261	86

Description

6500728261 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvcC yvcC Bacillus subtilis 1423 -11532119 7000692104 yvcC abc transporter atp-binding protein homolog yvcC (cl:atp-binding cassette homology) (db:pir2.dat) D70031 D70031 Bacillus subtilis 1423 -11532119  
1500694010 yvcC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to abc transporter (atp-binding protein)) (le:177255) (re:179024) (di:complement) BSUB0018 Z99121 g2635995 Bacillus subtilis 1423 -11532119  
7500963345 yvcC hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:probable abc transporter) (le:2647) (re:4416) (di:direct) BSZ94043 Z94043 g1945644 Bacillus subtilis 1423 -11532119

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814153	6302	28458	186	61

Description

6500728262 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvzA yvzA Bacillus subtilis 1423 -11532120  
7000694036 yvzA hypothetical protein yvza (db:pir2.dat) E70049 E70049 Bacillus subtilis 1423 -11532120 7500964821 yvza (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:179189) (re:179548) (di:complement) BSUB0018 Z99121 g2635996 Bacillus subtilis 1423 -11532120

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814154	6303	28459	285	94

Description

6500728263 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvcB yvcB Bacillus subtilis 1423 -11532121  
7000694003 yvcB hypothetical protein yvcB (db:pir2.dat) C70031 C70031 Bacillus subtilis 1423 -11532121 1500694009 yvcB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:179563) (re:181473) (di:complement) BSUB0018 Z99121 g2635997 Bacillus subtilis 1423 -11532121 7500964795 yvcB hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (le:198) (re:2108) (di:direct) BSZ94043 Z94043 g1945643 Bacillus subtilis 1423 -11532121

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814158	6304	28460	501	166

Description

6500728264 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvCA yvCA Bacillus subtilis 1423 -11532122  
7000694002 yvCA hypothetical protein yvCA (db:pir2.dat) B70031 B70031 Bacillus subtilis 1423 -11532122 5500701778 yvCA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:181475) (re:182200) (di:complement) BSUB0018 Z99121 g2635998 Bacillus subtilis 1423 -11532122 7500964794 yvra yvra (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (nt:putative lipoprotein) (le:45633) (re:46358) (di:direct) AF017113 AF017113 g2618872 Bacillus subtilis 1423 -11532122

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814168	6305	28461	315	104

Description

6500728265 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvpB yvpB Bacillus subtilis 1423 -11532123  
7000694025 yvpB hypothetical protein yvpB (db:pir2.dat) B70045 B70045 Bacillus subtilis 1423 -11532123 5500701769 yvpB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:189121) (re:189873) (di:direct) BSUB0018 Z99121 g2636007 Bacillus subtilis 1423 -11532123 7500964814 yvpB yvpB (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:37960) (re:38712) (di:complement) AF017113 AF017113 g2618863 Bacillus subtilis 1423 -11532123

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814179	6306	28462	603	201

Description

GTC ORF with score 248 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814182	6307	28463	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814189	6308	28464	387	128

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814190	6309	28465	573	191

Description

6500728266 hypothetical protein:similar to pectate lyase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvpA yvpA Bacillus subtilis 1423 -11532124 7000694351 yvpA pectate lyase homolog yvpA (db:pir2.dat) A70045 A70045 Bacillus subtilis 1423 -11532124 5500701768 yvpA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to pectate lyase) (le:190113) (re:190778) (di:direct) BSUB0018 Z99121 g2636008 Bacillus subtilis 1423 -11532124 7500965041 yvpA yvpA (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (nt:the n-terminal region is similar to pectate lyases) (le:37055) (re:37720) (di:complement) AF017113 AF017113 g2618862 Bacillus subtilis 1423 -11532124

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814196	6310	28466	405	134

Description

GTC ORF with score 97 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac f4i18 genomic sequence,complete sequence.) (nt:unknown protein) (le:58572:59030:59321) (re:58940:59240:59385) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814201	6311	28467	477	158

Description

GTC ORF with score 204 to: (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to cytochrome p450 / nadph-cytochrome p450) (le:173710) (re:176874) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814215	6312	28468	1305	435

Description

6500728267 hypothetical protein:similar to o-acetyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvoF yvoF Bacillus subtilis 1423 -11532125 7000694330 yvof o-acetyltransferase homolog yvof (db:pir2.dat) H70044 H70044 Bacillus subtilis 1423 -11532125 5500701767 yvof (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to o-acetyltransferase) (le:190798) (re:191316) (di:complement) BSUB0018 Z99121 g2636009 Bacillus subtilis 1423 -11532125 7500965025 yvof putative acetyltransferase (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:36517) (re:37035) (di:direct) AF017113 AF017113 g2618861 Bacillus subtilis 1423 -11532125

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814226	6313	28469	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814232	6314	28470	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814233	6315	28471	657	218

Description

6500728268 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvoD yvoD Bacillus subtilis 1423 -11532126  
7000694024 yvod hypothetical protein yvod (db:pir2.dat) F70044 F70044 Bacillus subtilis 1423 -11532126 5500701765 yvod (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:191967) (re:192905) (di:complement) BSUB0018 Z99121 g2636011 Bacillus subtilis 1423 -11532126 7500964813 yvod yvod (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:34928) (re:35866) (di:direct) AF017113 AF017113 g2618859 Bacillus subtilis 1423 -11532126

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814247	6316	28472	570	190

Description

6500728269 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvoB yvoB Bacillus subtilis 1423 -11532127 7000692839 yvob conserved hypothetical protein yvob (cl:hypothetical protein yvob) (db:pir2.dat) E70044 E70044 Bacillus subtilis 1423 -11532127 5500701763 yvob (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:193752) (re:194684) (di:complement) BSUB0018 Z99121 g2636013 Bacillus subtilis 1423 -11532127 7500955905 ptsk hpr ser kinase (fn:activation of the ccpa binding to cres) (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (nt:similar to the mycoplasma genitalium hypothetical) (le:33149) (re:34081) (di:direct) AF017113 AF017113 g2618857 Bacillus subtilis 1423 -11532127

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814259	6317	28473	441	146

Description

6500728270 hypothetical protein:similar to transcriptional regulator:gntr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvoA yvoA Bacillus subtilis 1423 -11532128 7000694742 yvoA transcription regulator gntr family homolog yvoA (cl:transcription regulator gntr) (db:pir2.dat) D70044 D70044 Bacillus subtilis 1423 -11532128 5500701760 yvoA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to transcriptional regulator (gntr family)) (le:196799) (re:197530) (di:direct) BSUB0018 Z99121 g2636016 Bacillus subtilis 1423 -11532128 7500965314 yvoA yvoA (fn:belongs to the gntr family of transcriptional) (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:30303) (re:31034) (di:complement) AF017113 AF017113 g2618854 Bacillus subtilis 1423 -11532128

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814261	6318	28474	294	97

Description

6500728271 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvnB yvnB Bacillus subtilis 1423 -11532129 7000694023 yvnB probable phosphoesterase:yvnB (cl:unassigned probable phosphoesterases:phosphoesterase core homology) (ec:3.1.-.-) (db:pir2.dat) C70044 C70044 Bacillus subtilis 1423 -11532129 5500701759 yvnB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:197550) (re:201419) (di:complement) BSUB0018 Z99121 g2636017 Bacillus subtilis 1423 -11532129 6000689221 yvnB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:10) (re:3879) (di:complement) BSUB0019 Z99122 g2636030 Bacillus subtilis 1423 -11532129 7500954189 yvnB yvnB (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:26414) (re:30283) (di:direct) AF017113 AF017113 g2618853 Bacillus subtilis 1423 -11532129



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814262	6319	28475	1053	350

Description

6500728272 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvna yvna Bacillus subtilis 1423 -11532130 7000692838 yvna conserved hypothetical protein yvna (cl:hypothetical protein yhj) (db:pir2.dat) B70044 B70044 Bacillus subtilis 1423 -11532130 5500701758 yvna (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins from b. subtilis) (le:201584) (re:202057) (di:direct) BSUB0018 Z99121 g2636018 Bacillus subtilis 1423 -11532130 6000689219 yvna (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to hypothetical proteins from b. subtilis) (le:4044) (re:4517) (di:direct) BSUB0019 Z99122 g2636031 Bacillus subtilis 1423 -11532130 7500955933 yvna yvna (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (nt:similar to bacillus subtilis yzha protein:) (le:25776) (re:26249) (di:complement) AF017113 AF017113 g2618852 Bacillus subtilis 1423 -11532130

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814279	6320	28476	186	61

Description

6500728273 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvmC yvmC Bacillus subtilis 1423 -11532131 7000692837 yvmC conserved hypothetical protein yvmC (db:pir2.dat) A70044 A70044 Bacillus subtilis 1423 -11532131 5500701756 yvmC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to hypothetical proteins) (le:203331) (re:204077) (di:complement) BSUB0018 Z99121 g2636020 Bacillus subtilis 1423 -11532131 6000689215 yvmC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to hypothetical proteins) (le:5791) (re:6537) (di:complement) BSUB0019 Z99122 g2636033 Bacillus subtilis 1423 -11532131 7500963890 yvmC yvmC (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:23756) (re:24502) (di:direct) AF017113 AF017113 g2618850 Bacillus subtilis 1423 -11532131

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814281	6321	28477	1470	489

Description

GTC ORF with score 141 to: (db:genpept-bct1) (de:methanobacterium thermoautotrophicum from bases 1698671 to 1709269(section 145 of 148) of the complete genome.) (nt:function code:10.08 - metabolism of macromolecules,) (le:8495) (re:9430) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814282	6322	28478	330	109

Description

5000689895 yzha:yvmb hypothetical protein:hypothetical 19.7 kd protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvmb yvmb Bacillus subtilis 1423 -11532132 7500952856 yvmb (de:hypothetical 19.7 kd protein in cypx-uvra intergenic region) (db:swissprot) YVMB\_BACSU P40762 BACILLUS SUBTILIS 1423 -11532132 7000688837 yvmb conserved hypothetical protein yvmb (cl:hypothetical protein yhj) (db:pir2.dat) S47218 S47218 Bacillus subtilis 1423 -11532132 5500684828 (db:genpept-bct1) (de:b.subtilis (bd170) protein secretion gene.) (nt:involved in protein secretion) (le:18) (re:527) (di:direct) BPROSEC Z36881 g535052 Bacillus subtilis 1423 -11532132 219554 yvmb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: yzha; similar to hypothetical) (le:204503) (re:205012) (di:direct) BSUB0018 Z99121 g2636021 Bacillus subtilis 1423 -11532132 6500728274 yvmb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: yzha; similar to hypothetical) (le:6963) (re:7472) (di:direct) BSUB0019 Z99122 g2636034 Bacillus subtilis 1423 -11532132 6000686043 yzha yzha (fn:involved in protein secretion) (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:22821) (re:23330) (di:complement) AF017113 AF017113 g2618849 Bacillus subtilis 1423 -11532132 117010 yvmb (de:hypothetical 19.7 kd protein in cypx-uvra intergenic region) (db:swissprot) YVMB\_BACSU P40762 BACILLUS SUBTILIS 1423 -11532132 170173 yvmb conserved hypothetical protein yvmb (cl:hypothetical protein yhj) (db:pir) S47218 S47218 Bacillus subtilis 1423 -11532132

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814289	6323	28479	594	198

Description

6500728275 hypothetical protein:similar to transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvmA yvmA Bacillus subtilis 1423 -11532133 7000694819 yvma transporter homolog yvma (db:pir2.dat) G70043 G70043 Bacillus subtilis 1423 -11532133 5500701755 yvma (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to transporter) (le:205033) (re:206244) (di:direct) BSUB0018 Z99121 g2636022 Bacillus subtilis 1423 -11532133 6000689213 yvma (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to transporter) (le:7493) (re:8704) (di:direct) BSUB0019 Z99122 g2636035 Bacillus subtilis 1423 -11532133 7500965373 yvma yvma (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (nt:belongs to the major facilitator family) (le:21589) (re:22800) (di:complement) AF017113 AF017113 g2618848 Bacillus subtilis 1423 -11532133

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814292	6324	28480	729	242

Description

6500728276 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvld yvld Bacillus subtilis 1423 -11532134 7000694022 yvld hypothetical protein yvld (cl:hypothetical protein yvld) (db:pir2.dat) F70043 F70043 Bacillus subtilis 1423 -11532134 5500701754 yvld (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:206272) (re:206631) (di:complement) BSUB0018 Z99121 g2636023 Bacillus subtilis 1423 -11532134 6000689211 yvld (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:8732) (re:9091) (di:complement) BSUB0019 Z99122 g2636036 Bacillus subtilis 1423 -11532134 7500955925 yvld yvld (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:21202) (re:21561) (di:direct) AF017113 AF017113 g2618847 Bacillus subtilis 1423 -11532134

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814301	6325	28481	735	244
<u>Description</u>				
6500728277 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvlC yvlC Bacillus subtilis 1423 -11532135 7000694021 yvlc hypothetical protein yvlc (db:pir2.dat) E70043 E70043 Bacillus subtilis 1423 -11532135 5500701753 yvlc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:206633) (re:206830) (di:complement) BSUB0018 Z99121 g2636024 Bacillus subtilis 1423 -11532135 6000689209 yvlc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:9093) (re:9290) (di:complement) BSUB0019 Z99122 g2636037 Bacillus subtilis 1423 -11532135 7500964812 yvlc yvlc (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (nt:shows weak similarity to escherichia coli phage) (le:21003) (re:21200) (di:direct) AF017113 AF017113 g2618846 Bacillus subtilis 1423 -11532135				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814302	6326	28482	789	262
<u>Description</u>				
6500728278 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvlB yvlB Bacillus subtilis 1423 -11532136 7000694020 yvlb hypothetical protein yvlb (db:pir2.dat) D70043 D70043 Bacillus subtilis 1423 -11532136 5500701752 yvlb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:206835) (re:207932) (di:complement) BSUB0018 Z99121 g2636025 Bacillus subtilis 1423 -11532136 6000689207 yvlb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:9295) (re:10392) (di:complement) BSUB0019 Z99122 g2636038 Bacillus subtilis 1423 -11532136 7500964811 yvlb yvlb (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:19901) (re:20998) (di:direct) AF017113 AF017113 g2618845 Bacillus subtilis 1423 -11532136				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814315	6327	28483	207	68
<u>Description</u>				
Hypothetical protein				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814318	6328	28484	477	158

Description

6500728279 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvlA yvlA Bacillus subtilis 1423 -11532137  
 7000694019 yvla hypothetical protein yvla (db:pir2.dat) C70043 C70043 Bacillus subtilis 1423 -11532137 5500701751 yvla (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:207957) (re:208283) (di:complement) BSUB0018 Z99121 g2636026 Bacillus subtilis 1423 -11532137 6000689205 yvla (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:10417) (re:10743) (di:complement) BSUB0019 Z99122 g2636039 Bacillus subtilis 1423 -11532137 7500964810 yvla yvla (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:19550) (re:19876) (di:direct) AF017113 AF017113 g2618844 Bacillus subtilis 1423 -11532137

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814327	6329	28485	747	248

Description

6500728280 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvkN yvkN Bacillus subtilis 1423 -11532138  
 7000694018 yvkn hypothetical protein yvkn (db:pir2.dat) B70043 B70043 Bacillus subtilis 1423 -11532138 5500701750 yvkn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:208501) (re:208731) (di:direct) BSUB0018 Z99121 g2636027 Bacillus subtilis 1423 -11532138 6000689203 yvkn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:10961) (re:11191) (di:direct) BSUB0019 Z99122 g2636040 Bacillus subtilis 1423 -11532138 7500964809 yvkn yvkn (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:19102) (re:19332) (di:complement) AF017113 AF017113 g2618843 Bacillus subtilis 1423 -11532138

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814333	6330	28486	324	107

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814334	6331	28487	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814347	6332	28488	297	98

Description

6500728281 hypothetical protein:similar to flagellin (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvzb yvzb Bacillus subtilis 1423 -11532139 7000692994 yvzb flagellin homolog yvzb (db:pir2.dat) F70049 F70049 Bacillus subtilis 1423 -11532139 6000691719 yvzb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to flagellin) (le:208930) (re:209412) (di:complement) BSUB0018 Z99121 g2636028 Bacillus subtilis 1423 -11532139 7500963987 yvzb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to flagellin) (le:11390) (re:11872) (di:complement) BSUB0019 Z99122 g2636041 Bacillus subtilis 1423 -11532139

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814348	6333	28489	237	78

Description

6500728282 hypothetical protein:similar to pyruvate:water dikinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvkC yvkC Bacillus subtilis 1423 -11532140 7000694486 yvkC pyruvate:water dikinase homolog yvkC (db:pir2.dat) A70043 A70043 Bacillus subtilis 1423 -11532140 5500701747 yvkC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to pyruvate,water dikinase) (le:17763) (re:20258) (di:direct) BSUB0019 Z99122 g2636045 Bacillus subtilis 1423 -11532140 7500965125 yvkC yvkC (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (nt:similar to pep-utilizing enzymes) (le:10035) (re:12530) (di:complement) AF017113 AF017113 g2618839 Bacillus subtilis 1423 -11532140

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814355	6334	28490	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814358	6335	28491	375	124

Description

GTC ORF with score 115 to: (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #261(30.0-30.3 min.)) (nt:orf\_id:o260#11; similar to (swissprot accession) (le:<1) (re:403) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814360	6336	28492	984	328

Description

6500728283 hypothetical protein:similar to transcriptional regulator:tetr/acrr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvkB yvkB Bacillus subtilis 1423 -11532141 7000694788 yvkB transcription regulator tetr/acrr family homolog yvkB (db:pir2.dat) H70042 H70042 Bacillus subtilis 1423 -11532141 5500701746 yvkB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to transcriptional regulator (tetr/acrr) (le:20334) (re:20903) (di:direct) BSUB0019 Z99122 g2636046 Bacillus subtilis 1423 -11532141 7500965349 yvkB yvkB (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (nt:belongs to the tetr/acrr family of transcriptional) (le:9390) (re:9959) (di:complement) AF017113 AF017113 g2618838 Bacillus subtilis 1423 -11532141

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814390	6337	28493	408	136

Description

6500728284 hypothetical protein:similar to multidrug-efflux transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvka yvka Bacillus subtilis 1423 -11532142 7000694259 yvka multidrug-efflux transporter homolog yvka (db:pir2.dat) G70042 G70042 Bacillus subtilis 1423 -11532142 5500701745 yvka (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to multidrug-efflux transporter) (le:20934) (re:22268) (di:direct) BSUB0019 Z99122 g2636047 Bacillus subtilis 1423 -11532142 7500964979 yvka yvka (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (nt:belongs to the major facilitator family) (le:8025) (re:9359) (di:complement) AF017113 AF017113 g2618837 Bacillus subtilis 1423 -11532142

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814393	6338	28494	465	154

Description

6500728285 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvjD yvjD Bacillus subtilis 1423 -11532143 7000694017 yvjD hypothetical protein yvjD (db:pir2.dat) F70042 F70042 Bacillus subtilis 1423 -11532143 5500701744 yvjD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:22316) (re:23509) (di:complement) BSUB0019 Z99122 g2636048 Bacillus subtilis 1423 -11532143 7500964808 yvjD yvjD (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (nt:transmembrane protein) (le:6784) (re:7977) (di:direct) AF017113 AF017113 g2618836 Bacillus subtilis 1423 -11532143

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814401	6339	28495	204	67

Description

6500728286 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yvzD yvzD Bacillus subtilis 1423 -11532144  
7000694038 yvzd hypothetical protein yvzd (db:pir2.dat) H70049 H70049  
Bacillus subtilis 1423 -11532144 7500964823 yvzd (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21):  
from 3597091to 3809700.) (le:23588) (re:23926) (di:complement) BSUB0019  
Z99122 g2636049 Bacillus subtilis 1423 -11532144

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814402	6340	28496	348	115

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814411	6341	28497	489	162

Description

6500728287 hypothetical protein:similar to carboxy-terminal processing  
protease (gtcfc:10.11) (ec:3.4.21.-) (keggfc:14.1) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yvjB yvjB Bacillus subtilis 1423 -11532145  
7000692322 yvjB carboxy-terminal processing proteinase homolog yvjB  
(cl:carboxyl-terminal processing proteinase) (db:pir2.dat) E70042 E70042  
Bacillus subtilis 1423 -11532145 5500701743 yvjB (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21):  
from 3597091to 3809700.) (nt:similar to carboxy-terminal processing  
protease) (le:24326) (re:25768) (di:complement) BSUB0019 Z99122 g2636050  
Bacillus subtilis 1423 -11532145 7500963491 yvjB putative protease  
(db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.)  
(le:4525) (re:5967) (di:direct) AF017113 AF017113 g2618834 Bacillus subtilis  
1423 -11532145

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814421	6342	28498	189	62

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814431	6343	28499	288	95

Description

6500728288 hypothetical protein:similar to hypothetical proteins  
 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvja  
 yvja Bacillus subtilis 1423 -11532146 7000692836 yvja conserved  
 hypothetical protein yvja (cl:conserved hypothetical protein yitt)  
 (db:pir2.dat) D70042 D70042 Bacillus subtilis 1423 -11532146 5500701739  
 yvja (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome  
 (section 19 of 21): from 3597091to 3809700.) (nt:similar to hypothetical  
 proteins) (le:28098) (re:28943) (di:complement) BSUB0019 Z99122 g2636054  
 Bacillus subtilis 1423 -11532146 7500963889 yvja yvja (db:genpept-bct2)  
 (de:bacillus subtilis 300-304 degree genomic sequence.) (nt:similar to  
 thermophilic bacterium ps-3 hypothetical) (le:1350) (re:2195) (di:direct)  
 AF017113 AF017113 g2618831 Bacillus subtilis 1423 -11532146

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814435	6344	28500	600	199

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501814450	6345	28501	798	265

#### Description

6500728289 yvii:yvyd hypothetical protein:hypothetical 22.0 kd protein in flit-seca intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvyD yvyD Bacillus subtilis 1423 -11532147

7500952866 yvyd (de:hypothetical 22.0 kd protein in flit-seca intergenic region) (db:swissprot) YVYD\_BACSU P28368 BACILLUS SUBTILIS 1423 -11532147

7000688630 yvyd ribosomal protein s30ae family homolog yvyd:hypothetical 13.6k protein div+ 5 region:hypothetical protein 189 flir 5 region (db:pir2.dat) I40400 I40400 Bacillus subtilis 1423 -11532147 5000689714 orf189 (db:genpept-bct1) (de:b.subtilis (hb2058) genes for flid, flis, flit proteins.) (le:3511) (re:4080) (di:direct) BSFLIDST Z31376 g499384 Bacillus subtilis 1423 -11532147 219213 yvyd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: yvii; similar to ribosomal) (le:32973) (re:33542) (di:complement) BSUB0019 Z99122 g2636057 Bacillus subtilis 1423 -11532147 298112 yvii sigma-54 modulator homolog (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj), ycr59c/yigz homolog (yvhk), histidine kinase (degs), transcriptional regulator of degradation enzyme (degu), (degv), (comfa), (comfb), (comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762348 Bacillus subtilis 1423 -11532147 116613 yvyd (de:hypothetical 22.0 kd protein in flit-seca intergenic region) (db:swissprot) YVYD\_BACSU P28368 BACILLUS SUBTILIS 1423 -11532147 170291 yvyd ribosomal protein s30ae family homolog yvyd:hypothetical 13.6k protein div+ 5 region:hypothetical protein 189 flir 5 region (db:pir) I40400 I40400 Bacillus subtilis 1423 -11532147 220129 yvii sigma-54 modulator homolog (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj), ycr59c/yigz homolog (yvhk), histidine kinase (degs), transcriptional regulator of degradation enzyme (degu), (degv), (comfa), (comfb), (comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762348 Bacillus subtilis 1423 -11532147

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814454	6346	28502	1647	548

Description

6500728290 yvih:yvyc hypothetical protein:hypothetical 13.0 kd protein in hag-flid intergenic region:orf 99 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvyC yvyC Bacillus subtilis 1423 -11532148  
7500952865 yvyc (de:hypothetical 13.0 kd protein in hag-flid intergenic region (orf 99)) (db:swissprot) YVYC\_BACSU P39737 BACILLUS SUBTILIS 1423 -11532148 7000688629 yvyc flagellar protein homolog yvyc (db:pir2.dat) I40396 I40396 Bacillus subtilis 1423 -11532148 5000689713 orf99 (db:genpept-bct1) (de:b.subtilis (hb2058) genes for flid, flis, flit proteins.) (le:329) (re:658) (di:direct) BSFLIDST Z31376 g580862 Bacillus subtilis 1423 -11532148 219209 yvyc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: yvih; similar to flagellar) (le:36395) (re:36724) (di:complement) BSUB0019 Z99122 g2636061 Bacillus subtilis 1423 -11532148 298108 yvih flagellar protein (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj), ycr59c/yigz homolog (yvhk), histidine kinase (degs), transcriptional regulator of degradation enzyme (degu), (degv), (comfa), (comfb), (comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762344 Bacillus subtilis 1423 -11532148 116612 yvyc (de:hypothetical 13.0 kd protein in hag-flid intergenic region (orf 99)) (db:swissprot) YVYC\_BACSU P39737 BACILLUS SUBTILIS 1423 -11532148  
170292 yvyc flagellar protein homolog yvyc (db:pir) I40396 I40396 Bacillus subtilis 1423 -11532148 220125 yvih flagellar protein (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj), ycr59c/yigz homolog (yvhk), histidine kinase (degs), transcriptional regulator of degradation enzyme (degu), (degv), (comfa), (comfb), (comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762344 Bacillus subtilis 1423 -11532148

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814455	6347	28503	393	131

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814469	6348	28504	1404	467

Description

6500728291 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yviF yviF Bacillus subtilis 1423 -11532149 7000692835 yvif conserved hypothetical protein yvif (db:pir2.dat) C70042 C70042 Bacillus subtilis 1423 -11532149 220122 yvif (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to hypothetical proteins from b. subtilis) (le:38234) (re:38665) (di:complement) BSUB0019 Z99122 g2636064 Bacillus subtilis 1423 -11532149 298105 yvif transmembrane protein (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj), ycr59c/yigz homolog (yvhk), histidine kinase (degs), transcriptional regulator of degradation enzyme (degu), (degv), (comfa), (comfb), (comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762341 Bacillus subtilis 1423 -11532149

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814472	6349	28505	387	128

Description

6500728292 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yviE yviE Bacillus subtilis 1423 -11532150 7000694016 yvie hypothetical protein yvie (db:pir2.dat) B70042 B70042 Bacillus subtilis 1423 -11532150 220121 yvie (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:38686) (re:39261) (di:complement) BSUB0019 Z99122 g2636065 Bacillus subtilis 1423 -11532150 298104 yvie (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj), ycr59c/yigz homolog (yvhk), histidine kinase (degs), transcriptional regulator of degradation enzyme (degu), (degv), (comfa), (comfb), (comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762340 Bacillus subtilis 1423 -11532150

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814486	6350	28506	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814495	6351	28507	612	203

Description

6500728293 yvic:yvyg hypothetical protein:hypothetical 18.2 kd protein in flgm-flgk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvyG yvyG Bacillus subtilis 1423 -11532151  
 116616 yvyg (de:hypothetical 18.2 kd protein in flgm-flgk intergenic region) (db:swissprot) YVYG\_BACSU P39808 BACILLUS SUBTILIS 1423 -11532151  
 7000688632 yvyg flagellar protein homolog yvyg (db:pir2.dat) C70049 C70049 Bacillus subtilis 1423 -11532151 215616 (sr:bacillus subtilis (strain w168) (library: lambda gtwes library) (db:genpept-bct1) (de:bacillus subtilis (clones pdm116 and pdm113) flagellin synthesisregulatory protein (flgm) and flagellar hook-filament junctionprotein (flgk) genes and orf139, orf...  
 BACFLGMK L14437 g451870 Bacillus subtilis 1423 -11532151 220118 yvyg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: yvic; similar to flagellar) (le:41757) (re:42239) (di:complement) BSUB0019 Z99122 g2636068 Bacillus subtilis 1423 -11532151 298101 yvic flagellar protein (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj), ycr59c/yigz homolog (yvhk), histidine kinase (degs), transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb), (comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762337 Bacillus subtilis 1423 -11532151 5000689717 (de:(yvyg) (pn:hypothetical 18) (gtcfc:13.07) (ec:) (yvyg\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yvyG yvyG Bacillus subtilis 1423 10058341

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814499	6352	28508	960	319

Description

6500728294 yvib:yvyf hypothetical protein:hypothetical 16.2 kd protein in comf-flgm intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvyF yvyF Bacillus subtilis 1423 -11532152 116615 yvyf (de:hypothetical 16.2 kd protein in comf-flgm intergenic region) (db:swissprot) YVYF\_BACSU P39807 BACILLUS SUBTILIS 1423 -11532152 7000688631 yvyf flagellar protein homolog yvyf (db:pir2.dat) B70049 B70049 Bacillus subtilis 1423 -11532152 215614 (sr:bacillus subtilis (strain w168) (library: lambda gtwes library) (db:genpept-bct1) (de:bacillus subtilis (clones pdm116 and pdm113) flagellin synthesisregulatory protein (flgm) and flagellar hook-filament junctionprotein (flgk) genes and orf139, orf... BACFLGMK L14437 g451868 Bacillus subtilis 1423 -11532152 220116 yvyf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: yvib; similar to flagellar) (le:42602) (re:43021) (di:complement) BSUB0019 Z99122 g2636070 Bacillus subtilis 1423 -11532152 298099 yvib flagellar protein (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj), ycr59c/yigz homolog (yvhk), histidine kinase (degs), transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb), (comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762335 Bacillus subtilis 1423 -11532152 5000689716 (de:(yvyf) (pn:hypothetical 16) (gtcfc:13.07) (ec:) (yvyf\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yvyF yvyF Bacillus subtilis 1423 10058340

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814511	6353	28509	237	78

Description

5000688891 degv:sacu:yvia hypothetical protein:degv protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yviA yviA Bacillus subtilis 1423 -11532153 7500880155 degv (de:degv protein) (db:swissprot) DEGV\_BACSU P32436 BACILLUS SUBTILIS 1423 -11532153 170253 yvia conserved hypothetical protein yvia (db:pir2.dat) D30191 I40386 Bacillus subtilis 1423 -11532153 219082 deguorf3 u3 (db:genpept-bct1) (de:b.subtilis comf gene.) (le:1) (re:846) (di:direct) BSCOMFG Z18629 g39848 Bacillus subtilis 1423 -11532153 6500728295 yvia (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: degv, sacu; similar to) (le:45634) (re:46479) (di:complement) BSUB0019 Z99122 g2636074 Bacillus subtilis 1423 -11532153 298095 degv (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj), ycr59c/yigz homolog (yvhk), histidine kinase (degs), transcriptional regulator of degradation enzyme (degu), (degv), (comfa), (comfb), (comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762331 Bacillus subtilis 1423 -11532153 68240 degv (de:degv protein) (db:swissprot) DEGV\_BACSU P32436 BACILLUS SUBTILIS 1423 -11532153 7000685006 yvia conserved hypothetical protein yvia (db:pir) D30191 D30191 Bacillus subtilis 1423 -11532153 220112 degv (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj), ycr59c/yigz homolog (yvhk), histidine kinase (degs), transcriptional regulator of degradation enzyme (degu), (degv), (comfa), (comfb), (comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762331 Bacillus subtilis 1423 -11532153

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814515	6354	28510	1404	467

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814529	6355	28511	546	181

Description

6500728296 yvhk:yvye hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvyE yvyE Bacillus subtilis 1423 -11532154 7500952867 yvye:yvhk (de:hypothetical 24.8 kd protein in degs-tago intergenic region) (db:swissprot) YVYE\_BACSU P32437 BACILLUS SUBTILIS 1423 -11532154 7000692852 yvye conserved hypothetical protein yvye (cl:hypothetical protein hi0722) (db:pir2.dat) A70049 A70049 Bacillus subtilis 1423 -11532154 298092 yvye (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: yvhk; similar to hypothetical) (le:48723) (re:49376) (di:direct) BSUB0019 Z99122 g2636077 Bacillus subtilis 1423 -11532154 220109 yvhk ycr59c/yigz homolog (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj), ycr59c/yigz homolog (yvhk), histidine kinase (degs), transcriptional regulator of degradation enzyme (degu), (degv), (comfa), (comfb), (comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762328 Bacillus subtilis 1423 -11532154

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814546	6356	28512	570	189

Description

6500728297 hypothetical protein:similar to transcriptional regulator (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvhJ yvhJ Bacillus subtilis 1423 -11532155 7000694790 yvhj probable transcription regulator yvhj (cl:bacillus subtilis probable transcription regulator yvhj) (db:pir2.dat) H70041 H70041 Bacillus subtilis 1423 -11532155 220108 yvhj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to transcriptional regulator) (le:49376) (re:50551) (di:direct) BSUB0019 Z99122 g2636078 Bacillus subtilis 1423 -11532155 298091 yvhj putative transcriptional regulator (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj), ycr59c/yigz homolog (yvhk), histidine kinase (degs), transcriptional regulator of degradation enzyme (degu), (degv), (comfa), (comfb), (comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762327 Bacillus subtilis 1423 -11532155



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814549	6357	28513	483	161

Description

6500728298 yvhi:tago hypothetical protein:teichoic acid linkage unit synthesis:synthesis of undecaprenylpyrophosphate-n-aetylglucosamine (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) tagO Bacillus subtilis 1423 -11532156 7000694666 tago teichoic acid linkage unit synthesis tago (cl:lipophilic protein lim) (db:pir2.dat) B69721 B69721 Bacillus subtilis 1423 -11532156 5500704943 tago putative undecaprenyl-phosphate (fn:involved in teichoic acid synthesis) (db:genpept-bct1) (de:bacillus subtilis tago gene.) (le:193) (re:1269) (di:direct) BSTAGO AJ004803 g2582651 Bacillus subtilis 1423 -11532156 7500965251 tago (fn:teichoic acid linkage unit synthesis (synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: yvhi) (le:50624) (re:51700) (di:complement) BSUB0019 Z99122 g2636079 Bacillus subtilis 1423 -11532156

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814550	6358	28514	978	325

Description

6500728299 yvhh:tuah hypothetical protein:biosynthesis of teichuronic acid (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) tuaH tuaH Bacillus subtilis 1423 -11532157 7000692283 tuah biosynthesis of teichuronic acid tuah (db:pir2.dat) B69728 B69728 Bacillus subtilis 1423 -11532157 7000692284 tuah unknown (db:genpept-bct1) (de:bacillus subtilis 168 teichuronic acid operon, tuaabcdefgh genes,complete sequence.) (le:8055) (re:9248) (di:direct) AF015609 AF015609 g2454563 Bacillus subtilis 1423 -11532157 7500963456 tuah (fn:biosynthesis of teichuronic acid) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: yvhh) (le:51845) (re:53038) (di:complement) BSUB0019 Z99122 g2636080 Bacillus subtilis 1423 -11532157

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814551	6359	28515	609	203

Description

6500728300 yvhg:tuag hypothetical protein:biosynthesis of teichuronic acid (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) tuaG tuaG Bacillus subtilis 1423 -11532158 7000692281 tuag biosynthesis of teichuronic acid tuag (db:pir2.dat) A69728 A69728 Bacillus subtilis 1423 -11532158 7000692282 tuag unknown (db:genpept-bct1) (de:bacillus subtilis 168 teichuronic acid operon, tuaabcdefgh genes,complete sequence.) (le:7268) (re:8026) (di:direct) AF015609 AF015609 g2454562 Bacillus subtilis 1423 -11532158 7500963455 tuag (fn:biosynthesis of teichuronic acid) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: yvhg) (le:53067) (re:53825) (di:complement) BSUB0019 Z99122 g2636081 Bacillus subtilis 1423 -11532158

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814564	6360	28516	375	124

Description

6500728301 yvhf:tuaf hypothetical protein:biosynthesis of teichuronic acid (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) tuaF tuaF Bacillus subtilis 1423 -11532159 7000692279 tuaf biosynthesis of teichuronic acid tuaf (db:pir2.dat) H69727 H69727 Bacillus subtilis 1423 -11532159 7000692280 tuaf unknown (db:genpept-bct1) (de:bacillus subtilis 168 teichuronic acid operon, tuaabcdefgh genes,complete sequence.) (le:6564) (re:7244) (di:direct) AF015609 AF015609 g2454561 Bacillus subtilis 1423 -11532159 7500963454 tuaf (fn:biosynthesis of teichuronic acid) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: yvhf) (le:53849) (re:54529) (di:complement) BSUB0019 Z99122 g2636082 Bacillus subtilis 1423 -11532159

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814565	6361	28517	1155	384

Description

6500728302 yvhe:tuae hypothetical protein:biosynthesis of teichuronic acid (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) tuaE tuaE Bacillus subtilis 1423 -11532160 7000692277 tuae biosynthesis of teichuronic acid tuae (db:pir2.dat) G69727 G69727 Bacillus subtilis 1423 -11532160 7000692278 tuae unknown (db:genpept-bct1) (de:bacillus subtilis 168 teichuronic acid operon, tuaabcdefgh genes,complete sequence.) (le:5069) (re:6535) (di:direct) AF015609 AF015609 g2454560 Bacillus subtilis 1423 -11532160 7500963453 tuae (fn:biosynthesis of teichuronic acid) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: yvhe) (le:54558) (re:56024) (di:complement) BSUB0019 Z99122 g2636083 Bacillus subtilis 1423 -11532160

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814583	6362	28518	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814595	6363	28519	327	108

Description

6500728303 yvhc:tuac hypothetical protein:biosynthesis of teichuronic acid (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) tuac tuac Bacillus subtilis 1423 -11532161 7000692275 tuac biosynthesis of teichuronic acid tuac (db:pir2.dat) E69727 E69727 Bacillus subtilis 1423 -11532161 7000692276 tuac unknown (db:genpept-bct1) (de:bacillus subtilis 168 teichuronic acid operon, tuaabcdefgh genes,complete sequence.) (le:2368) (re:3537) (di:direct) AF015609 AF015609 g2454558 Bacillus subtilis 1423 -11532161 7500963452 tuac (fn:biosynthesis of teichuronic acid) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: yvhc) (le:57556) (re:58725) (di:complement) BSUB0019 Z99122 g2636085 Bacillus subtilis 1423 -11532161

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814597	6364	28520	612	203

Description

6500728304 yvhb:tuab hypothetical protein:biosynthesis of teichuronic acid (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) tuaB tuaB Bacillus subtilis 1423 -11532162 7000692273 tuab biosynthesis of teichuronic acid tuab (cl:hypothetical protein b2046) (db:pir2.dat) D69727 D69727 Bacillus subtilis 1423 -11532162 7000692274 tuab unknown (db:genpept-bct1) (de:bacillus subtilis 168 teichuronic acid operon, tuaabcdefgh genes,complete sequence.) (le:920) (re:2371) (di:direct) AF015609 AF015609 g2454557 Bacillus subtilis 1423 -11532162 7500955941 tuab (fn:biosynthesis of teichuronic acid) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: yvhb) (le:58722) (re:60173) (di:complement) BSUB0019 Z99122 g2636086 Bacillus subtilis 1423 -11532162

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814598	6365	28521	765	254

Description

6500728305 yvha:tuaa hypothetical protein:biosynthesis of teichuronic acid (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) tuaA tuaA Bacillus subtilis 1423 -11532163 7000692271 tuaa biosynthesis of teichuronic acid tuaa (cl:pss2 protein) (db:pir2.dat) C69727 C69727 Bacillus subtilis 1423 -11532163 7000692272 tuaa unknown (db:genpept-bct1) (de:bacillus subtilis 168 teichuronic acid operon, tuaabcdefgh genes,complete sequence.) (le:231) (re:770) (di:direct) AF015609 AF015609 g2454556 Bacillus subtilis 1423 -11532163 7500963451 tuaa (fn:biosynthesis of teichuronic acid) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: yvha) (le:60323) (re:60862) (di:complement) BSUB0019 Z99122 g2636087 Bacillus subtilis 1423 -11532163

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814601	6366	28522	870	289

Description

6500728306 hypothetical protein:similar to metabolite transport protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywtG ywtG Bacillus subtilis 1423 -11532164 7000694206 ywtg metabolite transport protein homolog ywtg (cl:glucose transport protein) (db:pir2.dat) E70070 E70070 Bacillus subtilis 1423 -11532164 307942 ywtg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to metabolite transport protein) (le:94500) (re:95873) (di:complement) BSUB0019 Z99122 g2636109 Bacillus subtilis 1423 -11532164 7500964933 ywtg (db:genpept-bct1) (de:b.subtilis yws(a,b,c,d,e,f,g) and gerbc genes.) (nt:product highly similar to metabolite transport) (le:6609) (re:7982) (di:direct) BSZ92954 Z92954 g1894771 Bacillus subtilis 1423 -11532164

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814603	6367	28523	279	92

Description

6500728307 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywtE ywtE Bacillus subtilis 1423 -11532165 7000692869 ywte conserved hypothetical protein ywte (cl:hypothetical protein ywpj) (db:pir2.dat) C70070 C70070 Bacillus subtilis 1423 -11532165 307941 ywte (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to hypothetical proteins) (le:97330) (re:98190) (di:direct) BSUB0019 Z99122 g2636110 Bacillus subtilis 1423 -11532165 7500955885 ywte (db:genpept-bct1) (de:b.subtilis yws(a,b,c,d,e,f,g) and gerbc genes.) (nt:product similar to bacillus subtilis yxeh and ycse) (le:4292) (re:5152) (di:complement) BSZ92954 Z92954 g1894770 Bacillus subtilis 1423 -11532165

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814607	6368	28524	342	113

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814617	6369	28525	1197	398
<u>Description</u>				
6500728308 hypothetical protein:similar to murein hydrolase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywtD ywtD Bacillus subtilis 1423 -11532166 7000694266 ywtd murein hydrolase homolog ywtd (db:pir2.dat) B70070 B70070 Bacillus subtilis 1423 -11532166 307940 ywtd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to murein hydrolase) (le:98224) (re:99465) (di:complement) BSUB0019 Z99122 g2636111 Bacillus subtilis 1423 -11532166 7500964983 ywtd (db:genpept-bct1) (de:b.subtilis yws(a,b,c,d,e,f,g) and gerbc genes.) (nt:product similar to e. coli nlpc protein and to) (le:3017) (re:4258) (di:direct) BSZ92954 Z92954 g1894769 Bacillus subtilis 1423 -11532166				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814625	6370	28526	1095	364
<u>Description</u>				
6500728309 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywtC ywtC Bacillus subtilis 1423 -11532167 7000694069 ywtc hypothetical protein ywtc (db:pir2.dat) A70070 A70070 Bacillus subtilis 1423 -11532167 307939 ywtc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:99606) (re:99773) (di:complement) BSUB0019 Z99122 g2636112 Bacillus subtilis 1423 -11532167 7500964850 ywtc unknown (db:genpept-bct1) (de:b.subtilis yws(a,b,c,d,e,f,g) and gerbc genes.) (le:2709) (re:2876) (di:direct) BSZ92954 Z92954 g1894768 Bacillus subtilis 1423 -11532167				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814627	6371	28527	429	142
<u>Description</u>				
6500728310 hypothetical protein:similar to capsular polyglutamate biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywtB ywtB Bacillus subtilis 1423 -11532168 7000692306 ywtb capsular polyglutamate biosynthesis homolog ywtb (db:pir2.dat) H70069 H70069 Bacillus subtilis 1423 -11532168 307938 ywtb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to capsular polyglutamate biosynthesis) (le:99788) (re:100930) (di:complement) BSUB0019 Z99122 g2636113 Bacillus subtilis 1423 -11532168 7500963475 ywtb (db:genpept-bct1) (de:b.subtilis yws(a,b,c,d,e,f,g) and gerbc genes.) (nt:product highly similar to bacillus anthracis capa) (le:1552) (re:2694) (di:direct) BSZ92954 Z92954 g1894767 Bacillus subtilis 1423 -11532168				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814635	6372	28528	372	123

Description

6500728311 hypothetical protein:similar to capsular polyglutamate biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywtA ywtA Bacillus subtilis 1423 -11532169 7000692305 ywtA capsular polyglutamate biosynthesis homolog ywtA (db:pir2.dat) G70069 G70069 Bacillus subtilis 1423 -11532169 307937 ywtA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to capsular polyglutamate biosynthesis) (le:100949) (re:101398) (di:complement) BSUB0019 Z99122 g2636114 Bacillus subtilis 1423 -11532169 7500963474 ywtA (db:genpept-bct1) (de:b.subtilis yws(a,b,c,d,e,f,g) and gerbc genes.) (nt:product highly similar to bacillus anthracis capc) (le:1084) (re:1533) (di:direct) BSZ92954 Z92954 g1894766 Bacillus subtilis 1423 -11532169

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814639	6373	28529	462	153

Description

6500728312 hypothetical protein:similar to capsular polyglutamate biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywsc ywsc Bacillus subtilis 1423 -11532170 7000692304 ywsc capsular polyglutamate biosynthesis homolog ywsc (db:pir2.dat) F70069 F70069 Bacillus subtilis 1423 -11532170 7500963473 ywsc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to capsular polyglutamate biosynthesis) (le:101413) (re:102594) (di:complement) BSUB0019 Z99122 g2636115 Bacillus subtilis 1423 -11532170

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814644	6374	28530	1014	337

Description

6500728313 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywsB ywsB Bacillus subtilis 1423 -11532171 7000692868 ywsb conserved hypothetical protein ywsb (db:pir2.dat) E70069 E70069 Bacillus subtilis 1423 -11532171 307928 ywsb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to hypothetical proteins from b. subtilis) (le:109111) (re:109647) (di:direct) BSUB0019 Z99122 g2636122 Bacillus subtilis 1423 -11532171 7500963906 ywsb unknown (db:genpept-bct1) (de:b.subtilis yws(a,b,c) genes and rbs(a,c,d,k,r) genes.) (le:371) (re:907) (di:complement) BSZ92953 Z92953 g1894756 Bacillus subtilis 1423 -11532171

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814665	6375	28531	252	83
<u>Description</u>				
6500728314 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywsA ywsA Bacillus subtilis 1423 -11532172 7000694068 ywsA hypothetical protein ywsA (db:pir2.dat) D70069 D70069 Bacillus subtilis 1423 -11532172 7500964849 ywsA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:109803) (re:110099) (di:direct) BSUB0019 Z99122 g2636123 Bacillus subtilis 1423 -11532172				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814674	6376	28532	192	63
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814678	6377	28533	534	177
<u>Description</u>				
6500728315 hypothetical protein:similar to nad:ph oxidoreductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywro ywro Bacillus subtilis 1423 -11532173 1500693630 ywro (ec:1.6.99.-) (de:general stress protein 14 (gsp14),) (db:swissprot) GS14_BACSU P80871 BACILLUS SUBTILIS 1423 -11532173 7000694300 ywro nad p h oxidoreductase homolog ywro (cl:probable nad(p)h oxidoreductase yabf) (db:pir2.dat) C70069 C70069 Bacillus subtilis 1423 -11532173 7500882770 ywro (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to nad(p)h oxidoreductase) (le:110139) (re:110666) (di:complement) BSUB0019 Z99122 g2636124 Bacillus subtilis 1423 -11532173 7502851752 ywro (db:genpept-bct1) (de:b.subtilis dna; 15.2 kb fragment, from ywqn gene to ywro gene.) (nt:similar to hypothetical nad(p)h oxidoreductase) (le:14505) (re:15032) (di:direct) BSZ93767 Z93767 g1929342 Bacillus subtilis 1423 -11532173 7500882768 ywro (ec:1.6.99.-) (de:general stress protein 14 (gsp14),) (db:swissprot) GS14_BACSU P80871 BACILLUS SUBTILIS 1423 -11532173				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814686	6378	28534	939	312

Description

6500728316 hypothetical protein: similar to arsenical pump membrane protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywrK ywrK Bacillus subtilis 1423 -11532174 7000692231 ywrK arsenical pump membrane protein homolog ywrK (db:pir2.dat) B70069 B70069 Bacillus subtilis 1423 -11532174 1500693628 ywrK (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to arsenical pump membrane protein) (le:114584) (re:115912) (di:direct) BSUB0019 Z99122 g2636128 Bacillus subtilis 1423 -11532174 7500963430 ywrK (db:genpept-bct1) (de:b.subtilis dna; 15.2 kb fragment, from ywqn gene to ywro gene.) (nt:similar to arsb integral membrane protein) (le:9259) (re:10587) (di:complement) BSZ93767 Z93767 g1929338 Bacillus subtilis 1423 -11532174

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814729	6379	28535	420	139

Description

GTC ORF with score 211 to: (sr:aspergillus oryzae (strain:jcm02238) dna) (db:genpept-pln2) (de:aspergillus oryzae gene for hanc, complete cds.) (nt:putative component of ccaat binding complex: yeast) (le:304:816:993:1214) (re:460:926:1120:1465) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814734	6380	28536	189	62

Description

6500728317 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywrJ ywrJ Bacillus subtilis 1423 -11532175 7000694067 ywrJ hypothetical protein ywrJ (db:pir2.dat) A70069 A70069 Bacillus subtilis 1423 -11532175 1500693627 ywrJ (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:115969) (re:116646) (di:complement) BSUB0019 Z99122 g2636129 Bacillus subtilis 1423 -11532175 7500964848 ywrJ (db:genpept-bct1) (de:b.subtilis dna; 15.2 kb fragment, from ywqn gene to ywro gene.) (le:8525) (re:9202) (di:direct) BSZ93767 Z93767 g1929337 Bacillus subtilis 1423 -11532175

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814735	6381	28537	267	88

Description

GTC ORF with score 336 to: (sr:aspergillus oryzae (strain:jcm02238) dna)  
(db:genpept-pln2) (de:aspergillus oryzae gene for hapc, complete cds.)  
(nt:putative component of ccaat binding complex: yeast)  
(le:304:816:993:1214) (re:460:926:1120:1465) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814749	6382	28538	567	189

Description

6500728318 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) ywrF ywrF Bacillus subtilis 1423 -11532176  
7000694066 ywrf hypothetical protein ywrf (db:pir2.dat) H70068 H70068  
Bacillus subtilis 1423 -11532176 1500693624 ywrf (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21):  
from 3597091to 3809700.) (le:119966) (re:120583) (di:direct) BSUB0019 Z99122  
g2636133 Bacillus subtilis 1423 -11532176 7500964847 ywrf (db:genpept-bct1)  
(de:b.subtilis dna; 15.2 kb fragment, from ywqn gene to ywro gene.)  
(le:4588) (re:5205) (di:complement) BSZ93767 Z93767 g1929333 Bacillus  
subtilis 1423 -11532176

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814753	6383	28539	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814764	6384	28540	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814766	6385	28541	186	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814774	6386	28542	519	172

Description

6500728319 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywrE ywrE Bacillus subtilis 1423 -11532177  
7000694065 ywre hypothetical protein ywre (db:pir2.dat) G70068 G70068 Bacillus subtilis 1423 -11532177 1500693623 ywre (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:120761) (re:121096) (di:direct) BSUB0019 Z99122 g2636134 Bacillus subtilis 1423 -11532177 7500964846 ywre (db:genpept-bct1) (de:b.subtilis dna; 15.2 kb fragment, from ywqn gene to ywro gene.) (le:4075) (re:4410) (di:complement) BSZ93767 Z93767 g1929332 Bacillus subtilis 1423 -11532177

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814787	6387	28543	837	278

Description

6500728320 hypothetical protein:similar to gamma-glutamyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywrD ywrD Bacillus subtilis 1423 -11532178 7000693017 ywrD gamma-glutamyltransferase homolog ywrD (db:pir2.dat) F70068 F70068 Bacillus subtilis 1423 -11532178 1500693622 ywrD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to gamma-glutamyltransferase) (le:121101) (re:122678) (di:complement) BSUB0019 Z99122 g2636135 Bacillus subtilis 1423 -11532178 7500964002 ywrD (db:genpept-bct1) (de:b.subtilis dna; 15.2 kb fragment, from ywqn gene to ywro gene.) (nt:similar to gamma glutamyl transpeptidase precursor,) (le:2493) (re:4070) (di:direct) BSZ93767 Z93767 g1929331 Bacillus subtilis 1423 -11532178

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814800	6388	28544	687	228

Description

6500728321 hypothetical protein:similar to transcriptional regulator:lrp/asnc family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywrC ywrC Bacillus subtilis 1423 -11532179 7000694751 ywrc transcription regulator lrp/asnc family homolog ywrc (db:pir2.dat) E70068 E70068 Bacillus subtilis 1423 -11532179 1500693621 ywrc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to transcriptional regulator (lrp/asnc) (le:122892) (re:123368) (di:direct) BSUB0019 Z99122 g2636136 Bacillus subtilis 1423 -11532179 7500965321 ywrc (db:genpept-bct1) (de:b.subtilis dna; 15.2 kb fragment, from ywqn gene to ywro gene.) (nt:similar to leucine regulatory protein, lrp and asnc) (le:1803) (re:2279) (di:complement) BSZ93767 Z93767 g1929330 Bacillus subtilis 1423 -11532179

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814803	6389	28545	486	161

Description

GTC ORF with score 150 to: (sr:schizosaccharomyces pombe (library: pdb20 (from l. guarente)) cdn) (db:genpept-pln1) (ec:2.5.1.21) (de:schizosaccharomyces pombe squalene synthetase (erg9) mrna, completedcds.) (le:19) (re:1401) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814804	6390	28546	435	144

Description

6500728322 hypothetical protein:similar to chromate transport protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywrB ywrB Bacillus subtilis 1423 -11532180 7000692373 ywrB probable chromate transport protein (cl:probable chromate transport protein ywra) (db:pir2.dat) D70068 D70068 Bacillus subtilis 1423 -11532180 1500693620 ywrB (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to chromate transport protein) (le:123382) (re:123975) (di:direct) BSUB0019 Z99122 g2636137 Bacillus subtilis 1423 -11532180 7500963535 ywrB (db:genpept-bct1) (de:b.subtilis dna; 15.2 kb fragment, from ywqn gene to ywro gene.) (nt:similar to chromate transport protein, chra) (le:1196) (re:1789) (di:complement) BSZ93767 Z93767 g1929329 Bacillus subtilis 1423 -11532180

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814805	6391	28547	555	184

Description

6500728323 hypothetical protein:similar to chromate transport protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywra ywra Bacillus subtilis 1423 -11532181 7000692372 ywra probable chromate transport protein (cl:probable chromate transport protein ywra) (db:pir2.dat) C70068 C70068 Bacillus subtilis 1423 -11532181 1500693619 ywra (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to chromate transport protein) (le:123972) (re:124508) (di:direct) BSUB0019 Z99122 g2636138 Bacillus subtilis 1423 -11532181 7500963534 ywra (db:genpept-bct1) (de:b.subtilis dna; 15.2 kb fragment, from ywqn gene to ywro gene.) (nt:similar to chromate transport protein, chra) (le:663) (re:1199) (di:complement) BSZ93767 Z93767 g1929328 Bacillus subtilis 1423 -11532181

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814816	6392	28548	312	104

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814823	6393	28549	321	106

Description

6500728324 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywqO ywqO Bacillus subtilis 1423 -11532182  
7000694064 ywqo hypothetical protein ywqo (db:pir2.dat) B70068 B70068 Bacillus subtilis 1423 -11532182 307926 ywqo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:124535) (re:124756) (di:complement) BSUB0019 Z99122 g2636139 Bacillus subtilis 1423 -11532182 1500689799 ywqo unknown (db:genpept-bct1) (de:b.subtilis ywq(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) genes.) (le:13570) (re:13791) (di:direct) BSZ92952 Z92952 g1894753 Bacillus subtilis 1423 -11532182 7500964845 ywqo (db:genpept-bct1) (de:b.subtilis dna; 15.2 kb fragment, from ywqn gene to ywro gene.) (le:415) (re:636) (di:direct) BSZ93767 Z93767 g1929327 Bacillus subtilis 1423 -11532182

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814824	6394	28550	429	142

Description

6500728325 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywqN ywqN Bacillus subtilis 1423 -11532183 7000692867 ywqn conserved hypothetical protein ywqn (db:pir2.dat) A70068 A70068 Bacillus subtilis 1423 -11532183 307925 ywqn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to hypothetical proteins) (le:124753) (re:125298) (di:complement) BSUB0019 Z99122 g2636140 Bacillus subtilis 1423 -11532183 7500963905 ywqn unknown (db:genpept-bct1) (de:b.subtilis ywq(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) genes.) (le:13028) (re:13573) (di:direct) BSZ92952 Z92952 g1894752 Bacillus subtilis 1423 -11532183

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814828	6395	28551	219	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814830	6396	28552	477	158

Description

6500728326 hypothetical protein:similar to transcriptional regulator:lysr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywqM ywqM Bacillus subtilis 1423 -11532184 7000694762 ywqm transcription regulator lysr family homolog ywqm (cl:pseudomonas putida regulatory protein catr) (db:pir2.dat) H70067 H70067 Bacillus subtilis 1423 -11532184 307924 ywqm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to transcriptional regulator (lysr family)) (le:125421) (re:126302) (di:direct) BSUB0019 Z99122 g2636141 Bacillus subtilis 1423 -11532184 7500965332 ywqm (fn:lysr-type transcriptional regulator) (db:genpept-bct1) (de:b.subtilis ywq(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) genes.) (le:12024) (re:12905) (di:complement) BSZ92952 Z92952 g1894751 Bacillus subtilis 1423 -11532184

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814834	6397	28553	312	103

Description

6500728327 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywqL ywqL Bacillus subtilis 1423 -11532185 7000692866 ywql conserved hypothetical protein ywql (db:pir2.dat) G70067 G70067 Bacillus subtilis 1423 -11532185 307923 ywql (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to hypothetical proteins) (le:126387) (re:127103) (di:complement) BSUB0019 Z99122 g2636142 Bacillus subtilis 1423 -11532185 7500963904 ywql (db:genpept-bct1) (de:b.subtilis ywq(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) genes.) (nt:product similar to e.coli yjaf protein) (le:11223) (re:11939) (di:direct) BSZ92952 Z92952 g1894750 Bacillus subtilis 1423 -11532185

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814835	6398	28554	636	212

Description

6500728328 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywqK ywqK Bacillus subtilis 1423 -11532186 7000694063 ywqk hypothetical protein ywqk (db:pir2.dat) F70067 F70067 Bacillus subtilis 1423 -11532186 307922 ywqk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:127113) (re:127577) (di:complement) BSUB0019 Z99122 g2636143 Bacillus subtilis 1423 -11532186 7500964844 ywqk unknown (db:genpept-bct1) (de:b.subtilis ywq(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) genes.) (le:10749) (re:11213) (di:direct) BSZ92952 Z92952 g1894749 Bacillus subtilis 1423 -11532186

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814845	6399	28555	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814858	6400	28556	1428	476

Description

6500728329 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywqJ ywqJ Bacillus subtilis 1423 -11532187 7000692865 ywqj conserved hypothetical protein ywqj (db:pir2.dat) E70067 E70067 Bacillus subtilis 1423 -11532187 307921 ywqj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to hypothetical proteins from b. subtilis) (le:127567) (re:129375) (di:complement) BSUB0019 Z99122 g2636144 Bacillus subtilis 1423 -11532187 7500963903 ywqj (db:genpept-bct1) (de:b.subtilis ywq(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) genes.) (nt:product similar to bacillus subtilis yxid protein) (le:8951) (re:10759) (di:direct) BSZ92952 Z92952 g1894748 Bacillus subtilis 1423 -11532187

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814860	6401	28557	582	193

Description

6500728330 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywqI ywqI Bacillus subtilis 1423 -11532188 7000692864 ywqi conserved hypothetical protein ywqi (db:pir2.dat) D70067 D70067 Bacillus subtilis 1423 -11532188 307920 ywqi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to hypothetical proteins from b. subtilis) (le:129394) (re:129654) (di:complement) BSUB0019 Z99122 g2636145 Bacillus subtilis 1423 -11532188 7500963902 ywqi (db:genpept-bct1) (de:b.subtilis ywq(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) genes.) (nt:product similar to bacillus subtilis yxic protein) (le:8672) (re:8932) (di:direct) BSZ92952 Z92952 g1894747 Bacillus subtilis 1423 -11532188

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814870	6402	28558	729	242

Description

6500728331 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywqH ywqH Bacillus subtilis 1423 -11532189  
 7000694062 ywqh hypothetical protein ywqh (db:pir2.dat) C70067 C70067 Bacillus subtilis 1423 -11532189 307919 ywqh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:129664) (re:130086) (di:complement) BSUB0019 Z99122 g2636146 Bacillus subtilis 1423 -11532189 7500964843 ywqh unknown (db:genpept-bct1) (de:b.subtilis ywq(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) genes.) (le:8240) (re:8662) (di:direct) BSZ92952 Z92952 g1894746 Bacillus subtilis 1423 -11532189

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814873	6403	28559	321	107

Description

6500728332 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywqG ywqG Bacillus subtilis 1423 -11532190  
 7000694061 ywqg hypothetical protein ywqg (db:pir2.dat) B70067 B70067 Bacillus subtilis 1423 -11532190 307918 ywqg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:130478) (re:131263) (di:complement) BSUB0019 Z99122 g2636147 Bacillus subtilis 1423 -11532190 7500964842 ywqg unknown (db:genpept-bct1) (de:b.subtilis ywq(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) genes.) (le:7063) (re:7848) (di:direct) BSZ92952 Z92952 g1894745 Bacillus subtilis 1423 -11532190

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814896	6404	28560	285	95

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814899	6405	28561	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814903	6406	28562	189	63

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814917	6407	28563	912	303

Description

6500728333 hypothetical protein:similar to ndp-sugar dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywqF ywqF Bacillus subtilis 1423 -11532191 7000694313 ywqf ndp-sugar dehydrogenase homolog ywqf (cl:gdpmannose dehydrogenase) (db:pir2.dat) A70067 A70067 Bacillus subtilis 1423 -11532191 307917 ywqf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to ndp-sugar dehydrogenase) (le:131455) (re:132777) (di:complement) BSUB0019 Z99122 g2636148 Bacillus subtilis 1423 -11532191 7500965014 ywqf (db:genpept-bct1) (de:b.subtilis ywq(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) genes.) (nt:product similar to pseudomonas aeruginosa) (le:5549) (re:6871) (di:direct) BSZ92952 Z92952 gl894744 Bacillus subtilis 1423 -11532191

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814924	6408	28564	654	217

Description

GTC ORF with score 321 to: (sr:arabidopsis thaliana (strain:columbia) dna) (db:genpept-pln2) (de:arabidopsis thaliana mutm homologue gene, complete cds.) (nt:mutm homologue-1) (le:105:754:897:1040:1202) (re:333:805:954:1108:1327) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501814925	6409	28565	522	173

Description

GTC ORF with score 230 to: (sr:arabidopsis thaliana (strain:columbia) dna) (db:genpept-pln2) (de:arabidopsis thaliana mutm homologue gene, complete cds.) (nt:mutm homologue-1) (le:105:754:897:1040:1202) (re:333:805:954:1108:1327) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814952	6410	28566	1761	586

Description

6500728334 hypothetical protein:similar to capsular polysaccharide biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywqE ywqE Bacillus subtilis 1423 -11532192 7000692318 ywqe capsular polysaccharide biosynthesis homolog ywqe (db:pir2.dat) H70066 H70066 Bacillus subtilis 1423 -11532192 307916 ywqe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to capsular polysaccharide biosynthesis) (le:132972) (re:133736) (di:complement) BSUB0019 Z99122 g2636149 Bacillus subtilis 1423 -11532192 7500963486 ywqe (db:genpept-bct1) (de:b.subtilis ywq(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) genes.) (nt:product similar to staphylococcus aureus capc) (le:4590) (re:5354) (di:direct) BSZ92952 Z92952 g1894743 Bacillus subtilis 1423 -11532192

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814964	6411	28567	303	100

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814979	6412	28568	231	76

Description

6500728335 hypothetical protein:similar to capsular polysaccharide biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywqD ywqD Bacillus subtilis 1423 -11532193 7000692317 ywqd capsular polysaccharide biosynthesis homolog ywqd (cl:capsular polysaccharide biosynthesis protein cpse) (db:pir2.dat) G70066 G70066 Bacillus subtilis 1423 -11532193 307915 ywqd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to capsular polysaccharide biosynthesis) (le:133789) (re:134502) (di:complement) BSUB0019 Z99122 g2636150 Bacillus subtilis 1423 -11532193 7500963485 ywqd (db:genpept-bct1) (de:b.subtilis ywq(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) genes.) (nt:product similar to staphylococcus aureus capb) (le:3824) (re:4537) (di:direct) BSZ92952 Z92952 g1894742 Bacillus subtilis 1423 -11532193

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814987	6413	28569	489	163

Description

6500728336 hypothetical protein:similar to capsular polysaccharide biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywqC ywqC Bacillus subtilis 1423 -11532194 7000692316 ywqc capsular polysaccharide biosynthesis homolog ywqc (cl:streptococcus agalactiae cpsb protein) (db:pir2.dat) F70066 F70066 Bacillus subtilis 1423 -11532194 307914 ywqc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to capsular polysaccharide biosynthesis) (le:134492) (re:135238) (di:complement) BSUB0019 Z99122 g2636151 Bacillus subtilis 1423 -11532194 7500963484 ywqc (db:genpept-bct1) (de:b.subtilis ywq(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) genes.) (nt:product similar to staphylococcus aureus capa) (le:3088) (re:3834) (di:direct) BSZ92952 Z92952 g1894741 Bacillus subtilis 1423 -11532194

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814988	6414	28570	1155	384

Description

6500728337 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywqB ywqB Bacillus subtilis 1423 -11532195 7000694060 ywqb hypothetical protein ywqb (db:pir2.dat) E70066 E70066 Bacillus subtilis 1423 -11532195 307913 ywqb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:135819) (re:137429) (di:direct) BSUB0019 Z99122 g2636152 Bacillus subtilis 1423 -11532195 7500964841 ywqb unknown (db:genpept-bct1) (de:b.subtilis ywq(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) genes.) (le:897) (re:2507) (di:complement) BSZ92952 Z92952 g1894740 Bacillus subtilis 1423 -11532195

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501814991	6415	28571	345	114

Description

GTC ORF with score 291 to: (sr:yarrowia lipolytica (strain w29) dna) (db:genpept-pln1) (de:yarrowia lipolytica ras-like protein (ryl1) gene, complete cds.) (nt:ryl1, an essential gene belongs to ypt1 sub-family.) (le:618) (re:1229) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815002	6416	28572	408	135

Description

GTC ORF with score 113 to: (db:genpept-bct2) (de:mycobacterium smegmatis exochelin gene cluster, exit (exit) andfxbb (fxbb) genes, complete cds; and fxbc (fxbc) gene, partial cds.) (nt:abc transporter; this abc transporter probably) (le:489) (re:3857) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815005	6417	28573	627	209

Description

6500728338 hypothetical protein:similar to snf2 helicase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywqA ywqA Bacillus subtilis 1423 -11532196 7000694592 ywqa snf2 helicase homolog ywqa (db:pir2.dat) D70066 D70066 Bacillus subtilis 1423 -11532196 7500965191 ywqa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to snf2 helicase) (le:137416) (re:140184) (di:direct) BSUB0019 Z99122 g2636153 Bacillus subtilis 1423 -11532196

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815006	6418	28574	1134	377

Description

6500728339 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywpJ ywpJ Bacillus subtilis 1423 -11532197 7000692863 ywpj conserved hypothetical protein ywpj (cl:hypothetical protein ywpj) (db:pir2.dat) C70066 C70066 Bacillus subtilis 1423 -11532197 220412 ywpj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to hypothetical proteins) (le:140310) (re:141167) (di:complement) BSUB0019 Z99122 g2636154 Bacillus subtilis 1423 -11532197 7500955884 ywpj (db:genpept-bct1) (de:b.subtilis mbl, flh(o,p), rapd, ywp(b,c,d,e,f,g,h,i,j) and ywqagenes.) (nt:similar to b. subtilis ycse hypothetical protein) (le:8154) (re:9011) (di:direct) BSZ83337 Z83337 g1763711 Bacillus subtilis 1423 -11532197

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815023	6419	28575	342	113

#### Description

6500728340 hypothetical protein:similar to single-strand dna-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywpH ywpH Bacillus subtilis 1423 -11532198 7000694586 ywpH single-strand dna-binding protein homolog ywpH (cl:single-stranded dna-binding protein:single-stranded dna-binding protein homology) (db:pir2.dat) B70066 B70066 Bacillus subtilis 1423 -11532198 220410 ywpH (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to single-strand dna-binding protein) (le:142173) (re:142514) (di:complement) BSUB0019 Z99122 g2636156 Bacillus subtilis 1423 -11532198 7500965186 ywpH (db:genpept-bct1) (de:b.subtilis mbl, flh(o,p), rapd, ywp(b,c,d,e,f,g,h,i,j) and ywqagenes.) (nt:similar to single strand binding protein) (le:6807) (re:7148) (di:direct) BSZ83337 Z83337 g1763709 Bacillus subtilis 1423 -11532198

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815033	6420	28576	258	85

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815037	6421	28577	822	273

#### Description

6500728341 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywpG ywpG Bacillus subtilis 1423 -11532199 7000694059 ywpG hypothetical protein ywpG (db:pir2.dat) A70066 A70066 Bacillus subtilis 1423 -11532199 220409 ywpG (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:142591) (re:142974) (di:complement) BSUB0019 Z99122 g2636157 Bacillus subtilis 1423 -11532199 7500964840 ywpG (db:genpept-bct1) (de:b.subtilis mbl, flh(o,p), rapd, ywp(b,c,d,e,f,g,h,i,j) and ywqagenes.) (le:6347) (re:6730) (di:direct) BSZ83337 Z83337 g1763708 Bacillus subtilis 1423 -11532199

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815038	6422	28578	327	108

Description

6500728342 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywpF ywpF Bacillus subtilis 1423 -11532200  
 7000694058 ywpf hypothetical protein ywpf (db:pir2.dat) H70065 H70065  
 Bacillus subtilis 1423 -11532200 220408 ywpf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:143149) (re:143559) (di:direct) BSUB0019 Z99122 g2636158  
 Bacillus subtilis 1423 -11532200 7500964839 ywpf (db:genpept-bct1) (de:b.subtilis mbl, flh(o,p), rapd, ywp(b,c,d,e,f,g,h,i,j) and ywqagenes.) (le:5762) (re:6172) (di:complement) BSZ83337 Z83337 g1763707 Bacillus subtilis 1423 -11532200

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815042	6423	28579	414	137

Description

6500728343 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywpE ywpE Bacillus subtilis 1423 -11532201  
 7000694057 ywpe hypothetical protein ywpe (db:pir2.dat) G70065 G70065  
 Bacillus subtilis 1423 -11532201 220407 ywpe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:143698) (re:144006) (di:complement) BSUB0019 Z99122 g2636159  
 Bacillus subtilis 1423 -11532201 7500964838 ywpe (db:genpept-bct1) (de:b.subtilis mbl, flh(o,p), rapd, ywp(b,c,d,e,f,g,h,i,j) and ywqagenes.) (le:5315) (re:5623) (di:direct) BSZ83337 Z83337 g1763706 Bacillus subtilis 1423 -11532201

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815069	6424	28580	318	105

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815077	6425	28581	1311	437

Description

6500728344 hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywpD ywpD Bacillus subtilis 1423 -11532202 7000694863 ywpd two-component sensor histidine kinase homolog ywpd (db:pir2.dat) F70065 F70065 Bacillus subtilis 1423 -11532202 220406 ywpd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to two-component sensor histidine kinase) (le:144350) (re:145186) (di:direct) BSUB0019 Z99122 g2636160 Bacillus subtilis 1423 -11532202 7500965423 ywpd (db:genpept-bct1) (de:b.subtilis mbl, flh(o,p), rapd, ywp(b,c,d,e,f,g,h,i,j) and ywqagenes.) (le:4135) (re:4971) (di:complement) BSZ83337 Z83337 g1763705 Bacillus subtilis 1423 -11532202

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815080	6426	28582	585	195

Description

6500728345 hypothetical protein:similar to large conductance mechanosensitive channel protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywpc ywpc Bacillus subtilis 1423 -11532203 7000694157 ywpc large conductance mechanosensitive channel homolog ywpc (cl:yhdc protein) (db:pir2.dat) E70065 E70065 Bacillus subtilis 1423 -11532203 220405 ywpc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to large conductance mechanosensitive) (le:145233) (re:145625) (di:complement) BSUB0019 Z99122 g2636161 Bacillus subtilis 1423 -11532203 7500964890 ywpc (db:genpept-bct1) (de:b.subtilis mbl, flh(o,p), rapd, ywp(b,c,d,e,f,g,h,i,j) and ywqagenes.) (nt:highly similar to e. coli large conductance) (le:3696) (re:4088) (di:direct) BSZ83337 Z83337 g1763704 Bacillus subtilis 1423 -11532203

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815092	6427	28583	210	69

Description

6500728346 hypothetical protein:similar to hydroxymyristoyl-:acyl carrier protein dehydratase (gtcfc:14.1) (ec:4.2.1.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywpB ywpB Bacillus subtilis 1423 -11532204 7000693119 ywpb 3r -hydroxymyristoyl-acyl carrier protein dehydratase, ywpb) (cl:(3r)-hydroxymyristoyl-(acyl carrier protein) dehydratase) (ec:4.2.1.-) (db:pir2.dat) D70065 D70065 Bacillus subtilis 1423 -11532204 220404 ywpb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to hydroxymyristoyl-(acyl carrier protein)) (le:145724) (re:146122) (di:complement) BSUB0019 Z99122 g2636162 Bacillus subtilis 1423 -11532204 7500963284 ywpb (db:genpept-bct1) (de:bacillus subtilis mbl, flh(o,p), rapd, ywp(b,c,d,e,f,g,h,i,j) and ywqagenes.) (nt:similar to hydroxymyristoyl-(acyl carrier protein)) (le:3199) (re:3597) (di:direct) BSZ83337 Z83337 g1763703 Bacillus subtilis 1423 -11532204

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815096	6428	28584	816	272

Description

GTC ORF with score 1037 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone\_lib:mizukam) (db:genpept-pln1) (de:schizosaccharomyces pombe 37 kb genomic dna, clone c213.) (nt:similar to s.cerevisiae methionyl-trna synthetase:) (le:14661) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815102	6429	28585	324	107

Description

6500728347 hypothetical protein:required for translation of spoiiid (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) usd usd Bacillus subtilis 1423 -11532205 7000694492 usd required for translation of spoiiid usd (db:pir2.dat) E69729 E69729 Bacillus subtilis 1423 -11532205 7500965131 usd (fn:required for translation of spoiiid) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:150681) (re:150791) (di:complement) BSUB0019 Z99122 g2636168 Bacillus subtilis 1423 -11532205



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815103	6430	28586	1092	364

Description

6500728348 hypothetical protein:similar to transcriptional regulator:marr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywoH ywoH Bacillus subtilis 1423 -11532206 7000694774 ywoH transcription regulator marr family homolog ywoH (db:pir2.dat) C70065 C70065 Bacillus subtilis 1423 -11532206 220397 ywoH (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to transcriptional regulator (marr family)) (le:151016) (re:151429) (di:direct) BSUB0019 Z99122 g2636169 Bacillus subtilis 1423 -11532206 7500965337 ywoH unknown:similar to cytolysin slyA from (db:genpept-bct1) (de:b.subtilis ywo(a,b,c,d,e,f,g,h), nrg(a,b), spoiiid and mbl genes.) (le:9874) (re:10287) (di:complement) BSZ82987 Z82987 g1684652 Bacillus subtilis 1423 -11532206

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815112	6431	28587	468	156

Description

GTC ORF with score 155 to: (fn:controls germ tube growth and pathogenicity of) (db:genpept-pln1) (de:magnaporthe grisea putative transcriptional regulator (con7) gene,complete cds.) (nt:has zinc-finger motif and nuclear localization) (le:298:1253:1920)...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815132	6432	28588	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815133	6433	28589	222	73

Description

6500728349 hypothetical protein:similar to antibiotic resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywoG ywoG Bacillus subtilis 1423 -11532207 7000692217 ywoG antibiotic resistance protein homolog ywoG (db:pir2.dat) B70065 B70065 Bacillus subtilis 1423 -11532207 220396 ywoG (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to antibiotic resistance protein) (le:151451) (re:152641) (di:direct) BSUB0019 Z99122 g2636170 Bacillus subtilis 1423 -11532207 7500963423 ywoG unknown similar to quinolon resistance protein (db:genpept-bct1) (de:b.subtilis ywo(a,b,c,d,e,f,g,h), nrg(a,b), spoiiid and mbl genes.) (le:8662) (re:9852) (di:complement) BSZ82987 Z82987 g1684651 Bacillus subtilis 1423 -11532207

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815147	6434	28590	537	178

Description

6500728350 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywoF ywoF Bacillus subtilis 1423 -11532208  
 7000694056 ywof hypothetical protein ywof (db:pir2.dat) A70065 A70065  
 Bacillus subtilis 1423 -11532208 220395 ywof (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:152732) (re:154138) (di:complement) BSUB0019 Z99122 g2636171  
 Bacillus subtilis 1423 -11532208 7500964837 ywof unknown (db:genpept-bct1) (de:b.subtilis ywo(a,b,c,d,e,f,g,h), nrg(a,b), spoiiid and mb1 genes.) (le:7165) (re:8571) (di:direct) BSZ82987 Z82987 g1684650 Bacillus subtilis 1423 -11532208

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815162	6435	28591	285	94

Description

6500728351 hypothetical protein:hypothetical 54.0 kd protein in nrga-usd intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywoE ywoE Bacillus subtilis 1423 -11532209  
 7500952954 ywoe (de:hypothetical 54.0 kd protein in nrga-usd intergenic region) (db:swissprot) YWOE\_BACSU P94575 BACILLUS SUBTILIS 1423 -11532209  
 7000688707 ywoe permease homolog ywoe (cl:escherichia coli probable transport protein b0511) (db:pir2.dat) H70064 H70064 Bacillus subtilis 1423 -11532209 220394 ywoe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to permease) (le:154244) (re:155716) (di:complement) BSUB0019 Z99122 g2636172  
 Bacillus subtilis 1423 -11532209 7502851753 ywoe unknown:similar to uracil permease from (db:genpept-bct1) (de:b.subtilis ywo(a,b,c,d,e,f,g,h), nrg(a,b), spoiiid and mb1 genes.) (le:5587) (re:7059) (di:direct) BSZ82987 Z82987 g1684649 Bacillus subtilis 1423 -11532209 4000707552 ywoe (de:hypothetical 54.0 kd protein in nrga-usd intergenic region) (db:swissprot) YWOE\_BACSU P94575 BACILLUS SUBTILIS 1423 -11532209

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815168	6436	28592	318	105

Description

6500728352 hypothetical protein:similar to transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywoD ywoD Bacillus subtilis 1423 -11532210 7000694820 ywod transporter homolog ywod (cl:fosmidmycin resistance protein) (db:pir2.dat) G70064 G70064 Bacillus subtilis 1423 -11532210 220393 ywod (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to transporter) (le:155897) (re:157255) (di:complement) BSUB0019 Z99122 g2636173 Bacillus subtilis 1423 -11532210 7500955915 ywod unknown:similar to streptomyces glaucescens (db:genpept-bct1) (de:b.subtilis ywo(a,b,c,d,e,f,g,h), nrg(a,b), spoiiid and mbl genes.) (le:4048) (re:5406) (di:direct) BSZ82987 Z82987 gl684648 Bacillus subtilis 1423 -11532210

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815172	6437	28593	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815182	6438	28594	453	150

Description

GTC ORF with score 114 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid c11g6, complete sequence.) (nt:similar to phd-finger.; cdna est embl:t00556 comes) (le:19230:19333:20803:22572) (re:19263:19616:20996:23063) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815185	6439	28595	237	78

Description

6500728353 hypothetical protein:similar to isochorismatase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywoC ywoC Bacillus subtilis 1423 -11532211 7000694135 ywoc isochorismatase homolog ywoc (cl:hypothetical protein b1011) (db:pir2.dat) F70064 F70064 Bacillus subtilis 1423 -11532211 220392 ywoc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to isochorismatase) (le:157255) (re:157824) (di:complement) BSUB0019 Z99122 g2636174 Bacillus subtilis 1423 -11532211 7500955929 ywoc unknown:highly similar to e. coli yecd (db:genpept-bct1) (de:b.subtilis ywo(a,b,c,d,e,f,g,h), nrg(a,b), spoiid and mb1 genes.) (le:3479) (re:4048) (di:direct) BSZ82987 Z82987 g1684647 Bacillus subtilis 1423 -11532211

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815186	6440	28596	543	180

Description

6500728354 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywoB ywoB Bacillus subtilis 1423 -11532212 7000694055 ywob hypothetical protein ywob (db:pir2.dat) E70064 E70064 Bacillus subtilis 1423 -11532212 220391 ywob (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:158008) (re:158472) (di:complement) BSUB0019 Z99122 g2636175 Bacillus subtilis 1423 -11532212 7500964836 ywob unknown (db:genpept-bct1) (de:b.subtilis ywo(a,b,c,d,e,f,g,h), nrg(a,b), spoiid and mb1 genes.) (le:2831) (re:3295) (di:direct) BSZ82987 Z82987 g1684646 Bacillus subtilis 1423 -11532212

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815189	6441	28597	414	138

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815192	6442	28598	732	244

Description

6500728355 hypothetical protein:similar to bacteriocin transport permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywoA ywoA Bacillus subtilis 1423 -11532213 220388 ywoa (de:hypothetical 21.7 kd protein in nrgb-spoiiq intergenic region) (db:swissprot) YWOA\_BACSU P94571 BACILLUS SUBTILIS 1423 -11532213 7000692258 ywoa bacteriocin transport permease homolog ywoa (db:pir2.dat) D70064 D70064 Bacillus subtilis 1423 -11532213 7500952952 ywoa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to bacteriocin transport permease) (le:160511) (re:161092) (di:direct) BSUB0019 Z99122 g2636178 Bacillus subtilis 1423 -11532213 7502851754 ywoa unknown (db:genpept-bct1) (de:b.subtilis ywo(a,b,c,d,e,f,g,h), nrg(a,b), spoiiid and mbl genes.) (le:211) (re:792) (di:complement) BSZ82987 Z82987 g1684643 Bacillus subtilis 1423 -11532213 7500952950 ywoa (de:hypothetical 21.7 kd protein in nrgb-spoiiq intergenic region) (db:swissprot) YWOA\_BACSU P94571 BACILLUS SUBTILIS 1423 -11532213

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815200	6443	28599	306	101

Description

6500728356 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywnJ ywnJ Bacillus subtilis 1423 -11532214 7000694054 ywnj hypothetical protein ywnj (db:pir2.dat) C70064 C70064 Bacillus subtilis 1423 -11532214 220229 ywnj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:161133) (re:161555) (di:complement) BSUB0019 Z99122 g2636179 Bacillus subtilis 1423 -11532214 7500964835 ywnj unknown (db:genpept-bct1) (de:b.subtilis urease operon and downstream dna.) (le:9676) (re:10098) (di:direct) BSUEROP Y08559 g1592706 Bacillus subtilis 1423 -11532214

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815204	6444	28600	471	156

Description

6500728357 hypothetical protein:similar to phosphinothricin acetyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywnH ywnH Bacillus subtilis 1423 -11532215 7000694402 ywnh probable phosphinothricin n-acetyltransferase:ywnh (cl:phosphinothricin n-acetyltransferase) (ec:2.3.1.-) (db:pir2.dat) B70064 B70064 Bacillus subtilis 1423 -11532215 220227 ywnh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to phosphinothricin acetyltransferase) (le:162658) (re:163149) (di:direct) BSUB0019 Z99122 g2636181 Bacillus subtilis 1423 -11532215 7500955851 ywnh unknown:similar to streptomyces coelicolor (db:genpept-bct1) (de:b.subtilis urease operon and downstream dna.) (le:8082) (re:8573) (di:complement) BSUEROP Y08559 g1592704 Bacillus subtilis 1423 -11532215

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815221	6445	28601	597	198

Description

6500728358 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywnG ywnG Bacillus subtilis 1423 -11532216 7000692862 ywnG conserved hypothetical protein ywnG (cl:hypothetical protein ywnG) (db:pir2.dat) A70064 A70064 Bacillus subtilis 1423 -11532216 220226 ywnG (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to hypothetical proteins from b. subtilis) (le:163146) (re:163664) (di:direct) BSUB0019 Z99122 g2636182 Bacillus subtilis 1423 -11532216 7500955928 ywnG unknown (db:genpept-bct1) (de:b.subtilis urease operon and downstream dna.) (le:7567) (re:8085) (di:complement) BSUEROP Y08559 g1592703 Bacillus subtilis 1423 -11532216

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815225	6446	28602	552	183

Description

6500728359 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywnF ywnF Bacillus subtilis 1423 -11532217 7000694053 ywnf hypothetical protein ywnf (db:pir2.dat) H70063 H70063 Bacillus subtilis 1423 -11532217 220225 ywnf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:163951) (re:164385) (di:complement) BSUB0019 Z99122 g2636183 Bacillus subtilis 1423 -11532217 7500964834 ywnf unknown (db:genpept-bct1) (de:b.subtilis urease operon and downstream dna.) (le:6846) (re:7280) (di:direct) BSUEROP Y08559 g1592702 Bacillus subtilis 1423 -11532217

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815226	6447	28603	345	114

Description

6500728360 hypothetical protein:similar to cardiolipin synthase (gtcfc:14.1) (ec:2.7.8.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywnE ywnE Bacillus subtilis 1423 -11532218 7500952946 ywne (de:hypothetical 55.8 kd protein in spoiiq-mta intergenic region) (db:swissprot) YWNE\_BACSU P71040 BACILLUS SUBTILIS 1423 -11532218 7000692326 ywne cardiolipin synthase homolog ywne (cl:bacillus probable cardiolipin synthetase) (db:pir2.dat) G70063 G70063 Bacillus subtilis 1423 -11532218 7500952948 ywne (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to cardiolipin synthase) (le:164628) (re:166076) (di:direct) BSUB0019 Z99122 g2636184 Bacillus subtilis 1423 -11532218 220224 ywne unknown (db:genpept-bct1) (de:b.subtilis urease operon and downstream dna.) (nt:product similar to escherichia coli cardiolipin) (le:5155) (re:6603) (di:complement) BSUEROP Y08559 g1592701 Bacillus subtilis 1423 -11532218

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815230	6448	28604	243	80

Description

6500728361 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywnC ywnC Bacillus subtilis 1423 -11532219 7000692861 ywnc conserved hypothetical protein ywnc (cl:hypothetical protein ywnc) (db:pir2.dat) F70063 F70063 Bacillus subtilis 1423 -11532219 220222 ywnc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to hypothetical proteins from b. subtilis) (le:167015) (re:167398) (di:direct) BSUB0019 Z99122 g2636186 Bacillus subtilis 1423 -11532219 7500955927 ywnc unknown (db:genpept-bct1) (de:b.subtilis urease operon and downstream dna.) (le:3833) (re:4216) (di:complement) BSUEROP Y08559 g1592699 Bacillus subtilis 1423 -11532219

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815232	6449	28605	798	265

Description

6500728362 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywnB ywnB Bacillus subtilis 1423 -11532220  
7000694052 ywnb hypothetical protein ywnb (db:pir2.dat) E70063 E70063 Bacillus subtilis 1423 -11532220 220221 ywnb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:167433) (re:168074) (di:complement) BSUB0019 Z99122 g2636187 Bacillus subtilis 1423 -11532220 7500964833 ywnb unknown (db:genpept-bct1) (de:b.subtilis urease operon and downstream dna.) (le:3157) (re:3798) (di:direct) BSUEROP Y08559 g1592698 Bacillus subtilis 1423 -11532220

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815249	6450	28606	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815252	6451	28607	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815255	6452	28608	1608	535

Description

6500728363 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywnA ywnA Bacillus subtilis 1423 -11532221  
7000694051 ywna hypothetical protein ywna (db:pir2.dat) D70063 D70063 Bacillus subtilis 1423 -11532221 220220 ywna (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:168142) (re:168543) (di:complement) BSUB0019 Z99122 g2636188 Bacillus subtilis 1423 -11532221 7500964832 ywna unknown (db:genpept-bct1) (de:b.subtilis urease operon and downstream dna.) (le:2688) (re:3089) (di:direct) BSUEROP Y08559 g1592697 Bacillus subtilis 1423 -11532221



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815261	6453	28609	1098	365

Description

6500728364 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywmG ywmG Bacillus subtilis 1423 -11532222  
7000694050 ywmG hypothetical protein ywmG (db:pir2.dat) C70063 C70063 Bacillus subtilis 1423 -11532222 219036 ywmh unknown (db:genpept-bct1) (de:b.subtilis atpc gene.) (le:10910) (re:11098) (di:direct) BSATPC Z81356 g1648859 Bacillus subtilis 1423 -11532222 304089 ywmG (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:172069) (re:172257) (di:complement) BSUB0019 Z99122 g2636192 Bacillus subtilis 1423 -11532222

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815264	6454	28610	459	152

Description

6500728365 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywmF ywmF Bacillus subtilis 1423 -11532223  
7000694049 ywmF hypothetical protein ywmF (db:pir2.dat) B70063 B70063 Bacillus subtilis 1423 -11532223 219035 ywmG unknown (db:genpept-bct1) (de:b.subtilis atpc gene.) (le:10358) (re:10837) (di:direct) BSATPC Z81356 g1648858 Bacillus subtilis 1423 -11532223 304088 ywmF (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:172330) (re:172809) (di:complement) BSUB0019 Z99122 g2636193 Bacillus subtilis 1423 -11532223

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815272	6455	28611	423	140

Description

6500728366 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywmE ywmE Bacillus subtilis 1423 -11532224  
7000694048 ywmE hypothetical protein ywmE (db:pir2.dat) A70063 A70063 Bacillus subtilis 1423 -11532224 219030 ywme unknown (db:genpept-bct1) (de:b.subtilis atpc gene.) (le:6641) (re:6802) (di:direct) BSATPC Z81356 g1648862 Bacillus subtilis 1423 -11532224 304083 ywme (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:176365) (re:176526) (di:complement) BSUB0019 Z99122 g2636197 Bacillus subtilis 1423 -11532224

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815275	6456	28612	1569	523

Description

6500728367 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywmD ywmD Bacillus subtilis 1423 -11532225 7000692860 ywmD conserved hypothetical protein ywmD (cl:hypothetical protein ywmD) (db:pir2.dat) H70062 H70062 Bacillus subtilis 1423 -11532225 219029 ywmD unknown (db:genpept-bct1) (de:b.subtilis atpc gene.) (le:5873) (re:6547) (di:direct) BSATPC Z81356 g1648854 Bacillus subtilis 1423 -11532225 304082 ywmD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to hypothetical proteins from b. subtilis) (le:176620) (re:177294) (di:complement) BSUB0019 Z99122 g2636198 Bacillus subtilis 1423 -11532225

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815276	6457	28613	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815291	6458	28614	402	133

Description

6500728368 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywmC ywmC Bacillus subtilis 1423 -11532226 7000692859 ywmC conserved hypothetical protein ywmC (cl:hypothetical protein ywmC) (db:pir2.dat) G70062 G70062 Bacillus subtilis 1423 -11532226 219028 ywmC unknown (db:genpept-bct1) (de:b.subtilis atpc gene.) (le:4866) (re:5549) (di:direct) BSATPC Z81356 g1648853 Bacillus subtilis 1423 -11532226 304081 ywmC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to hypothetical proteins from b. subtilis) (le:177618) (re:178301) (di:complement) BSUB0019 Z99122 g2636199 Bacillus subtilis 1423 -11532226

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815295	6459	28615	834	277

Description

6500728369 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywmB ywmB Bacillus subtilis 1423 -11532227  
7000694047 ywmb hypothetical protein ywmb (db:pir2.dat) F70062 F70062 Bacillus subtilis 1423 -11532227 7500964831 ywmb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:181258) (re:181998) (di:complement) BSUB0019 Z99122 g2636202 Bacillus subtilis 1423 -11532227

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815298	6460	28616	345	114

Description

6500728370 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywzB ywzB Bacillus subtilis 1423 -11532228  
7000694070 ywzb hypothetical protein ywzb (db:pir2.dat) G70070 G70070 Bacillus subtilis 1423 -11532228 7500964851 ywzb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:182127) (re:182357) (di:complement) BSUB0019 Z99122 g2636203 Bacillus subtilis 1423 -11532228

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815313	6461	28617	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815318	6462	28618	444	147

Description

6500728371 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywma ywma Bacillus subtilis 1423 -11532229  
7000694046 ywma hypothetical protein ywma (db:pir2.dat) E70062 E70062 Bacillus subtilis 1423 -11532229 219024 ywma unknown (db:genpept-bct1) (de:b.subtilis atpc gene.) (le:170) (re:643) (di:complement) BSATPC Z81356 g1648850 Bacillus subtilis 1423 -11532229 304077 ywma (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:182527) (re:183000) (di:direct) BSUB0019 Z99122 g2636204 Bacillus subtilis 1423 -11532229

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815320	6463	28619	519	172

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815333	6464	28620	1284	427

Description

6500728372 ipc-33d:ylg hypothetical protein:hypothetical 19.4 kd protein in spoir-glyc intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylg ylg Bacillus subtilis 1423 -11532230  
7500952945 ylg:ipc-33d (de:hypothetical 19.4 kd protein in spoir-glyc intergenic region) (db:swissprot) YWLG\_BACSU P39157 BACILLUS SUBTILIS 1423 -11532230 7000688706 ylg:ipc-33d hypothetical protein ylg:ipc-33d protein (db:pir2.dat) I40482 I40482 Bacillus subtilis 1423 -11532230 5000689788 ipc-33d unknown (db:genpept-bct1) (de:b.subtilis spoir-r, glyc and upp genes.) (le:4750) (re:5292) (di:direct) BSSPORUPP Z38002 g556885 Bacillus subtilis 1423 -11532230 219666 ylg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: ipc-33d) (le:192609) (re:193151) (di:complement) BSUB0019 Z99122 g2636216 Bacillus subtilis 1423 -11532230 116730 ylg:ipc-33d (de:hypothetical 19.4 kd protein in spoir-glyc intergenic region) (db:swissprot) YWLG\_BACSU P39157 BACILLUS SUBTILIS 1423 -11532230 170298 ylg:ipc-33d hypothetical protein ylg:ipc-33d protein (db:pir) I40482 I40482 Bacillus subtilis 1423 -11532230

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815345	6465	28621	729	242

Description

6500728373 ipc-32d:ywlf hypothetical protein:hypothetical laca/rpib family protein in spoiiir-glyc intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywlf ywlf Bacillus subtilis 1423 -11532231 7500952944 ywlf:ipc-32d (de:region) (db:swissprot) YWLF\_BACSU P39156 BACILLUS SUBTILIS 1423 -11532231 7000688705 ywlf:ipc-32d ribose 5-phosphate epimerase pentose phosphate homolog ywlf:yjca homolog ipc-32d (cl:galactoside o-acetyltransferase) (db:pir2.dat) I40481 I40481 Bacillus subtilis 1423 -11532231 5000689787 ipc-32d similar to escherichia coli yjca gene product (db:genpept-bct1) (de:b.subtilis spoii-r, glyc and upp genes.) (le:4288) (re:4737) (di:direct) BSSPORUPP Z38002 g556884 Bacillus subtilis 1423 -11532231 219665 ywlf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: ipc-32d; similar to ribose) (le:193164) (re:193613) (di:complement) BSUB0019 Z99122 g2636217 Bacillus subtilis 1423 -11532231 116729 ywlf:ipc-32d (de:region) (db:swissprot) YWLF\_BACSU P39156 BACILLUS SUBTILIS 1423 -11532231 170671 ywlf:ipc-32d ribose 5-phosphate epimerase pentose phosphate homolog ywlf:yjca homolog ipc-32d (db:pir) I40481 I40481 Bacillus subtilis 1423 -11532231

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815346	6466	28622	267	89

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815365	6467	28623	330	109

#### Description

6500728374 ipc-31d:ywle hypothetical protein:putative low molecular weight protein-tyrosine-phosphatase (gtcfc:14.1) (ec:3.1.3.48) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywle ywle Bacillus subtilis 1423 -11532232 7500952943 ywle:ipc-31d (ec:3.1.3.48) (de:(ec 3.1.3.48)) (db:swissprot) YWLE\_BACSU P39155 BACILLUS SUBTILIS 1423 -11532232 124306 ywle:ipc-31d protein-tyrosine-phosphatase:homolog ywle:low molecular weight:ipc-31d protein (cl:protein-tyrosine-phosphatase, low molecular weight) (ec:3.1.3.48) (db:pir1.dat) S49360 I40479 Bacillus subtilis 1423 -11532232 5000689786 ipc-31d unknown (db:genpept-bct1) (de:b.subtilis spoii-r, glyc and upp genes.) (le:3679) (re:4131) (di:direct) BSSPORUPP Z38002 g556883 Bacillus subtilis 1423 -11532232 219664 ywle (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: ipc-31d; similar to) (le:193770) (re:194222) (di:complement) BSUB0019 Z99122 g2636218 Bacillus subtilis 1423 -11532232 116728 ywle:ipc-31d (ec:3.1.3.48) (de:(ec 3.1.3.48)) (db:swissprot) YWLE\_BACSU P39155 BACILLUS SUBTILIS 1423 -11532232 7000688704 ywle:ipc-31d protein-tyrosine-phosphatase:homolog ywle:low molecular weight:ipc-31d protein (cl:protein-tyrosine-phosphatase, low molecular weight) (ec:3.1.3.48) (db:pir) S49360 B70062 Bacillus subtilis 1423 -11532232

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815371	6468	28624	735	244

#### Description

6500728375 ipc-30d:ywld hypothetical protein:hypothetical 19.7 kd protein in spoii-r-glyc intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywld ywld Bacillus subtilis 1423 -11532233 7500952942 ywld:ipc-30d (de:hypothetical 19.7 kd protein in spoii-r-glyc intergenic region) (db:swissprot) YWLD\_BACSU P39154 BACILLUS SUBTILIS 1423 -11532233 7000688703 ywld:ipc-30d conserved hypothetical protein ywld:ipc-30d protein (cl:escherichia coli conserved hypothetical protein b1821) (db:pir2.dat) I40478 I40478 Bacillus subtilis 1423 -11532233 5000689785 ipc-30d unknown (db:genpept-bct1) (de:b.subtilis spoii-r, glyc and upp genes.) (le:3046) (re:3603) (di:direct) BSSPORUPP Z38002 g556882 Bacillus subtilis 1423 -11532233 219663 ywld (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: ipc-30d; similar to) (le:194298) (re:194855) (di:complement) BSUB0019 Z99122 g2636219 Bacillus subtilis 1423 -11532233 116727 ywld:ipc-30d (de:hypothetical 19.7 kd protein in spoii-r-glyc intergenic region) (db:swissprot) YWLD\_BACSU P39154 BACILLUS SUBTILIS 1423 -11532233 170297 ywld:ipc-30d conserved hypothetical protein ywld:ipc-30d protein (db:pir) I40478 I40478 Bacillus subtilis 1423 -11532233

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815408	6469	28625	813	271

Description

GTC ORF with score 141 to: (sr:baker's yeast strain=s288c (ab972))  
(db:genpept-pln1) (de:saccharomyces cerevisiae chromosome xii cosmid 8083.)  
(nt:similar to kluyveromyces lactis deoxyribonucleic) (le:23775) (re:26219)  
(di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815411	6470	28626	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815434	6471	28627	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815436	6472	28628	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815437	6473	28629	804	267

#### Description

6500728376 ipc-29d:ylwc hypothetical protein:hypothetical 37.0 kd protein in spoir-glyc intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylwc ylwc Bacillus subtilis 1423 -11532234  
7500952941 ylwc:ipc-29d (de:hypothetical 37.0 kd protein in spoir-glyc intergenic region) (db:swissprot) YWLC\_BACSU P39153 BACILLUS SUBTILIS 1423 -11532234 7000688702 ylwc:ipc-29d conserved hypothetical protein ylwc:sua5 homolog ipc-29d (db:pir2.dat) I40476 I40476 Bacillus subtilis 1423 -11532234 5000689784 ipc-29d similar to saccharomyces cerevisiae sua5 (db:genpept-bct1) (de:b.subtilis spoii-r, glyc and upp genes.) (le:1927) (re:2967) (di:direct) BSSPORUPP Z38002 g556881 Bacillus subtilis 1423 -11532234 219662 ylwc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: ipc-29d; similar to) (le:194934) (re:195974) (di:complement) BSUB0019 Z99122 g2636220 Bacillus subtilis 1423 -11532234 116726 ylwc:ipc-29d (de:hypothetical 37.0 kd protein in spoir-glyc intergenic region) (db:swissprot) YWLC\_BACSU P39153 BACILLUS SUBTILIS 1423 -11532234 170610 ylwc:ipc-29d conserved hypothetical protein ylwc:sua5 homolog ipc-29d (db:pir) I40476 I40476 Bacillus subtilis 1423 -11532234

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815451	6474	28630	387	128

#### Description

6500728377 ipc-28d:ylwb hypothetical protein:hypothetical 16.5 kd protein in spoir-glyc intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylwb ylwb Bacillus subtilis 1423 -11532235  
7500952940 ylwb:ipc-28d (de:hypothetical 16.5 kd protein in spoir-glyc intergenic region) (db:swissprot) YWLB\_BACSU P39152 BACILLUS SUBTILIS 1423 -11532235 7000688701 ylwb:ipc-28d hypothetical protein ylwb:ipc-28d protein (db:pir2.dat) I40475 I40475 Bacillus subtilis 1423 -11532235 5000689783 ipc-28d unknown (db:genpept-bct1) (de:b.subtilis spoii-r, glyc and upp genes.) (le:1327) (re:1770) (di:direct) BSSPORUPP Z38002 g556880 Bacillus subtilis 1423 -11532235 219661 ylwb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: ipc-28d) (le:196131) (re:196574) (di:complement) BSUB0019 Z99122 g2636221 Bacillus subtilis 1423 -11532235 116725 ylwb:ipc-28d (de:hypothetical 16.5 kd protein in spoir-glyc intergenic region) (db:swissprot) YWLB\_BACSU P39152 BACILLUS SUBTILIS 1423 -11532235 170296 ylwb:ipc-28d hypothetical protein ylwb:ipc-28d protein (db:pir) I40475 I40475 Bacillus subtilis 1423 -11532235



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815454	6475	28631	294	98

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815456	6476	28632	1401	466

Description

6500728378 ipc-26r:ywla hypothetical protein:hypothetical 13.9 kd protein in prfa-spoir intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywla ywla Bacillus subtilis 1423 -11532236  
7500952939 ywla:ipc-26r (de:hypothetical 13.9 kd protein in prfa-spoir intergenic region) (db:swissprot) YWLA\_BACSU P39150 BACILLUS SUBTILIS 1423 -11532236 7000688700 ywla:ipc-26r conserved hypothetical protein ywla:ipc-26r protein (db:pir2.dat) I40473 I40473 Bacillus subtilis 1423 -11532236 5000689782 ipc-26r unknown (db:genpept-bct1) (de:b.subtilis spoiir-r, glyc and upp genes.) (le:83) (re:445) (di:complement) BSSPORUPP Z38002 g556878 Bacillus subtilis 1423 -11532236 219659 ywla (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: ipc-26r; similar to) (le:197456) (re:197818) (di:direct) BSUB0019 Z99122 g2636223 Bacillus subtilis 1423 -11532236 116724 ywla:ipc-26r (de:hypothetical 13.9 kd protein in prfa-spoir intergenic region) (db:swissprot) YWLA\_BACSU P39150 BACILLUS SUBTILIS 1423 -11532236 170295 ywla:ipc-26r conserved hypothetical protein ywla:ipc-26r protein (db:pir) I40473 I40473 Bacillus subtilis 1423 -11532236

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815465	6477	28633	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815467	6478	28634	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815474	6479	28635	1083	360

Description

5000689781 hypothetical protein:hypothetical 10.1 kd protein in prfa-spoiir intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywkF ywkF Bacillus subtilis 1423 -11532237 304127 ywkf (de:hypothetical 10.1 kd protein in prfa-spoiir intergenic region) (db:swissprot) YWKF\_BACSU P45874 BACILLUS SUBTILIS 1423 -11532237 7000688699 ywkf hypothetical protein ywkf (db:pir2.dat) S55439 S55439 Bacillus subtilis 1423 -11532237 7500952938 ywkf (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (le:25621) (re:25908) (di:direct) BSDNA320D Z49782 g853778 Bacillus subtilis 1423 -11532237 7502851755 ywkf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:197835) (re:198122) (di:complement) BSUB0019 Z99122 g2636224 Bacillus subtilis 1423 -11532237 116723 ywkf (de:hypothetical 10.1 kd protein in prfa-spoiir intergenic region) (db:swissprot) YWKF\_BACSU P45874 BACILLUS SUBTILIS 1423 -11532237 170683 ywkf hypothetical protein ywkf (db:pir) S55439 S55439 Bacillus subtilis 1423 -11532237 219155 ywkf (db:genpept-bct2) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (le:25621) (re:25908) (di:direct) BSDNA320D Z49782 g853778 Bacillus subtilis 1423 -11532237 6500728379 hypothetical protein:hypothetical 10.1 kd protein in prfa-spoiir intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywkF ywkF Bacillus subtilis 1423 -11532237

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815491	6480	28636	549	183

Description

5000689780 hypothetical protein:hypothetical 14.8 kd protein in tdk-prfa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) ywkD ywkD Bacillus subtilis 1423 -11532238  
304124 ywkD (de:hypothetical 14.8 kd protein in tdk-prfa intergenic region)  
(db:swissprot) YWKD\_BACSU P45871 BACILLUS SUBTILIS 1423 -11532238  
7000688698 ywkD conserved hypothetical protein ywkD (db:pir2.dat) S55436  
S55436 Bacillus subtilis 1423 -11532238 7500952937 ywkD unknown  
(db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321 degrees).)  
(le:23111) (re:23497) (di:complement) BSDNA320D Z49782 g853775 Bacillus  
subtilis 1423 -11532238 7502851756 ywkD (fn:unknown) (db:genpept-bct1)  
(de:bacillus subtilis complete genome (section 19 of 21): from 3597091to  
3809700.) (nt:similar to hypothetical proteins) (le:200246) (re:200632)  
(di:direct) BSUB0019 Z99122 g2636227 Bacillus subtilis 1423 -11532238  
116722 ywkD (de:hypothetical 14.8 kd protein in tdk-prfa intergenic region)  
(db:swissprot) YWKD\_BACSU P45871 BACILLUS SUBTILIS 1423 -11532238 170681  
ywkD conserved hypothetical protein ywkD (db:pir) S55436 S55436 Bacillus  
subtilis 1423 -11532238 219152 ywkD unknown (db:genpept-bct2)  
(de:b.subtilis chromosomal dna (region 320-321 degrees).) (le:23111)  
(re:23497) (di:complement) BSDNA320D Z49782 g853775 Bacillus subtilis 1423  
-11532238 6500728380 hypothetical protein:hypothetical 14.8 kd protein in  
tdk-prfa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) ywkD ywkD Bacillus subtilis 1423 -11532238

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815492	6481	28637	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815494	6482	28638	204	67

Description

5000689779 hypothetical protein:hypothetical 21.1 kd protein in tdk-prfa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) ywkc ywkc Bacillus subtilis 1423 -11532239  
304123 ywkc (de:hypothetical 21.1 kd protein in tdk-prfa intergenic region)  
(db:swissprot) YWKC\_BACSU P45870 BACILLUS SUBTILIS 1423 -11532239  
7000688697 ywkc hypothetical protein ywkc (db:pir2.dat) S55435 S55435  
Bacillus subtilis 1423 -11532239 7500952936 ywkc unknown (db:genpept-bct1)  
(de:b.subtilis chromosomal dna (region 320-321 degrees).) (le:22435)  
(re:22989) (di:complement) BSDNA320D Z49782 g853774 Bacillus subtilis 1423  
-11532239 7502851757 ywkc (fn:unknown) (db:genpept-bct1) (de:bacillus  
subtilis complete genome (section 19 of 21): from 3597091to 3809700.)  
(le:200754) (re:201308) (di:direct) BSUB0019 Z99122 g2636228 Bacillus  
subtilis 1423 -11532239 116721 ywkc (de:hypothetical 21.1 kd protein in  
tdk-prfa intergenic region) (db:swissprot) YWKC\_BACSU P45870 BACILLUS  
SUBTILIS 1423 -11532239 170680 ywkc hypothetical protein ywkc (db:pir)  
S55435 S55435 Bacillus subtilis 1423 -11532239 219151 ywkc unknown  
(db:genpept-bct2) (de:b.subtilis chromosomal dna (region 320-321 degrees).)  
(le:22435) (re:22989) (di:complement) BSDNA320D Z49782 g853774 Bacillus  
subtilis 1423 -11532239 6500728381 hypothetical protein:hypothetical 21.1  
kd protein in tdk-prfa intergenic region (gtcfc:14.1) (keggfc:14.2)  
(bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywkc ywkc Bacillus subtilis 1423  
-11532239

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815496	6483	28639	336	111

Description

5000689778 hypothetical protein:hypothetical 33.6 kd protein in tdk-prfa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywkb ywkb Bacillus subtilis 1423 -11532240 304122 ywkb (de:hypothetical 33.6 kd protein in tdk-prfa intergenic region) (db:swissprot) YWKB\_BACSU P45869 BACILLUS SUBTILIS 1423 -11532240 7000688696 ywkb conserved hypothetical protein ywkb (db:pir2.dat) S55434 S55434 Bacillus subtilis 1423 -11532240 6000685896 ywkb (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (nt:ttg start codon) (le:21442) (re:22401) (di:direct) BSDNA320D Z49782 g853773 Bacillus subtilis 1423 -11532240 7500952935 ywkb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to hypothetical proteins) (le:201342) (re:202301) (di:complement) BSUB0019 Z99122 g2636229 Bacillus subtilis 1423 -11532240 219150 ywkb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to hypothetical proteins) (le:32) (re:991) (di:complement) BSUB0020 Z99123 g2636241 Bacillus subtilis 1423 -11532240 116720 ywkb (de:hypothetical 33.6 kd protein in tdk-prfa intergenic region) (db:swissprot) YWKB\_BACSU P45869 BACILLUS SUBTILIS 1423 -11532240 170679 ywkb conserved hypothetical protein ywkb (db:pir) S55434 S55434 Bacillus subtilis 1423 -11532240 6500728382 hypothetical protein:hypothetical 33.6 kd protein in tdk-prfa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywkb ywkb Bacillus subtilis 1423 -11532240

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815500	6484	28640	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815502	6485	28641	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815503	6486	28642	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815519	6487	28643	396	131

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815558	6488	28644	453	150

Description

5000689777 hypothetical protein:hypothetical 34.0 kd protein in rho-mura intergenic region:orfq (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywji ywji Bacillus subtilis 1423 -11532241 304117 ywji (de:hypothetical 34.0 kd protein in rho-mura intergenic region (orfq)) (db:swissprot) YWJI\_BACSU Q03224 BACILLUS SUBTILIS 1423 -11532241 7000688695 ywji glycerol-inducible protein homolog ywji (db:pir2.dat) S55429 S55429 Bacillus subtilis 1423 -11532241 7500952934 orfq orfq (fn:unknown) (sr:bacillus subtilis (transposon tn917 insertional library) dna) (db:genpept-bct1) (de:bacillus subtilis orfr, 3' end; orfq; transcriptional terminator(rho) gene; ribosomal protein l31; thymidine kinase (tdk) gene,complete cds.) (nt:may f... BACRHOTDKX M97678 g143433 Bacillus subtilis 1423 -11532241 6000685894 ywji (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (le:15723) (re:16688) (di:direct) BSDNA320D Z49782 g853768 Bacillus subtilis 1423 -11532241 216589 ywji (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to glycerol-inducible protein) (le:207055) (re:208020) (di:complement) BSUB0019 Z99122 g2636234 Bacillus subtilis 1423 -11532241 219145 ywji (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to glycerol-inducible protein) (le:5745) (re:6710) (di:complement) BSUB0020 Z99123 g2636246 Bacillus subtilis 1423 -11532241 116719 ywji (de:hypothetical 34.0 kd protein in rho-mura intergenic region (orfq)) (db:swissprot) YWJI\_BACSU Q03224 BACILLUS SUBTILIS 1423 -11532241 170678 ywji glycerol-inducible protein homolog ywji (db:pir) S55429 S55429 Bacillus subtilis 1423 -11532241 6500728383 hypothetical protein:hypothetical 34.0 kd protein in rho-mura intergenic region:orfq (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywji ywji Bacillus subtilis 1423 -11532241

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815584	6489	28645	723	240

#### Description

6500728384 hypothetical protein:transaldolase-like protein:20 kd  
phosphoprotein orfu:csi9 (gtcfc:14.1) (ec:2.2.1.-) (keggfc:14.1)  
(bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywjH ywjH Bacillus subtilis 1423  
-11532242 6000684963 ywjh (ec:2.2.1.-) (de:(csi9)) (db:swissprot)  
ORFU\_BACSU P19669 BACILLUS SUBTILIS 1423 -11532242 131107 ywjh  
transaldolase pentose phosphate homolog ywjh:23k phosphoprotein orfu tsr 3  
region:hypothetical protein u (cl:bacillus subtilis 23k phosphoprotein orfu)  
(db:pir1.dat) F32354 F32354 Bacillus subtilis 1423 -11532242 5000689776  
ywjh hypothetical protein u (db:genpept-bct1) (de:b.subtilis chromosomal dna  
(region 320-321 degrees).) (le:13388) (re:13948) (di:direct) BSDNA320D  
Z49782 g853766 Bacillus subtilis 1423 -11532242 219143 ywjh (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21):  
from 3597091to 3809700.) (nt:similar to transaldolase (pentose phosphate))  
(le:209795) (re:210355) (di:complement) BSUB0019 Z99122 g2636236 Bacillus  
subtilis 1423 -11532242 304115 ywjh (fn:unknown) (db:genpept-bct1)  
(de:bacillus subtilis complete genome (section 20 of 21): from 3798401to  
4010550.) (nt:similar to transaldolase (pentose phosphate)) (le:8485)  
(re:9045) (di:complement) BSUB0020 Z99123 g2636248 Bacillus subtilis 1423  
-11532242 87869 ywjh (ec:2.2.1.-) (de:(csi9)) (db:swissprot) ORFU\_BACSU  
P19669 BACILLUS SUBTILIS 1423 -11532242

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815605	6490	28646	186	61

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815619	6491	28647	1785	594

#### Description

GTC ORF with score 775 to: (fn:hydrolyzes the amide bond between the)  
(sr:human) (db:genpept-pri2) (de:homo sapiens ubiquitin hydrolyzing enzyme i  
(ubh1) mrna, partialcds.) (nt:member of the deubiquitinating enzyme (dub)  
family;) (le:<153) (re:1220) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501815631	6492	28648	204	67

Description

5000689775 hypothetical protein: hypothetical 19.1 kd protein in spo0f-pyrg intergenic region: orfs (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywjG ywjG Bacillus subtilis 1423 -11532243 304112 ywjg (de: hypothetical 19.1 kd protein in spo0f-pyrg intergenic region (orfs)) (db:swissprot) YWJG\_BACSU P06629 BACILLUS SUBTILIS 1423 -11532243 7000688694 ywjg:spoof hypothetical protein ywjg:spoof protein (db:pir2.dat) I40471 I40471 Bacillus subtilis 1423 -11532243 6000685892 ywjg (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (le:11169) (re:11690) (di:complement) BSDNA320D Z49782 g853763 Bacillus subtilis 1423 -11532243 7500952933 spoof (db:genpept-bct1) (de:bacillus subtilis gene required at an early stage of sporulation. (gene code spoof).) (le:541) (re:1062) (di:direct) BSSPOO V00105 g40177 Bacillus subtilis 1423 -11532243 219140 ywjg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:212053) (re:212574) (di:direct) BSUB0019 Z99122 g2636239 Bacillus subtilis 1423 -11532243 219651 ywjg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:10743) (re:11264) (di:direct) BSUB0020 Z99123 g2636251 Bacillus subtilis 1423 -11532243 116718 ywjg (de: hypothetical 19.1 kd protein in spo0f-pyrg intergenic region (orfs)) (db:swissprot) YWJG\_BACSU P06629 BACILLUS SUBTILIS 1423 -11532243 170563 ywjg:spoof hypothetical protein ywjg:spoof protein (db:pir) I40471 I40471 Bacillus subtilis 1423 -11532243 6500728385 hypothetical protein: hypothetical 19.1 kd protein in spo0f-pyrg intergenic region: orfs (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywjG ywjG Bacillus subtilis 1423 -11532243



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815636	6493	28649	609	202

Description

5000689774 hypothetical protein:hypothetical 79.2 kd protein in acda 5region  
 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywjF  
 ywjF Bacillus subtilis 1423 -11532244 304108 ywjf (de:hypothetical 79.2 kd  
 protein in acda 5'region) (db:swissprot) YWJF\_BACSU P45866 BACILLUS SUBTILIS  
 1423 -11532244 7000688693 ywjf conserved hypothetical protein ywjf  
 (db:pir2.dat) S55420 S55420 Bacillus subtilis 1423 -11532244 7500952932  
 ywjf (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321  
 degrees).) (le:5281) (re:7398) (di:direct) BSDNA320D Z49782 g853759 Bacillus  
 subtilis 1423 -11532244 7502851758 ywjf (fn:unknown) (db:genpept-bct1)  
 (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to  
 4010550.) (nt:similar to hypothetical proteins) (le:15035) (re:17152)  
 (di:complement) BSUB0020 Z99123 g2636255 Bacillus subtilis 1423 -11532244  
 116717 ywjf (de:hypothetical 79.2 kd protein in acda 5'region)  
 (db:swissprot) YWJF\_BACSU P45866 BACILLUS SUBTILIS 1423 -11532244 170677  
 ywjf conserved hypothetical protein ywjf (db:pir) S55420 S55420 Bacillus  
 subtilis 1423 -11532244 219136 ywjf (db:genpept-bct2) (de:b.subtilis  
 chromosomal dna (region 320-321 degrees).) (le:5281) (re:7398) (di:direct)  
 BSDNA320D Z49782 g853759 Bacillus subtilis 1423 -11532244 6500728386  
 hypothetical protein:hypothetical 79.2 kd protein in acda 5region  
 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywjF  
 ywjF Bacillus subtilis 1423 -11532244

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815637	6494	28650	285	94

Description

5000689773 hypothetical protein:hypothetical 45.8 kd protein in acda 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywjE ywjE Bacillus subtilis 1423 -11532245 304107 ywje (de:hypothetical 45.8 kd protein in acda-nari intergenic region) (db:swissprot) YWJE\_BACSU P45865 BACILLUS SUBTILIS 1423 -11532245 7000688692 ywje cardiolipin synthetase homolog ywje (cl:bacillus probable cardiolipin synthetase) (db:pir2.dat) S55419 S55419 Bacillus subtilis 1423 -11532245 7500952931 ywje unknown (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (nt:similar to e. coli cardiolipin synthetase) (le:3930) (re:5126) (di:complement) BSDNA320D Z49782 g853758 Bacillus subtilis 1423 -11532245 7502851759 ywje (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to cardiolipin synthetase) (le:17307) (re:18503) (di:direct) BSUB0020 Z99123 g2636256 Bacillus subtilis 1423 -11532245 116716 ywje (de:hypothetical 45.8 kd protein in acda-nari intergenic region) (db:swissprot) YWJE\_BACSU P45865 BACILLUS SUBTILIS 1423 -11532245 170676 ywje cardiolipin synthetase homolog ywje (db:pir) S55419 S55419 Bacillus subtilis 1423 -11532245 219135 ywje unknown (db:genpept-bct2) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (nt:similar to e. coli cardiolipin synthetase) (le:3930) (re:5126) (di:complement) BSDNA320D Z49782 g853758 Bacillus subtilis 1423 -11532245 6500728387 hypothetical protein:hypothetical 45.8 kd protein in acda 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywjE ywjE Bacillus subtilis 1423 -11532245

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815651	6495	28651	501	166

Description

5000689772 hypothetical protein:hypothetical 36.9 kd protein in acda 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywjd ywjd Bacillus subtilis 1423 -11532246 304106 ywjd (de:hypothetical 36.9 kd protein in acda 5'region) (db:swissprot) YWJD\_BACSU P45864 BACILLUS SUBTILIS 1423 -11532246 7000688691 ywjd uv-endonuclease homolog ywjd (db:pir2.dat) S55418 S55418 Bacillus subtilis 1423 -11532246 7500952930 ywjd unknown (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (le:2955) (re:3917) (di:complement) BSDNA320D Z49782 g853757 Bacillus subtilis 1423 -11532246 7502851760 ywjd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to uv-endonuclease) (le:18516) (re:19478) (di:direct) BSUB0020 Z99123 g2636257 Bacillus subtilis 1423 -11532246 116715 ywjd (de:hypothetical 36.9 kd protein in acda 5'region) (db:swissprot) YWJD\_BACSU P45864 BACILLUS SUBTILIS 1423 -11532246 170675 ywjd uv-endonuclease homolog ywjd (db:pir) S55418 S55418 Bacillus subtilis 1423 -11532246 219134 ywjd unknown (db:genpept-bct2) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (le:2955) (re:3917) (di:complement) BSDNA320D Z49782 g853757 Bacillus subtilis 1423 -11532246 6500728388 hypothetical protein:hypothetical 36.9 kd protein in acda 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywjd ywjd Bacillus subtilis 1423 -11532246

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815657	6496	28652	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815660	6497	28653	564	187

Description

5000689771 hypothetical protein:hypothetical 10.5 kd protein in acda 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywjc ywjc Bacillus subtilis 1423 -11532247 304105 ywjc (de:hypothetical 10.5 kd protein in acda 5'region) (db:swissprot) YWJC\_BACSU P45863 BACILLUS SUBTILIS 1423 -11532247 7000688690 ywjc hypothetical protein ywjc (db:pir2.dat) S55417 S55417 Bacillus subtilis 1423 -11532247 7500952929 ywjc unknown (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (le:2602) (re:2874) (di:complement) BSDNA320D Z49782 g853756 Bacillus subtilis 1423 -11532247 7502851761 ywjc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:19559) (re:19831) (di:direct) BSUB0020 Z99123 g2636258 Bacillus subtilis 1423 -11532247 116714 ywjc (de:hypothetical 10.5 kd protein in acda 5'region) (db:swissprot) YWJC\_BACSU P45863 BACILLUS SUBTILIS 1423 -11532247 170674 ywjc hypothetical protein ywjc (db:pir) S55417 S55417 Bacillus subtilis 1423 -11532247 219133 ywjc unknown (db:genpept-bct2) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (le:2602) (re:2874) (di:complement) BSDNA320D Z49782 g853756 Bacillus subtilis 1423 -11532247 6500728389 hypothetical protein:hypothetical 10.5 kd protein in acda 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywjc ywjc Bacillus subtilis 1423 -11532247

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815661	6498	28654	402	133

Description

5000689770 hypothetical protein:hypothetical 19.6 kd protein in acda 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywjB ywjB Bacillus subtilis 1423 -11532248 304104 ywjb (de:hypothetical 19.6 kd protein in acda 5'region) (db:swissprot) YWJB\_BACSU P45862 BACILLUS SUBTILIS 1423 -11532248 7000688689 ywjb conserved hypothetical protein ywjb (db:pir2.dat) S55416 S55416 Bacillus subtilis 1423 -11532248 7500952928 ywjb unknown (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (le:2036) (re:2560) (di:direct) BSDNA320D Z49782 g853755 Bacillus subtilis 1423 -11532248 7502851762 ywjb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to hypothetical proteins) (le:19873) (re:20397) (di:complement) BSUB0020 Z99123 g2636259 Bacillus subtilis 1423 -11532248 116713 ywjb (de:hypothetical 19.6 kd protein in acda 5'region) (db:swissprot) YWJB\_BACSU P45862 BACILLUS SUBTILIS 1423 -11532248 170673 ywjb conserved hypothetical protein ywjb (db:pir) S55416 S55416 Bacillus subtilis 1423 -11532248 219132 ywjb unknown (db:genpept-bct2) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (le:2036) (re:2560) (di:direct) BSDNA320D Z49782 g853755 Bacillus subtilis 1423 -11532248 6500728390 hypothetical protein:hypothetical 19.6 kd protein in acda 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywjB ywjB Bacillus subtilis 1423 -11532248

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815674	6499	28655	648	215

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815679	6500	28656	453	150

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815690	6501	28657	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815694	6502	28658	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815703	6503	28659	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815724	6504	28660	918	305

Description

5000688778 hypothetical protein: hypothetical abc transporter atp-binding protein in acda 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywja ywja Bacillus subtilis 1423 -11532249 304103 ywja (de: hypothetical abc transporter atp-binding protein in acda 5' region) (db:swissprot) YWJA\_BACSU P45861 BACILLUS SUBTILIS 1423 -11532249 7000688688 ywja atp-binding transport protein ywja: abc transporter atp-binding protein ywja (cl: unassigned atp-binding cassette proteins: atp-binding cassette homology) (db:pir2.dat) S55415 S55415 Bacillus subtilis 1423 -11532249 7500952927 ywja abc transporter (db:genpept-bct1) (de: b. subtilis chromosomal dna (region 320-321 degrees).) (nt:gtg start codon) (le:299) (re:2026) (di:direct) BSDNA320D Z49782 g853754 Bacillus subtilis 1423 -11532249 7502851763 ywja (fn:unknown) (db:genpept-bct1) (de: bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt: similar to abc transporter (atp-binding protein)) (le:20407) (re:22134) (di:complement) BSUB0020 Z99123 g2636260 Bacillus subtilis 1423 -11532249 116712 ywja (de: hypothetical abc transporter atp-binding protein in acda 5' region) (db:swissprot) YWJA\_BACSU P45861 BACILLUS SUBTILIS 1423 -11532249 169838 ywja atp-binding transport protein ywja: abc transporter atp-binding protein ywja (cl: unassigned atp-binding cassette proteins: atp-binding cassette homology) (db:pir) S55415 S55415 Bacillus subtilis 1423 -11532249 219131 ywja abc transporter (db:genpept-bct2) (de: b. subtilis chromosomal dna (region 320-321 degrees).) (nt:gtg start codon) (le:299) (re:2026) (di:direct) BSDNA320D Z49782 g853754 Bacillus subtilis 1423 -11532249 6500728391 hypothetical protein: hypothetical abc transporter atp-binding protein in acda 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywja ywja Bacillus subtilis 1423 -11532249

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815725	6505	28661	324	107

Description

5000689769 hypothetical protein:hypothetical 58.2 protein in nari-acda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywiE ywiE Bacillus subtilis 1423 -11532250 219420 ywie (de:hypothetical 58.2 protein in acda-nari intergenic region) (db:swissprot) YWIE\_BACSU P45860 BACILLUS SUBTILIS 1423 -11532250 7000688687 ywie cardiolipin synthetase homolog ywie (cl:bacillus probable cardiolipin synthetase) (db:pir2.dat) S60089 S60089 Bacillus subtilis 1423 -11532250 7500952926 ywie unknown:similar to e.coli cardiolipin synthase (db:genpept-bct1) (de:b.subtilis nar(g,h,i,j,k), ywi(c,d,e) and args genes.) (le:10928) (re:12430) (di:direct) BSNARYWI Z49884 g971345 Bacillus subtilis 1423 -11532250 7502851764 ywie (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to cardiolipin synthetase) (le:22223) (re:23725) (di:complement) BSUB0020 Z99123 g2636261 Bacillus subtilis 1423 -11532250 116710 ywie (de:hypothetical 58.2 protein in acda-nari intergenic region) (db:swissprot) YWIE\_BACSU P45860 BACILLUS SUBTILIS 1423 -11532250 170287 ywie cardiolipin synthetase homolog ywie (db:pir) S60089 S60089 Bacillus subtilis 1423 -11532250 6500728392 hypothetical protein:hypothetical 58.2 protein in nari-acda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywiE ywiE Bacillus subtilis 1423 -11532250

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815740	6506	28662	957	318

Description

5000689768 hypothetical protein:hypothetical 18.1 kd protein in nark-narg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywiD ywiD Bacillus subtilis 1423 -11532251 219415 ywid (de:hypothetical 18.1 kd protein in nark-narg intergenic region) (db:swissprot) YWID\_BACSU P46910 BACILLUS SUBTILIS 1423 -11532251 7000688686 ywid hypothetical protein ywid (db:pir2.dat) S60084 S60084 Bacillus subtilis 1423 -11532251 7500952925 ywid unknown (db:genpept-bct1) (de:b.subtilis nar(g,h,i,j,k), ywi(c,d,e) and args genes.) (le:3383) (re:3859) (di:direct) BSNARYWI Z49884 g971340 Bacillus subtilis 1423 -11532251 7502851765 ywid (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:30794) (re:31270) (di:complement) BSUB0020 Z99123 g2636266 Bacillus subtilis 1423 -11532251 116709 ywid (de:hypothetical 18.1 kd protein in nark-narg intergenic region) (db:swissprot) YWID\_BACSU P46910 BACILLUS SUBTILIS 1423 -11532251 170286 ywid hypothetical protein ywid (db:pir) S60084 S60084 Bacillus subtilis 1423 -11532251 6500728393 hypothetical protein:hypothetical 18.1 kd protein in nark-narg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywiD ywiD Bacillus subtilis 1423 -11532251

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815744	6507	28663	1368	456

Description

5000689767 hypothetical protein:hypothetical 27.6 kd protein in fnr-narg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) ywiC ywiC Bacillus subtilis 1423 -11532252  
219414 ywic (de:hypothetical 27.6 kd protein in fnr-narg intergenic region)  
(db:swissprot) YWIC\_BACSU P46909 BACILLUS SUBTILIS 1423 -11532252  
7000688685 ywic conserved hypothetical protein ywic (db:pir2.dat) S60083  
S60083 Bacillus subtilis 1423 -11532252 7500952924 ywic unknown  
(db:genpept-bct1) (de:b.subtilis nar(g,h,i,j,k), ywi(c,d,e) and args genes.)  
(le:2520) (re:3239) (di:complement) BSNARYWI Z49884 g971339 Bacillus  
subtilis 1423 -11532252 7502851766 ywic (fn:unknown) (db:genpept-bct1)  
(de:bacillus subtilis complete genome (section 20 of 21): from 3798401to  
4010550.) (nt:similar to hypothetical proteins) (le:31414) (re:32133)  
(di:direct) BSUB0020 Z99123 g2636267 Bacillus subtilis 1423 -11532252  
116708 ywic (de:hypothetical 27.6 kd protein in fnr-narg intergenic region)  
(db:swissprot) YWIC\_BACSU P46909 BACILLUS SUBTILIS 1423 -11532252 170285  
ywic conserved hypothetical protein ywic (db:pir) S60083 S60083 Bacillus  
subtilis 1423 -11532252 6500728394 hypothetical protein:hypothetical 27.6  
kd protein in fnr-narg intergenic region (gtcfc:14.1) (keggfc:14.2)  
(bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywiC ywiC Bacillus subtilis 1423  
-11532252

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815745	6508	28664	477	158

Description

6500728395 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) ywiB ywiB Bacillus subtilis 1423 -11532253  
7000694045 ywib hypothetical protein ywib (db:pir2.dat) C70059 C70059  
Bacillus subtilis 1423 -11532253 4000714662 ywib (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21):  
from 3798401to 4010550.) (le:35970) (re:36398) (di:complement) BSUB0020  
Z99123 g2636271 Bacillus subtilis 1423 -11532253 7500964830 ywib  
(db:genpept-bct1) (de:bacillus subtilis ywia, sbo, ywib, args and nark  
genes.) (le:1255) (re:1683) (di:direct) BSZ97024 Z97024 g2224755 Bacillus  
subtilis 1423 -11532253

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815748	6509	28665	192	63

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815763	6510	28666	360	119

Description

6500728396 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywiA ywiA Bacillus subtilis 1423 -11532254 7000692858 ywia conserved hypothetical protein ywia (db:pir2.dat) B70059 B70059 Bacillus subtilis 1423 -11532254 7500963901 ywia unknown (db:genpept-bct1) (de:b.subtilis thrz downstream chromosomal region.) (le:18392) (re:19738) (di:complement) BSTHRZ Z80360 g1565254 Bacillus subtilis 1423 -11532254 219719 ywia (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to hypothetical proteins) (le:36976) (re:38322) (di:direct) BSUB0020 Z99123 g2636273 Bacillus subtilis 1423 -11532254

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815767	6511	28667	522	173

Description

6500728397 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywhR ywhR Bacillus subtilis 1423 -11532255 7000694044 ywhr hypothetical protein ywhr (db:pir2.dat) A70059 A70059 Bacillus subtilis 1423 -11532255 7500964829 ywhr unknown (db:genpept-bct1) (de:b.subtilis thrz downstream chromosomal region.) (le:18218) (re:18379) (di:complement) BSTHRZ Z80360 g1565253 Bacillus subtilis 1423 -11532255 219718 ywhr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:38335) (re:38496) (di:direct) BSUB0020 Z99123 g2636274 Bacillus subtilis 1423 -11532255

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815769	6512	28668	405	134

Description

6500728398 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywhQ ywhQ Bacillus subtilis 1423 -11532256 7000692107 ywhq abc transporter atp-binding protein homolog ywhq (cl:atp-binding cassette homology) (db:pir2.dat) H70058 H70058 Bacillus subtilis 1423 -11532256 7500963348 ywhq unknown:similar to abc transporter (db:genpept-bct1) (de:b.subtilis thrz downstream chromosomal region.) (le:17502) (re:18221) (di:complement) BSTHRZ Z80360 g1565252 Bacillus subtilis 1423 -11532256 219717 ywhq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to abc transporter (atp-binding protein)) (le:38493) (re:39212) (di:direct) BSUB0020 Z99123 g2636275 Bacillus subtilis 1423 -11532256

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815770	6513	28669	402	133

Description

6500728399 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywhP ywhP Bacillus subtilis 1423 -11532257  
7000694043 ywhp hypothetical protein ywhp (db:pir2.dat) G70058 G70058 Bacillus subtilis 1423 -11532257 7500964828 ywhp unknown (db:genpept-bct1) (de:b.subtilis thrz downstream chromosomal region.) (le:16199) (re:17509) (di:complement) BSTHRZ Z80360 g1565251 Bacillus subtilis 1423 -11532257  
219716 ywhp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:39205) (re:40515) (di:direct) BSUB0020 Z99123 g2636276 Bacillus subtilis 1423 -11532257

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815774	6514	28670	855	284

Description

6500728400 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywhO ywhO Bacillus subtilis 1423 -11532258  
7000694042 ywho hypothetical protein ywho (db:pir2.dat) F70058 F70058 Bacillus subtilis 1423 -11532258 7500964827 ywho unknown (db:genpept-bct1) (de:b.subtilis thrz downstream chromosomal region.) (le:15049) (re:16209) (di:complement) BSTHRZ Z80360 g1565250 Bacillus subtilis 1423 -11532258  
219715 ywho (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:40505) (re:41665) (di:direct) BSUB0020 Z99123 g2636277 Bacillus subtilis 1423 -11532258

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815779	6515	28671	1455	484

Description

6500728401 hypothetical protein:similar to ubiquinol-cytochrome c reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywhN ywhN Bacillus subtilis 1423 -11532259 7000694888 ywhn ubiquinol-cytochrome c reductase homolog ywhn (db:pir2.dat) E70058 E70058 Bacillus subtilis 1423 -11532259 7500965427 ywhn unknown:similar to peptidases (db:genpept-bct1) (de:b.subtilis thrz downstream chromosomal region.) (le:13764) (re:15044) (di:complement) BSTHRZ Z80360 g1565249 Bacillus subtilis 1423 -11532259  
219714 ywhn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to ubiquinol-cytochrome c reductase) (le:41670) (re:42950) (di:direct) BSUB0020 Z99123 g2636278 Bacillus subtilis 1423 -11532259

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815804	6516	28672	732	244

Description

6500728402 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywhM ywhM Bacillus subtilis 1423 -11532260  
7000694041 ywhm hypothetical protein ywhm (db:pir2.dat) D70058 D70058 Bacillus subtilis 1423 -11532260 7500964826 ywhm unknown (db:genpept-bct1) (de:b.subtilis thrz downstream chromosomal region.) (le:13066) (re:13767) (di:complement) BSTHRZ Z80360 g1565248 Bacillus subtilis 1423 -11532260 219713 ywhm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:42947) (re:43648) (di:direct) BSUB0020 Z99123 g2636279 Bacillus subtilis 1423 -11532260

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815809	6517	28673	1617	538

Description

6500728403 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywhL ywhL Bacillus subtilis 1423 -11532261 7000692857 ywhl conserved hypothetical protein ywhl (cl:hypothetical protein ywhk) (db:pir2.dat) C70058 C70058 Bacillus subtilis 1423 -11532261 7500963900 ywhl unknown (db:genpept-bct1) (de:b.subtilis thrz downstream chromosomal region.) (le:11684) (re:13060) (di:direct) BSTHRZ Z80360 g1565247 Bacillus subtilis 1423 -11532261 219712 ywhl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to hypothetical proteins) (le:43654) (re:45030) (di:complement) BSUB0020 Z99123 g2636280 Bacillus subtilis 1423 -11532261

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815845	6518	28674	1020	339

Description

6500728404 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywhK ywhK Bacillus subtilis 1423 -11532262 7000692856 ywhk conserved hypothetical protein ywhk (cl:hypothetical protein ywhk) (db:pir2.dat) B70058 B70058 Bacillus subtilis 1423 -11532262 7500963899 ywhk unknown (db:genpept-bct1) (de:b.subtilis thrz downstream chromosomal region.) (le:10290) (re:11645) (di:direct) BSTHRZ Z80360 g1565246 Bacillus subtilis 1423 -11532262 219711 ywhk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to hypothetical proteins) (le:45069) (re:46424) (di:complement) BSUB0020 Z99123 g2636281 Bacillus subtilis 1423 -11532262

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815851	6519	28675	366	121

Description

6500728405 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywhH ywhH Bacillus subtilis 1423 -11532263 7000692855 ywhh conserved hypothetical protein ywhh (db:pir2.dat) A70058 A70058 Bacillus subtilis 1423 -11532263 7500963898 ywhh unknown (db:genpept-bct1) (de:b.subtilis thrz downstream chromosomal region.) (le:8240) (re:8713) (di:complement) BSTHRZ Z80360 g1565243 Bacillus subtilis 1423 -11532263 219708 ywhh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to hypothetical proteins) (le:48001) (re:48474) (di:direct) BSUB0020 Z99123 g2636284 Bacillus subtilis 1423 -11532263

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815852	6520	28676	324	107

Description

6500728406 hypothetical protein:similar to penicillin-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywhE ywhE Bacillus subtilis 1423 -11532264 7000694356 ywhe penicillin-binding protein homolog ywhe (db:pir2.dat) F70057 F70057 Bacillus subtilis 1423 -11532264 7500965046 ywhe unknown:highly similar to penicillin binding (db:genpept-bct1) (de:b.subtilis thrz downstream chromosomal region.) (le:4300) (re:6243) (di:complement) BSTHRZ Z80360 g1565240 Bacillus subtilis 1423 -11532264 219705 ywhe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to penicillin-binding protein) (le:50471) (re:52414) (di:direct) BSUB0020 Z99123 g2636287 Bacillus subtilis 1423 -11532264

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815867	6521	28677	1458	485

Description

6500728407 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywhD ywhD Bacillus subtilis 1423 -11532265 7000694040 ywhd hypothetical protein ywhd (db:pir2.dat) E70057 E70057 Bacillus subtilis 1423 -11532265 7500964825 ywhd unknown (db:genpept-bct1) (de:b.subtilis thrz downstream chromosomal region.) (le:3358) (re:3876) (di:direct) BSTHRZ Z80360 g1565239 Bacillus subtilis 1423 -11532265 219704 ywhd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:52838) (re:53356) (di:complement) BSUB0020 Z99123 g2636288 Bacillus subtilis 1423 -11532265

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815878	6522	28678	585	194

Description

6500728408 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywhC ywhC Bacillus subtilis 1423 -11532266 7000692854 ywhc conserved hypothetical protein ywhc (db:pir2.dat) D70057 D70057 Bacillus subtilis 1423 -11532266 7500963897 ywhc unknown (db:genpept-bct1) (de:b.subtilis thrz downstream chromosomal region.) (le:2685) (re:3344) (di:direct) BSTHRZ Z80360 g1565238 Bacillus subtilis 1423 -11532266 219703 ywhc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to hypothetical proteins) (le:53370) (re:54029) (di:complement) BSUB0020 Z99123 g2636289 Bacillus subtilis 1423 -11532266

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815886	6523	28679	765	254

Description

6500728409 hypothetical protein:similar to 4-oxalocrotonate tautomerase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywhB ywhB Bacillus subtilis 1423 -11532267 7000692067 ywhb 4-oxalocrotonate tautomerase homolog ywhb (cl:4-oxalocrotonate tautomerase) (db:pir2.dat) C70057 C70057 Bacillus subtilis 1423 -11532267 7500963311 ywhb unknown:highly similar to pseudomonas putida (db:genpept-bct1) (de:b.subtilis thrz downstream chromosomal region.) (le:2388) (re:2576) (di:complement) BSTHRZ Z80360 g1565237 Bacillus subtilis 1423 -11532267 219702 ywhb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to 4-oxalocrotonate tautomerase) (le:54138) (re:54326) (di:direct) BSUB0020 Z99123 g2636290 Bacillus subtilis 1423 -11532267

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815887	6524	28680	888	295

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815914	6525	28681	429	142

Description

GTC ORF with score 119 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k06a9.) (nt:partial cds; coded for by c. elegans cdna yk50c7.5) (le:27212:27374:27536:27666) (re:27323:27486:27619:27751) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815932	6526	28682	330	109

Description

6500728410 hypothetical protein:similar to transcriptional regulator:marr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywhA ywhA Bacillus subtilis 1423 -11532268 7000694773 ywha transcription regulator marr family homolog ywha (db:pir2.dat) B70057 B70057 Bacillus subtilis 1423 -11532268 7500965336 ywha unknown:similar to regulatory proteins (db:genpept-bct1) (de:b.subtilis thrz downstream chromosomal region.) (le:1926) (re:2345) (di:direct) BSTHRZ Z80360 g1565236 Bacillus subtilis 1423 -11532268 219701 ywha (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to transcriptional regulator (marr family)) (le:54369) (re:54788) (di:complement) BSUB0020 Z99123 g2636291 Bacillus subtilis 1423 -11532268

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815933	6527	28683	435	144

Description

6500728411 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywgb ywgb Bacillus subtilis 1423 -11532269 7000692853 ywgb conserved hypothetical protein ywgb (db:pir2.dat) A70057 A70057 Bacillus subtilis 1423 -11532269 220234 ywgb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to hypothetical proteins) (le:58816) (re:59286) (di:complement) BSUB0020 Z99123 g2636294 Bacillus subtilis 1423 -11532269 7500963896 ywgb unknown (db:genpept-bct1) (de:b.subtilis ywfo, ywga and ywgb genes.) (le:2216) (re:2686) (di:direct) BSUWFO Z80355 g1561569 Bacillus subtilis 1423 -11532269

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815934	6528	28684	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815946	6529	28685	420	139

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815957	6530	28686	321	106

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815960	6531	28687	612	203

Description

GTC ORF with score 127 to: (sr:neurospora crassa strain=74-or23-1va)  
(db:genpept-pln1) (de:neurospora crassa two-component histidine kinase  
(nik-1) gene, 5'region and partial cds.) (nt:two-component histidine kinase)  
(le:1619:2488:3404:3732) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815975	6532	28688	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815980	6533	28689	528	175

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815982	6534	28690	309	102

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501815995	6535	28691	345	115

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501815998	6536	28692	1914	637

Description

6500728412 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywgA ywgA Bacillus subtilis 1423 -11532270  
7000694039 ywga hypothetical protein ywga (db:pir2.dat) H70056 H70056 Bacillus subtilis 1423 -11532270 220233 ywga (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:59398) (re:59898) (di:complement) BSUB0020 Z99123 g2636295 Bacillus subtilis 1423 -11532270 7500964824 ywga unknown (db:genpept-bct1) (de:bacillus subtilis ywfo, ywga and ywgb genes.) (le:1604) (re:2104) (di:direct) BSUWFO Z80355 g1561568 Bacillus subtilis 1423 -11532270

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816023	6537	28693	204	67

Description

6500728413 ipa-93d:ywfo hypothetical protein:hypothetical 51.0 kd protein in pta 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywfo ywfo Bacillus subtilis 1423 -11532271 7500952923 ywfo:ipa-93d (de:hypothetical 51.0 kd protein in pta 3'region) (db:swissprot) YWFO\_BACSU P39651 BACILLUS SUBTILIS 1423 -11532271  
7000688684 ywfo ywfo protein:hypothetical protein ipa-93d (db:pir2.dat) G70056 G70056 Bacillus subtilis 1423 -11532271 220232 ywfo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-93d; similar to) (le:59934) (re:61235) (di:complement) BSUB0020 Z99123 g2636296 Bacillus subtilis 1423 -11532271 5000689766 ywfo unknown (db:genpept-bct1) (de:bacillus subtilis ywfo, ywga and ywgb genes.) (le:267) (re:1568) (di:direct) BSUWFO Z80355 g1561567 Bacillus subtilis 1423 -11532271 116707 ywfo:ipa-93d (de:hypothetical 51.0 kd protein in pta 3'region) (db:swissprot) YWFO\_BACSU P39651 BACILLUS SUBTILIS 1423 -11532271

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816038	6538	28694	546	181

Description

6500728414 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywzC ywzC Bacillus subtilis 1423 -11532272  
7000694071 ywzc hypothetical protein ywzc (db:pir2.dat) H70070 H70070 Bacillus subtilis 1423 -11532272 7500964852 ywzc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:61397) (re:61621) (di:complement) BSUB0020 Z99123 g2636297 Bacillus subtilis 1423 -11532272



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816042	6539	28695	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816047	6540	28696	315	104

Description

6500728415 ipa-92r:ywfn hypothetical protein:hypothetical 29.7 kd protein in pta 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywfn ywfn Bacillus subtilis 1423 -11532273 7500952922 ywfn:ipa-92r (de:hypothetical 29.7 kd protein in pta 3'region) (db:swissprot) YWFN\_BACSU P39650 BACILLUS SUBTILIS 1423 -11532273 7000688683 ywfn ywfn protein:hypothetical protein ipa-92r (cl:hypothetical protein ylbo) (db:pir2.dat) S39747 S39747 Bacillus subtilis 1423 -11532273 5000689765 ipa-92r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:95347) (re:96123) (di:complement) BSGENR X73124 g414016 Bacillus subtilis 1423 -11532273 219329 ywfn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-92r; similar to) (le:61836) (re:62612) (di:direct) BSUB0020 Z99123 g2636298 Bacillus subtilis 1423 -11532273 116706 ywfn:ipa-92r (de:hypothetical 29.7 kd protein in pta 3'region) (db:swissprot) YWFN\_BACSU P39650 BACILLUS SUBTILIS 1423 -11532273 170170 ywfn conserved hypothetical protein ywfn (cl:hypothetical protein ylbo) (db:pir) S39747 S39747 Bacillus subtilis 1423 -11532273

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816050	6541	28697	315	104

Description

6500728416 ipa-91d:ywfm hypothetical protein:hypothetical 31.3 kd protein in pta 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywfm ywfm Bacillus subtilis 1423 -11532274 7500952921 ywfm:ipa-91d (de:hypothetical 31.3 kd protein in pta 3'region) (db:swissprot) YWFM\_BACSU P39649 BACILLUS SUBTILIS 1423 -11532274 7000688682 ywfm hypothetical protein ywfm:hypothetical protein ipa-91d (db:pir2.dat) S39746 S39746 Bacillus subtilis 1423 -11532274 5000689764 ipa-91d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:94313) (re:95203) (di:direct) BSGENR X73124 g414015 Bacillus subtilis 1423 -11532274 219328 ywfm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-91d; similar to) (le:62756) (re:63646) (di:complement) BSUB0020 Z99123 g2636299 Bacillus subtilis 1423 -11532274 116705 ywfm:ipa-91d (de:hypothetical 31.3 kd protein in pta 3'region) (db:swissprot) YWFM\_BACSU P39649 BACILLUS SUBTILIS 1423 -11532274 170169 ywfm conserved hypothetical protein ywfm (db:pir) S39746 S39746 Bacillus subtilis 1423 -11532274

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816053	6542	28698	417	139

Description

6500728417 ipa-90d:ywfl hypothetical protein:hypothetical 31.4 kd protein in pta 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywfl ywfl Bacillus subtilis 1423 -11532275 7500952920 ywfl:ipa-90d (de:hypothetical 31.4 kd protein in pta 3'region) (db:swissprot) YWFL\_BACSU P39648 BACILLUS SUBTILIS 1423 -11532275 7000688681 ywfl ywfl protein:hypothetical protein ipa-90d (db:pir2.dat) S39745 S39745 Bacillus subtilis 1423 -11532275 5000689763 ipa-90d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:93300) (re:94145) (di:direct) BSGENR X73124 g414014 Bacillus subtilis 1423 -11532275 219327 ywfl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-90d) (le:63814) (re:64659) (di:complement) BSUB0020 Z99123 g2636300 Bacillus subtilis 1423 -11532275 116704 ywfl:ipa-90d (de:hypothetical 31.4 kd protein in pta 3'region) (db:swissprot) YWFL\_BACSU P39648 BACILLUS SUBTILIS 1423 -11532275 170168 ywfl hypothetical protein ywfl (db:pir) S39745 S39745 Bacillus subtilis 1423 -11532275

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816068	6543	28699	471	156

Description

6500728418 ipa-89d:ywfk hypothetical protein:hypothetical transcriptional regulator in pta 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywfk ywfk Bacillus subtilis 1423 -11532276 7500952919 ywfk:ipa-89d (de:hypothetical transcriptional regulator in mmr-pta intergenic region) (db:swissprot) YWFK\_BACSU P39647 BACILLUS SUBTILIS 1423 -11532276 7000688680 ywfk transcription regulator lysr family homolog ywfk (cl:transcription activator lysr-type) (db:pir2.dat) S39744 S39744 Bacillus subtilis 1423 -11532276 5000688929 ipa-89d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:92352) (re:93251) (di:direct) BSGENR X73124 g580884 Bacillus subtilis 1423 -11532276 219326 ywfk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-89d; similar to) (le:64708) (re:65607) (di:complement) BSUB0020 Z99123 g2636301 Bacillus subtilis 1423 -11532276 116703 ywfk:ipa-89d (de:hypothetical transcriptional regulator in mmr-pta intergenic region) (db:swissprot) YWFK\_BACSU P39647 BACILLUS SUBTILIS 1423 -11532276 170167 ywfk transcriptional regulator lysr family homolog ywfk (db:pir) S39744 S39744 Bacillus subtilis 1423 -11532276

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816072	6544	28700	714	237

Description

GTC ORF with score 370 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome iii cosmid c1020.) (nt:spcc1020.07, unknown, len:236aa, similar eg. to s.) (le:23174:23378:23486:23606) (re:23206:23420:23548:24177) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816079	6545	28701	651	216

Description

GTC ORF with score 106 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c56c10.) (nt:similar to tpr domain of p59 protein (hsp binding) (le:18300:18520:18724) (re:18443:18681:18834) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816091	6546	28702	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816100	6547	28703	504	167

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816107	6548	28704	444	147

Description

6500728419 ipa-87r:ywfi hypothetical protein:hypothetical 29.5 kd protein in rocc-pta intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywfi ywfi Bacillus subtilis 1423 -11532277 7500952918 ywfi:ipa-87r (de:hypothetical 29.5 kd protein in rocc-pta intergenic region) (db:swissprot) YWFI\_BACSU P39645 BACILLUS SUBTILIS 1423 -11532277 7000688679 ywfi ywfi protein:hypothetical protein ipa-87r (db:pir2.dat) S39742 S39742 Bacillus subtilis 1423 -11532277 5000689762 ipa-87r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:90200) (re:90964) (di:complement) BSGENR X73124 g414011 Bacillus subtilis 1423 -11532277 219324 ywfi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-87r; similar to) (le:66995) (re:67759) (di:direct) BSUB0020 Z99123 g2636303 Bacillus subtilis 1423 -11532277 116702 ywfi:ipa-87r (de:hypothetical 29.5 kd protein in rocc-pta intergenic region) (db:swissprot) YWFI\_BACSU P39645 BACILLUS SUBTILIS 1423 -11532277 170165 ywfi conserved hypothetical protein ywfi (db:pir) S39742 S39742 Bacillus subtilis 1423 -11532277

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816116	6549	28705	564	187

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816117	6550	28706	549	182

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816125	6551	28707	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816127	6552	28708	714	237

Description

6500728420 ipa-86r:ywfH hypothetical protein:hypothetical oxidoreductase in rocc-pta intergenic region (gtcfc:14.1) (ec:1.-.-.) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywfH ywfH Bacillus subtilis 1423 -11532278 7500952917 ywfH:ipa-86r (ec:1.-.-.) (de:(ec 1.-.-.)) (db:swissprot) YWFH\_BACSU P39644 BACILLUS SUBTILIS 1423 -11532278 7000688678 ywfH 3-oxoacyl-acyl-carrier protein reductase homolog ywfH (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) S39741 S39741 Bacillus subtilis 1423 -11532278 5000689761 ipa-86r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:89288) (re:90067) (di:complement) BSGENR X73124 g580882 Bacillus subtilis 1423 -11532278 219323 ywfH (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-86r; similar to 3-oxoacyl-) (le:67892) (re:68671) (di:direct) BSUB0020 Z99123 g2636304 Bacillus subtilis 1423 -11532278 116701 ywfH:ipa-86r (ec:1.-.-.) (de:(ec 1.-.-.)) (db:swissprot) YWFH\_BACSU P39644 BACILLUS SUBTILIS 1423 -11532278 170164 ywfH 3-oxoacyl-acyl-carrier protein reductase homolog ywfH (db:pir) S39741 S39741 Bacillus subtilis 1423 -11532278

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816129	6553	28709	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816148	6554	28710	1083	360

Description

6500728421 ipa-84d:ywff hypothetical protein:hypothetical 43.4 kd protein in rocc-pta intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywff ywff Bacillus subtilis 1423 -11532279  
7500952916 ywff:ipa-84d (de:hypothetical 43.4 kd protein in rocc-pta intergenic region) (db:swissprot) YWFF\_BACSU P39642 BACILLUS SUBTILIS 1423 -11532279 7000688677 ywff efflux protein homolog ywff:protein ipa-84d (db:pir2.dat) S39739 S39739 Bacillus subtilis 1423 -11532279 5000689760 ipa-84d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:86889) (re:88073) (di:direct) BSGENR X73124 g414008 Bacillus subtilis 1423 -11532279 219321 ywff (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-84d; similar to efflux) (le:69886) (re:71070) (di:complement) BSUB0020 Z99123 g2636306 Bacillus subtilis 1423 -11532279 116700 ywff:ipa-84d (de:hypothetical 43.4 kd protein in rocc-pta intergenic region) (db:swissprot) YWFF\_BACSU P39642 BACILLUS SUBTILIS 1423 -11532279 170162 ywff efflux protein homolog ywff (db:pir) S39739 S39739 Bacillus subtilis 1423 -11532279

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816167	6555	28711	339	113

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816179	6556	28712	342	113

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816195	6557	28713	408	135

Description

GTC ORF with score 111 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c25a11.) (nt:coded for by c. elegans cdna yk13e11.5; coded for) (le:4444:5497:6022:6206) (re:4638:5565:6135:7125) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816200	6558	28714	804	267

Description

6500728422 ipa-83d:ywfe hypothetical protein:hypothetical 52.3 kd protein in rocc-pta intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywfe ywfe Bacillus subtilis 1423 -11532280  
7500952915 ywfe:ipa-83d (de:hypothetical 52.3 kd protein in rocc-pta intergenic region) (db:swissprot) YWFE\_BACSU P39641 BACILLUS SUBTILIS 1423 -11532280 7000688676 ywfe ywfe protein:hypothetical protein ipa-83d (db:pir2.dat) S39738 S39738 Bacillus subtilis 1423 -11532280 5000689759 ipa-83d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:85474) (re:86892) (di:direct) BSGENR X73124 g414007 Bacillus subtilis 1423 -11532280 219320 ywfe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-83d) (le:71067) (re:72485) (di:complement) BSUB0020 Z99123 g2636307 Bacillus subtilis 1423 -11532280 116699 ywfe:ipa-83d (de:hypothetical 52.3 kd protein in rocc-pta intergenic region) (db:swissprot) YWFE\_BACSU P39641 BACILLUS SUBTILIS 1423 -11532280 170161 ywfe hypothetical protein ywfe (db:pir) S39738 S39738 Bacillus subtilis 1423 -11532280

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816204	6559	28715	1242	413

Description

6500728423 ipa-82d:ywfd hypothetical protein:hypothetical oxidoreductase in rocc-pta intergenic region (gtcfc:14.1) (ec:1.-.-.) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywfd ywfd Bacillus subtilis 1423 -11532281 7500952914 ywfd:ipa-82d (ec:1.-.-.) (de:(ec 1.-.-.)) (db:swissprot) YWFD\_BACSU P39640 BACILLUS SUBTILIS 1423 -11532281 7000688675 ywfd glucose 1-dehydrogenase homolog ywfd:protein ipa-82d (cl:ribitol dehydrogenase:short-chain alcohol dehydrogenase homology) (db:pir2.dat) S39737 S39737 Bacillus subtilis 1423 -11532281 5000689758 ipa-82d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:84688) (re:85455) (di:direct) BSGENR X73124 g414006 Bacillus subtilis 1423 -11532281 219319 ywfd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-82d; similar to glucose) (le:72504) (re:73271) (di:complement) BSUB0020 Z99123 g2636308 Bacillus subtilis 1423 -11532281 116698 ywfd:ipa-82d (ec:1.-.-.) (de:(ec 1.-.-.)) (db:swissprot) YWFD\_BACSU P39640 BACILLUS SUBTILIS 1423 -11532281 170160 ywfd glucose 1-dehydrogenase homolog ywfd (cl:ribitol dehydrogenase:short-chain alcohol dehydrogenase homology) (db:pir) S39737 S39737 Bacillus subtilis 1423 -11532281

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816223	6560	28716	267	88

Description

6500728424 ipa-81d:ywfc hypothetical protein:hypothetical 26.8 kd protein in rocc-pta intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywfc ywfc Bacillus subtilis 1423 -11532282  
7500952913 ywfc:ipa-81d (de:hypothetical 26.8 kd protein in rocc-pta intergenic region) (db:swissprot) YWFC\_BACSU P39639 BACILLUS SUBTILIS 1423 -11532282 7000688674 ywfc ywfc protein:hypothetical protein ipa-81d (db:pir2.dat) S39736 S39736 Bacillus subtilis 1423 -11532282 5000689757 ipa-81d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:83984) (re:84691) (di:direct) BSGENR X73124 g414005 Bacillus subtilis 1423 -11532282 219318 ywfc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-81d) (le:73268) (re:73975) (di:complement) BSUB0020 Z99123 g2636309 Bacillus subtilis 1423 -11532282 116697 ywfc:ipa-81d (de:hypothetical 26.8 kd protein in rocc-pta intergenic region) (db:swissprot) YWFC\_BACSU P39639 BACILLUS SUBTILIS 1423 -11532282 170159 ywfc hypothetical protein ywfc (db:pir) S39736 S39736 Bacillus subtilis 1423 -11532282

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816224	6561	28717	315	104

Description

6500728425 ipa-80d:ywfb hypothetical protein:hypothetical 23.3 kd protein in rocc-pta intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywfb ywfb Bacillus subtilis 1423 -11532283  
7500952912 ywfb:ipa-80d (de:hypothetical 23.3 kd protein in rocc-pta intergenic region) (db:swissprot) YWFB\_BACSU P39638 BACILLUS SUBTILIS 1423 -11532283 7000688673 ywfb ywfb protein:hypothetical protein ipa-80d (db:pir2.dat) S39735 S39735 Bacillus subtilis 1423 -11532283 5000689756 ipa-80d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:83380) (re:83994) (di:direct) BSGENR X73124 g414004 Bacillus subtilis 1423 -11532283 219317 ywfb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-80d) (le:73965) (re:74579) (di:complement) BSUB0020 Z99123 g2636310 Bacillus subtilis 1423 -11532283 116696 ywfb:ipa-80d (de:hypothetical 23.3 kd protein in rocc-pta intergenic region) (db:swissprot) YWFB\_BACSU P39638 BACILLUS SUBTILIS 1423 -11532283 170158 ywfb hypothetical protein ywfb (db:pir) S39735 S39735 Bacillus subtilis 1423 -11532283



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816235	6562	28718	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816249	6563	28719	825	275

Description

6500728426 ipa-79d: ywfa hypothetical protein: hypothetical 44.5 kd protein in rocc-pta intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywfa ywfa Bacillus subtilis 1423 -11532284  
7500952911 ywfa: ipa-79d (de: hypothetical 44.5 kd protein in rocc-pta intergenic region) (db:swissprot) YWFA\_BACSU P39637 BACILLUS SUBTILIS 1423 -11532284 7000688672 ywfa chloramphenicol resistance homolog ywfa: conserved hypothetical protein ipa-79d (cl: chloramphenicol resistance homolog ywfa) (db:pir2.dat) S39734 S39734 Bacillus subtilis 1423 -11532284 5000689755 ipa-79d (db:genpept-bct1) (de: b. subtilis genomic region (325 to 333).) (le:81990) (re:83228) (di:direct) BSGENR X73124 g414003 Bacillus subtilis 1423 -11532284 219316 ywfa (fn:unknown) (db:genpept-bct1) (de: bacillus subtilis complete genome (section 20 of 21): from 3798401 to 4010550.) (nt: alternate gene name: ipa-79d; similar to) (le:74731) (re:75969) (di: complement) BSUB0020 Z99123 g2636311 Bacillus subtilis 1423 -11532284 116695 ywfa: ipa-79d (de: hypothetical 44.5 kd protein in rocc-pta intergenic region) (db:swissprot) YWFA\_BACSU P39637 BACILLUS SUBTILIS 1423 -11532284 170157 ywfa chloramphenicol resistance homolog ywfa: conserved hypothetical protein ipa-79d (db:pir) S39734 S39734 Bacillus subtilis 1423 -11532284

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816290	6564	28720	528	176

#### Description

6500728427 ipa-74d:ywea hypothetical protein:hypothetical 16.7 kd protein in ung-roca intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yweA yweA Bacillus subtilis 1423 -11532285  
7500952909 ywea:ipa-74d (de:hypothetical 16.7 kd protein in ung-roca intergenic region) (db:swissprot) YWEA\_BACSU P39632 BACILLUS SUBTILIS 1423 -11532285 7000688671 ywea ywea protein:hypothetical protein ipa-74d (db:pir2.dat) S39729 S39729 Bacillus subtilis 1423 -11532285 5000689754 ipa-74d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:74907) (re:75371) (di:direct) BSGENR X73124 g413998 Bacillus subtilis 1423 -11532285 219311 ywea (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-74d; similar to) (le:82590) (re:83054) (di:complement) BSUB0020 Z99123 g2636316 Bacillus subtilis 1423 -11532285 116693 ywea:ipa-74d (de:hypothetical 16.7 kd protein in ung-roca intergenic region) (db:swissprot) YWEA\_BACSU P39632 BACILLUS SUBTILIS 1423 -11532285 170153 ywea conserved hypothetical protein ywea (db:pir) S39729 S39729 Bacillus subtilis 1423 -11532285

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816299	6565	28721	879	292

#### Description

6500728428 ipa-62r:ywdl hypothetical protein:hypothetical 20.3 kd protein in ung-roca intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywdL ywdL Bacillus subtilis 1423 -11532286  
7500952908 ywdl:ipa-62r (de:hypothetical 20.3 kd protein in ung-roca intergenic region) (db:swissprot) YWDL\_BACSU P39620 BACILLUS SUBTILIS 1423 -11532286 7000688670 ywdl ywdl protein:hypothetical protein ipa-62r (db:pir2.dat) S39717 S39717 Bacillus subtilis 1423 -11532286 5000689753 ipa-62r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:63583) (re:64128) (di:complement) BSGENR X73124 g413986 Bacillus subtilis 1423 -11532286 219299 ywdl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-62r) (le:93834) (re:94379) (di:direct) BSUB0020 Z99123 g2636327 Bacillus subtilis 1423 -11532286 116692 ywdl:ipa-62r (de:hypothetical 20.3 kd protein in ung-roca intergenic region) (db:swissprot) YWDL\_BACSU P39620 BACILLUS SUBTILIS 1423 -11532286 170141 ywdl hypothetical protein ywdl (db:pir) S39717 S39717 Bacillus subtilis 1423 -11532286

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816304	6566	28722	1656	552

Description

6500728429 ipa-61d:ywdk hypothetical protein:hypothetical 12.0 kd protein in ung-roca intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywdK ywdK Bacillus subtilis 1423 -11532287  
7500952907 ywdk:ipa-61d (de:hypothetical 12.0 kd protein in ung-roca intergenic region) (db:swissprot) YWDK\_BACSU P39619 BACILLUS SUBTILIS 1423 -11532287 7000688669 ywdk ywdk protein:hypothetical protein ipa-61d (db:pir2.dat) S39716 S39716 Bacillus subtilis 1423 -11532287 5000689752 ipa-61d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:63169) (re:63510) (di:direct) BSGENR X73124 g413985 Bacillus subtilis 1423 -11532287 219298 ywdk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-61d; similar to) (le:94452) (re:94793) (di:complement) BSUB0020 Z99123 g2636328 Bacillus subtilis 1423 -11532287 116691 ywdk:ipa-61d (de:hypothetical 12.0 kd protein in ung-roca intergenic region) (db:swissprot) YWDK\_BACSU P39619 BACILLUS SUBTILIS 1423 -11532287 170140 ywdk conserved hypothetical protein ywdk (db:pir) S39716 S39716 Bacillus subtilis 1423 -11532287

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816319	6567	28723	312	103

Description

6500728430 ipa-60d:ywdj hypothetical protein:hypothetical 50.0 kd protein in ung-roca intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywdJ ywdJ Bacillus subtilis 1423 -11532288  
7500952906 ywdj:ipa-60d (de:hypothetical 50.0 kd protein in ung-roca intergenic region) (db:swissprot) YWDJ\_BACSU P39618 BACILLUS SUBTILIS 1423 -11532288 7000688668 ywdj conserved hypothetical protein ywdj (db:pir2.dat) S39715 S39715 Bacillus subtilis 1423 -11532288 5000689751 ipa-60d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:61786) (re:63168) (di:direct) BSGENR X73124 g580876 Bacillus subtilis 1423 -11532288 219297 ywdj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-60d; similar to) (le:94794) (re:96176) (di:complement) BSUB0020 Z99123 g2636329 Bacillus subtilis 1423 -11532288 116690 ywdj:ipa-60d (de:hypothetical 50.0 kd protein in ung-roca intergenic region) (db:swissprot) YWDJ\_BACSU P39618 BACILLUS SUBTILIS 1423 -11532288 170139 ywdj conserved hypothetical protein ywdj (db:pir) S39715 S39715 Bacillus subtilis 1423 -11532288

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816327	6568	28724	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816344	6569	28725	435	144

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816355	6570	28726	225	74

Description

6500728431 ipa-59d:ywdi hypothetical protein:hypothetical 11.8 kd protein in ung-roca intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywdI ywdI Bacillus subtilis 1423 -11532289 7500952905 ywdi:ipa-59d (de:hypothetical 11.8 kd protein in ung-roca intergenic region) (db:swissprot) YWDI\_BACSU P39617 BACILLUS SUBTILIS 1423 -11532289 7000688667 ywdi ywdi protein:hypothetical protein ipa-59d (db:pir2.dat) S39714 S39714 Bacillus subtilis 1423 -11532289 5000689750 ipa-59d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:61449) (re:61766) (di:direct) BSGENR X73124 g413983 Bacillus subtilis 1423 -11532289 219296 ywdi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-59d) (le:96196) (re:96513) (di:complement) BSUB0020 Z99123 g2636330 Bacillus subtilis 1423 -11532289 116689 ywdi:ipa-59d (de:hypothetical 11.8 kd protein in ung-roca intergenic region) (db:swissprot) YWDI\_BACSU P39617 BACILLUS SUBTILIS 1423 -11532289 170138 ywdi hypothetical protein ywdi (db:pir) S39714 S39714 Bacillus subtilis 1423 -11532289

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816361	6571	28727	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816381	6572	28728	399	132

Description

GTC ORF with score 124 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome iii cosmid c285.) (nt:spcc285.08, len:240, (only corresponds to n-term) (le:13748:13795:13893:14367) (re:13750:13834:14296:14642) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816382	6573	28729	855	285

Description

6500728432 ipa-56d:ywdf hypothetical protein:hypothetical 30.6 kd protein in saca-ung intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywdf ywdf Bacillus subtilis 1423 -11532290  
7500952904 ywdf:ipa-56d (de:hypothetical 30.6 kd protein in saca-ung intergenic region) (db:swissprot) YWDF\_BACSU P39614 BACILLUS SUBTILIS 1423 -11532290 7000688666 ywdf ywdf protein:hypothetical protein ipa-56d (db:pir2.dat) S39711 S39711 Bacillus subtilis 1423 -11532290 5000689749 ipa-56d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:58386) (re:59192) (di:direct) BSGENR X73124 g413980 Bacillus subtilis 1423 -11532290 219293 ywdf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-56d; similar to) (le:98770) (re:99576) (di:complement) BSUB0020 Z99123 g2636333 Bacillus subtilis 1423 -11532290 116688 ywdf:ipa-56d (de:hypothetical 30.6 kd protein in saca-ung intergenic region) (db:swissprot) YWDF\_BACSU P39614 BACILLUS SUBTILIS 1423 -11532290 170136 ywdf conserved hypothetical protein ywdf (db:pir) S39711 S39711 Bacillus subtilis 1423 -11532290

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816384	6574	28730	705	234

Description

GTC ORF with score 548 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome iii cosmid c285.) (nt:spcc285.08, len:240, (only corresponds to n-term) (le:13748:13795:13893:14367) (re:13750:13834:14296:14642) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816393	6575	28731	195	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816404	6576	28732	402	133

Description

6500728433 ipa-55d:ywde hypothetical protein:hypothetical 19.9 kd protein in saca-ung intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywde ywde Bacillus subtilis 1423 -11532291 7500952903 ywde:ipa-55d (de:hypothetical 19.9 kd protein in saca-ung intergenic region precursor) (db:swissprot) YWDE\_BACSU P39613 BACILLUS SUBTILIS 1423 -11532291 7000688665 ywde hypothetical protein ywde (db:pir2.dat) S39710 S39710 Bacillus subtilis 1423 -11532291 5000689748 ipa-55d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:57762) (re:58295) (di:direct) BSGENR X73124 g580874 Bacillus subtilis 1423 -11532291 219292 ywde (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-55d) (le:99667) (re:100200) (di:complement) BSUB0020 Z99123 g2636334 Bacillus subtilis 1423 -11532291 116687 ywde:ipa-55d (de:hypothetical 19.9 kd protein in saca-ung intergenic region precursor) (db:swissprot) YWDE\_BACSU P39613 BACILLUS SUBTILIS 1423 -11532291 170135 ywde hypothetical protein ywde (db:pir) S39710 S39710 Bacillus subtilis 1423 -11532291

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816414	6577	28733	222	73

Description

6500728434 ipa-54d:ywdd hypothetical protein:hypothetical 18.4 kd protein in saca-ung intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywdd ywdd Bacillus subtilis 1423 -11532292 7500952902 ywdd:ipa-54d (de:hypothetical 18.4 kd protein in saca-ung intergenic region) (db:swissprot) YWDD\_BACSU P39612 BACILLUS SUBTILIS 1423 -11532292 7000688664 ywdd ywdd protein:hypothetical protein ipa-54d (db:pir2.dat) S39709 S39709 Bacillus subtilis 1423 -11532292 5000689747 ipa-54d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:57223) (re:57714) (di:direct) BSGENR X73124 g413978 Bacillus subtilis 1423 -11532292 219291 ywdd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-54d) (le:100248) (re:100739) (di:complement) BSUB0020 Z99123 g2636335 Bacillus subtilis 1423 -11532292 116686 ywdd:ipa-54d (de:hypothetical 18.4 kd protein in saca-ung intergenic region) (db:swissprot) YWDD\_BACSU P39612 BACILLUS SUBTILIS 1423 -11532292 170134 ywdd hypothetical protein ywdd (db:pir) S39709 S39709 Bacillus subtilis 1423 -11532292

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816422	6578	28734	531	176

Description

GTC ORF with score 415 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1110.) (nt:unnamed protein product) (le:<1) (re:1106) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816427	6579	28735	531	176

Description

GTC ORF with score 163 to: (fn:morphogenesis in fission yeast) (sr:fission yeast) (db:genpept-pln2) (de:schizosaccharomyces pombe putative alpha-glucan synthase (ags1)mrna, partial cds.) (nt:agslp) (le:<1) (re:1008) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816435	6580	28736	594	198

Description

6500728435 ipa-53r:ywdc hypothetical protein:hypothetical 16.8 kd protein in saca-ung intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywdC ywdC Bacillus subtilis 1423 -11532293  
7500952901 ywdc:ipa-53r (de:hypothetical 16.8 kd protein in saca-ung intergenic region) (db:swissprot) YWDC\_BACSU P39611 BACILLUS SUBTILIS 1423 -11532293 7000688663 ywdc ywdc protein:hypothetical protein ipa-53r (db:pir2.dat) S39708 S39708 Bacillus subtilis 1423 -11532293 5000689746 ipa-53r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:56752) (re:57180) (di:complement) BSGENR X73124 g413977 Bacillus subtilis 1423 -11532293 219290 ywdc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-53r) (le:100782) (re:101210) (di:direct) BSUB0020 Z99123 g2636336 Bacillus subtilis 1423 -11532293  
116685 ywdc:ipa-53r (de:hypothetical 16.8 kd protein in saca-ung intergenic region) (db:swissprot) YWDC\_BACSU P39611 BACILLUS SUBTILIS 1423 -11532293  
170133 ywdc hypothetical protein ywdc (db:pir) S39708 S39708 Bacillus subtilis 1423 -11532293

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816452	6581	28737	1368	456

Description

GTC ORF with score 864 to: (sr:n.crassa (strain 74a) dna, clones psv50-5:4g) (db:genpept-pln1) (de:n.crassa tryptophan synthetase (trp3) alpha-2 subunit gene,complete cds.) (nt:tryptophan synthetase) (le:483:608:838) (re:530:766:2757) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816455	6582	28738	1581	527

#### Description

6500728436 ipa-51d:ywda hypothetical protein:hypothetical 9.6 kd protein in saca-ung intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywda ywda Bacillus subtilis 1423 -11532294  
7500952900 ywda:ipa-51d (de:hypothetical 9.6 kd protein in saca-ung intergenic region) (db:swissprot) YWDA\_BACSU P39609 BACILLUS SUBTILIS 1423 -11532294 7000688662 ywda hypothetical protein ywda (db:pir2.dat) S39706 S39706 Bacillus subtilis 1423 -11532294 5000689744 ipa-51d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:55450) (re:55698) (di:direct) BSGENR X73124 g580873 Bacillus subtilis 1423 -11532294 219288 ywda (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-51d) (le:102264) (re:102512) (di:complement) BSUB0020 Z99123 g2636338 Bacillus subtilis 1423 -11532294 116683 ywda:ipa-51d (de:hypothetical 9.6 kd protein in saca-ung intergenic region) (db:swissprot) YWDA\_BACSU P39609 BACILLUS SUBTILIS 1423 -11532294 170131 ywda hypothetical protein ywda (db:pir) S39706 S39706 Bacillus subtilis 1423 -11532294

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816456	6583	28739	279	92

#### Description

6500728437 ipa-48r:ycwj hypothetical protein:hypothetical 28.4 kd protein in sact-sacp intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywcJ ywcJ Bacillus subtilis 1423 -11532295  
7500952899 ywcj:ipa-48r (de:hypothetical 28.4 kd protein in sact-sacp intergenic region) (db:swissprot) YWCJ\_BACSU P39608 BACILLUS SUBTILIS 1423 -11532295 7000688661 ywcj nitrite transport protein homolog ywcj:protein ipa-48r (cl:formate dehydrogenase focb) (db:pir2.dat) S39703 S39703 Bacillus subtilis 1423 -11532295 5000688777 ipa-48r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:51463) (re:52233) (di:complement) BSGENR X73124 g413972 Bacillus subtilis 1423 -11532295 219285 ywcj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-48r; similar to nitrite) (le:105729) (re:106499) (di:direct) BSUB0020 Z99123 g2636341 Bacillus subtilis 1423 -11532295 116682 ywcj:ipa-48r (de:hypothetical 28.4 kd protein in sact-sacp intergenic region) (db:swissprot) YWCJ\_BACSU P39608 BACILLUS SUBTILIS 1423 -11532295 170130 ywcj nitrite transporter homolog ywcj (db:pir) S39703 S39703 Bacillus subtilis 1423 -11532295



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816478	6584	28740	1710	569

#### Description

6500728438 ipa-46d:ywci hypothetical protein:hypothetical 11.8 kd protein in vpr-sact intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywci ywci Bacillus subtilis 1423 -11532296  
7500952898 ywci:ipa-46d (de:hypothetical 11.8 kd protein in vpr-sact intergenic region) (db:swissprot) YWCI\_BACSU P39607 BACILLUS SUBTILIS 1423 -11532296 7000688660 ywci ywci protein:hypothetical protein ipa-46d (db:pir2.dat) S39701 S39701 Bacillus subtilis 1423 -11532296 5000689743 ipa-46d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:50252) (re:50554) (di:direct) BSGENR X73124 g413970 Bacillus subtilis 1423 -11532296 219283 ywci (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-46d) (le:107408) (re:107710) (di:complement) BSUB0020 Z99123 g2636343 Bacillus subtilis 1423 -11532296 116681 ywci:ipa-46d (de:hypothetical 11.8 kd protein in vpr-sact intergenic region) (db:swissprot) YWCI\_BACSU P39607 BACILLUS SUBTILIS 1423 -11532296 170129 ywci hypothetical protein ywci (db:pir) S39701 S39701 Bacillus subtilis 1423 -11532296

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816480	6585	28741	435	144

#### Description

6500728439 ipa-44d:ywch hypothetical protein:hypothetical 36.6 kd protein in qoxd-vpr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywch ywch Bacillus subtilis 1423 -11532297  
7500952897 ywch:ipa-44d (de:hypothetical 36.6 kd protein in qoxd-vpr intergenic region) (db:swissprot) YWCH\_BACSU P39606 BACILLUS SUBTILIS 1423 -11532297 7000688659 ywch monooxygenase homolog ywch:protein ipa-44d (cl:ynbw protein) (db:pir2.dat) S39699 S39699 Bacillus subtilis 1423 -11532297 5000689742 ipa-44d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:46263) (re:47264) (di:direct) BSGENR X73124 g413968 Bacillus subtilis 1423 -11532297 219281 ywch (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-44d; similar to) (le:110698) (re:111699) (di:complement) BSUB0020 Z99123 g2636345 Bacillus subtilis 1423 -11532297 116680 ywch:ipa-44d (de:hypothetical 36.6 kd protein in qoxd-vpr intergenic region) (db:swissprot) YWCH\_BACSU P39606 BACILLUS SUBTILIS 1423 -11532297 170128 ywch monooxygenase homolog ywch (cl:ynbw protein) (db:pir) S39699 S39699 Bacillus subtilis 1423 -11532297

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816484	6586	28742	372	123

Description

6500728440 ipa-43d:ycg hypothetical protein:hypothetical 28.3 kd protein in qoxd-vpr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywcG ywcG Bacillus subtilis 1423 -11532298  
7500952896 ywcg:ipa-43d (de:hypothetical 28.3 kd protein in qoxd-vpr intergenic region) (db:swissprot) YWCG\_BACSU P39605 BACILLUS SUBTILIS 1423 -11532298 7000688658 ywcg nadph-flavin oxidoreductase homolog ywcg:protein ipa-43d (cl:nadph-flavin oxidoreductase homolog) (db:pir2.dat) S39698 S39698 Bacillus subtilis 1423 -11532298 5000689741 ipa-43d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:45340) (re:46089) (di:direct) BSGENR X73124 g413967 Bacillus subtilis 1423 -11532298 219280 ywcg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-43d; similar to) (le:111873) (re:112622) (di:complement) BSUB0020 Z99123 g2636346 Bacillus subtilis 1423 -11532298 116679 ywcg:ipa-43d (de:hypothetical 28.3 kd protein in qoxd-vpr intergenic region) (db:swissprot) YWCG\_BACSU P39605 BACILLUS SUBTILIS 1423 -11532298 170127 ywcg nadph-flavin oxidoreductase homolog ywcg (db:pir) S39698 S39698 Bacillus subtilis 1423 -11532298

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816487	6587	28743	1488	495

Description

6500728441 ipa-41r:ywce hypothetical protein:hypothetical 10.0 kd protein in qoxd-vpr intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywCE ywCE Bacillus subtilis 1423 -11532299 7500952894 ywce:ipa-41r (de:hypothetical 10.0 kd protein in qoxd-vpr intergenic region precursor) (db:swissprot) YWCE\_BACSU P39603 BACILLUS SUBTILIS 1423 -11532299 7000688656 ywce ywce protein:hypothetical protein ipa-41r (db:pir2.dat) S39696 S39696 Bacillus subtilis 1423 -11532299 5000689740 ipa-41r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:43294) (re:43557) (di:complement) BSGENR X73124 g413965 Bacillus subtilis 1423 -11532299 219278 ywce (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-41r) (le:114405) (re:114668) (di:direct) BSUB0020 Z99123 g2636348 Bacillus subtilis 1423 -11532299 116677 ywce:ipa-41r (de:hypothetical 10.0 kd protein in qoxd-vpr intergenic region precursor) (db:swissprot) YWCE\_BACSU P39603 BACILLUS SUBTILIS 1423 -11532299 170125 ywce hypothetical protein ywce (db:pir) S39696 S39696 Bacillus subtilis 1423 -11532299

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816495	6588	28744	1668	556

Description

GTC ORF with score 1468 to: (sr:baker's yeast) (db:genpept-pln1)  
(de:saccharomyces cerevisiae cobalamin-independent methionine synthase(met6)  
gene, complete cds.) (nt:5-methyltetrahydrofolate homocysteine) (le:522)  
(re:2825) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816502	6589	28745	531	176

Description

6500728442 hypothetical protein:similar to hypothetical proteins from  
b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus  
subtilis) ywzA ywzA Bacillus subtilis 1423 -11532300 7000692870 ywza  
conserved hypothetical protein ywza (db:pir2.dat) F70070 F70070 Bacillus  
subtilis 1423 -11532300 7500963907 ywza (fn:unknown) (db:genpept-bct1)  
(de:bacillus subtilis complete genome (section 20 of 21): from 3798401to  
4010550.) (nt:similar to hypothetical proteins from b. subtilis) (le:119268)  
(re:119417) (di:direct) BSUB0020 Z99123 g2636353 Bacillus subtilis 1423  
-11532300

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816504	6590	28746	255	84

Description

6500728443 ipa-34d:ywcd hypothetical protein:hypothetical 14.3 kd protein in  
epr-galk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) ywcd ywcd Bacillus subtilis 1423 -11532301  
7500952893 ywcd:ipa-34d (de:hypothetical 14.3 kd protein in epr-galk  
intergenic region) (db:swissprot) YWCD\_BACSU P39602 BACILLUS SUBTILIS 1423  
-11532301 7000688655 ywcd ywcd protein:hypothetical protein ipa-34d  
(db:pir2.dat) S39689 S39689 Bacillus subtilis 1423 -11532301 5000689739  
ipa-34d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).)  
(le:35289) (re:35672) (di:direct) BSGENR X73124 g413958 Bacillus subtilis  
1423 -11532301 219271 ywcd (fn:unknown) (db:genpept-bct1) (de:bacillus  
subtilis complete genome (section 20 of 21): from 3798401to 4010550.)  
(nt:alternate gene name: ipa-34d) (le:122287) (re:122670) (di:complement)  
BSUB0020 Z99123 g2636356 Bacillus subtilis 1423 -11532301 116676  
ywcd:ipa-34d (de:hypothetical 14.3 kd protein in epr-galk intergenic region)  
(db:swissprot) YWCD\_BACSU P39602 BACILLUS SUBTILIS 1423 -11532301 170123  
ywcd hypothetical protein ywcd (db:pir) S39689 S39689 Bacillus subtilis 1423  
-11532301

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816510	6591	28747	354	117

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816514	6592	28748	441	146

Description

GTC ORF with score 369 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone\_lib:mizukam) (db:genpept-pln2) (de:schizosaccharomyces pombe 42.8 kb genomic dna, clone c973.) (nt:similar to s.cerevisiae hypothetical protein) (le:32916) (re:35417) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816518	6593	28749	573	190

Description

6500728444 ipa-33d:ywcc hypothetical protein:hypothetical 26.1 kd protein in epr-galk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywcc ywcc Bacillus subtilis 1423 -11532302 7500952892 ywcc:ipa-33d (de:hypothetical 26.1 kd protein in epr-galk intergenic region) (db:swissprot) YWCC\_BACSU P39601 BACILLUS SUBTILIS 1423 -11532302 7000688654 ywcc ywcc protein:hypothetical protein ipa-33d (db:pir2.dat) S39688 S39688 Bacillus subtilis 1423 -11532302 5000689738 ipa-33d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:34600) (re:35271) (di:direct) BSGENR X73124 g413957 Bacillus subtilis 1423 -11532302 219270 ywcc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-33d) (le:122688) (re:123359) (di:complement) BSUB0020 Z99123 g2636357 Bacillus subtilis 1423 -11532302 116675 ywcc:ipa-33d (de:hypothetical 26.1 kd protein in epr-galk intergenic region) (db:swissprot) YWCC\_BACSU P39601 BACILLUS SUBTILIS 1423 -11532302 170122 ywcc hypothetical protein ywcc (db:pir) S39688 S39688 Bacillus subtilis 1423 -11532302

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816530	6594	28750	570	189

#### Description

6500728445 ipa-32r:ywcb hypothetical protein:hypothetical 11.7 kd protein in epr-galk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywcb ywcb Bacillus subtilis 1423 -11532303 7500952891 ywcb:ipa-32r (de:hypothetical 11.7 kd protein in epr-galk intergenic region) (db:swissprot) YWCB\_BACSU P39600 BACILLUS SUBTILIS 1423 -11532303 7000688653 ywcb ywcb protein:hypothetical protein ipa-32r (db:pir2.dat) S39687 S39687 Bacillus subtilis 1423 -11532303 5000689737 ipa-32r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:33335) (re:33643) (di:complement) BSGENR X73124 g413956 Bacillus subtilis 1423 -11532303 219269 ywcb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-32r) (le:124316) (re:124624) (di:direct) BSUB0020 Z99123 g2636358 Bacillus subtilis 1423 -11532303 116674 ywcb:ipa-32r (de:hypothetical 11.7 kd protein in epr-galk intergenic region) (db:swissprot) YWCB\_BACSU P39600 BACILLUS SUBTILIS 1423 -11532303 170121 ywcb hypothetical protein ywcb (db:pir) S39687 S39687 Bacillus subtilis 1423 -11532303

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816532	6595	28751	462	153

#### Description

6500728446 ipa-31r:ywca hypothetical protein:hypothetical 55.0 kd protein in epr-galk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywca ywca Bacillus subtilis 1423 -11532304 219268 ywca:ipa-31r (de:hypothetical 55.0 kd protein in epr-galk intergenic region) (db:swissprot) YWCA\_BACSU P39599 BACILLUS SUBTILIS 1423 -11532304 7000688652 ywca na+-dependent symport homolog ywca:conserved hypothetical protein ipa-31r (cl:proline carrier protein) (db:pir2.dat) S39686 S39686 Bacillus subtilis 1423 -11532304 5000689736 ipa-31r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:31798) (re:33348) (di:complement) BSGENR X73124 g580869 Bacillus subtilis 1423 -11532304 7500952890 ywca (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-31r; similar to) (le:124611) (re:126161) (di:direct) BSUB0020 Z99123 g2636359 Bacillus subtilis 1423 -11532304 116673 ywca:ipa-31r (de:hypothetical 55.0 kd protein in epr-galk intergenic region) (db:swissprot) YWCA\_BACSU P39599 BACILLUS SUBTILIS 1423 -11532304

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816541	6596	28752	378	125

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816547	6597	28753	498	165

Description

6500728447 ipa-30d:ywbo hypothetical protein:hypothetical 22.6 kd protein in epr-galk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywbO ywbO Bacillus subtilis 1423 -11532305 7500952889 ywbo:ipa-30d (de:hypothetical 22.6 kd protein in epr-galk intergenic region) (db:swissprot) YWBO\_BACSU P39598 BACILLUS SUBTILIS 1423 -11532305 7000688651 ywbo ywbo protein:hypothetical protein ipa-30d (db:pir2.dat) S39685 S39685 Bacillus subtilis 1423 -11532305 5000689735 ipa-30d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:31165) (re:31767) (di:direct) BSGENR X73124 g413954 Bacillus subtilis 1423 -11532305 219267 ywbo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-30d) (le:126192) (re:126794) (di:complement) BSUB0020 Z99123 g2636360 Bacillus subtilis 1423 -11532305 116672 ywbo:ipa-30d (de:hypothetical 22.6 kd protein in epr-galk intergenic region) (db:swissprot) YWBO\_BACSU P39598 BACILLUS SUBTILIS 1423 -11532305 170119 ywbo hypothetical protein ywbo (db:pir) S39685 S39685 Bacillus subtilis 1423 -11532305

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816553	6598	28754	864	287

Description

6500728448 ipa-29d:ywbn hypothetical protein:hypothetical 45.7 kd protein in epr-galk intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywbN ywbN Bacillus subtilis 1423 -11532306 7500952888 ywbn:ipa-29d (de:hypothetical 45.7 kd protein in epr-galk intergenic region precursor) (db:swissprot) YWBN\_BACSU P39597 BACILLUS SUBTILIS 1423 -11532306 7000688650 ywbn ywbn protein:hypothetical protein ipa-29d (cl:hypothetical protein ycdb) (db:pir2.dat) S39684 S39684 Bacillus subtilis 1423 -11532306 5000689734 ipa-29d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:29631) (re:30881) (di:direct) BSGENR X73124 g413953 Bacillus subtilis 1423 -11532306 219266 ywbn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-29d; similar to) (le:127078) (re:128328) (di:complement) BSUB0020 Z99123 g2636361 Bacillus subtilis 1423 -11532306 116671 ywbn:ipa-29d (de:hypothetical 45.7 kd protein in epr-galk intergenic region precursor) (db:swissprot) YWBN\_BACSU P39597 BACILLUS SUBTILIS 1423 -11532306 170118 ywbn conserved hypothetical protein ywbn (db:pir) S39684 S39684 Bacillus subtilis 1423 -11532306

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816561	6599	28755	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816576	6600	28756	243	80

Description

6500728449 ipa-28d:ywbm hypothetical protein:hypothetical 42.8 kd protein in epr-galk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywbm ywbm Bacillus subtilis 1423 -11532307  
7500952887 ywbm:ipa-28d (de:hypothetical 42.8 kd protein in epr-galk intergenic region) (db:swissprot) YWBM\_BACSU P39596 BACILLUS SUBTILIS 1423 -11532307 7000688649 ywbm ywbm protein:hypothetical protein ipa-28d (db:pir2.dat) S39683 S39683 Bacillus subtilis 1423 -11532307 5000689733 ipa-28d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:28455) (re:29612) (di:direct) BSGENR X73124 g413952 Bacillus subtilis 1423 -11532307 219265 ywbm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-28d; similar to) (le:128347) (re:129504) (di:complement) BSUB0020 Z99123 g2636362 Bacillus subtilis 1423 -11532307 116670 ywbm:ipa-28d (de:hypothetical 42.8 kd protein in epr-galk intergenic region) (db:swissprot) YWBM\_BACSU P39596 BACILLUS SUBTILIS 1423 -11532307 170117 ywbm conserved hypothetical protein ywbm (db:pir) S39683 S39683 Bacillus subtilis 1423 -11532307

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816578	6601	28757	1512	503

Description

6500728450 ipa-27d:ywbl hypothetical protein:hypothetical 52.4 kd protein in epr-galk intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywbL ywbL Bacillus subtilis 1423 -11532308 7500952886 ywbl:ipa-27d (de:hypothetical 52.4 kd protein in epr-galk intergenic region precursor) (db:swissprot) YWBL\_BACSU P39595 BACILLUS SUBTILIS 1423 -11532308 7000688648 ywbl ywbl protein:hypothetical protein ipa-27d (cl:conserved hypothetical protein ywbl) (db:pir2.dat) S39682 S39682 Bacillus subtilis 1423 -11532308 5000689732 ipa-27d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:27013) (re:28458) (di:direct) BSGENR X73124 g413951 Bacillus subtilis 1423 -11532308 219264 ywbl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-27d; similar to) (le:129501) (re:130946) (di:complement) BSUB0020 Z99123 g2636363 Bacillus subtilis 1423 -11532308 116669 ywbl:ipa-27d (de:hypothetical 52.4 kd protein in epr-galk intergenic region precursor) (db:swissprot) YWBL\_BACSU P39595 BACILLUS SUBTILIS 1423 -11532308 170116 ywbl conserved hypothetical protein ywbl (db:pir) S39682 S39682 Bacillus subtilis 1423 -11532308

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816582	6602	28758	531	176

Description

6500728451 ipa-24d:ywbi hypothetical protein:hypothetical transcriptional regulator in epr-galk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywbI ywbI Bacillus subtilis 1423 -11532309 7500952885 ywbi:ipa-24d (de:hypothetical transcriptional regulator in thik-epr intergenic region) (db:swissprot) YWBI\_BACSU P39592 BACILLUS SUBTILIS 1423 -11532309 7000688647 ywbi transcription regulator homolog ywbi:protein ipa-24d (cl:probable transcription regulator lysr) (db:pir2.dat) S39679 S39679 Bacillus subtilis 1423 -11532309 5000688928 ipa-24d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:24460) (re:25365) (di:direct) BSGENR X73124 g413948 Bacillus subtilis 1423 -11532309 219261 ywbi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-24d; similar to) (le:132594) (re:133499) (di:complement) BSUB0020 Z99123 g2636366 Bacillus subtilis 1423 -11532309 116666 ywbi:ipa-24d (de:hypothetical transcriptional regulator in thik-epr intergenic region) (db:swissprot) YWBI\_BACSU P39592 BACILLUS SUBTILIS 1423 -11532309 170113 ywbi transcriptional regulator lysr family homolog ywbi (db:pir) S39679 S39679 Bacillus subtilis 1423 -11532309



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816597	6603	28759	768	255

Description

6500728452 ipa-23r:ywbh hypothetical protein:hypothetical 14.3 kd protein in epr-galk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywbH ywbH Bacillus subtilis 1423 -11532310  
7500952884 ywbh:ipa-23r (de:hypothetical 14.3 kd protein in epr-galk intergenic region) (db:swissprot) YWBH BACSU P39591 BACILLUS SUBTILIS 1423 -11532310 7000688646 ywbh ywbh protein:hypothetical protein ipa-23r (cl:conserved hypothetical protein hil297) (db:pir2.dat) S39678 S39678 Bacillus subtilis 1423 -11532310 5000689729 ipa-23r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:23968) (re:24354) (di:complement) BSGENR X73124 g413947 Bacillus subtilis 1423 -11532310 219260 ywbh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-23r) (le:133605) (re:133991) (di:direct) BSUB0020 Z99123 g2636367 Bacillus subtilis 1423 -11532310 116665 ywbh:ipa-23r (de:hypothetical 14.3 kd protein in epr-galk intergenic region) (db:swissprot) YWBH\_BACSU P39591 BACILLUS SUBTILIS 1423 -11532310 170112 ywbh hypothetical protein ywbh (db:pir) S39678 S39678 Bacillus subtilis 1423 -11532310

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816603	6604	28760	222	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816611	6605	28761	1149	382

Description

6500728453 ipa-22r:ywbG hypothetical protein:hypothetical 25.8 kd protein in epr-galk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywbG ywbG Bacillus subtilis 1423 -11532311  
7500952883 ywbG:ipa-22r (de:hypothetical 25.8 kd protein in epr-galk intergenic region) (db:swissprot) YWBG\_BACSU P39590 BACILLUS SUBTILIS 1423 -11532311 7000688645 ywbG conserved hypothetical protein ywbG (cl:yohk protein) (db:pir2.dat) S39677 S39677 Bacillus subtilis 1423 -11532311  
5000689728 ipa-22r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:23261) (re:23986) (di:complement) BSGENR X73124 g580868 Bacillus subtilis 1423 -11532311 219259 ywbG (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-22r; similar to) (le:133973) (re:134698) (di:direct) BSUB0020 Z99123 g2636368 Bacillus subtilis 1423 -11532311 116664 ywbG:ipa-22r (de:hypothetical 25.8 kd protein in epr-galk intergenic region) (db:swissprot) YWBG\_BACSU P39590 BACILLUS SUBTILIS 1423 -11532311 170111 ywbG conserved hypothetical protein ywbG (cl:yohk protein) (db:pir) S39677 S39677 Bacillus subtilis 1423 -11532311

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816619	6606	28762	612	203

Description

6500728454 ipa-21r:ywbF hypothetical protein:hypothetical 44.0 kd protein in epr-galk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywbF ywbF Bacillus subtilis 1423 -11532312  
7500952882 ywbF:ipa-21r (de:hypothetical 44.0 kd protein in epr-galk intergenic region) (db:swissprot) YWBF\_BACSU P39589 BACILLUS SUBTILIS 1423 -11532312 7000688644 ywbF sugar permease homolog ywbF:protein ipa-21r (cl:maltose permease) (db:pir2.dat) S39676 S39676 Bacillus subtilis 1423 -11532312 5000689727 ipa-21r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:22007) (re:23206) (di:complement) BSGENR X73124 g413945 Bacillus subtilis 1423 -11532312 219258 ywbF (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-21r; similar to sugar) (le:134753) (re:135952) (di:direct) BSUB0020 Z99123 g2636369 Bacillus subtilis 1423 -11532312 116663 ywbF:ipa-21r (de:hypothetical 44.0 kd protein in epr-galk intergenic region) (db:swissprot) YWBF\_BACSU P39589 BACILLUS SUBTILIS 1423 -11532312 170110 ywbF sugar permease homolog ywbF (db:pir) S39676 S39676 Bacillus subtilis 1423 -11532312

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816629	6607	28763	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816641	6608	28764	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816644	6609	28765	183	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816656	6610	28766	264	87

Description

6500728455 ipa-20r:ywbe hypothetical protein:hypothetical 7.3 kd protein in epr-galk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywbe ywbe Bacillus subtilis 1423 -11532313 7500952881 ywbe:ipa-20r (de:hypothetical 7.3 kd protein in epr-galk intergenic region) (db:swissprot) YWBE\_BACSU P39588 BACILLUS SUBTILIS 1423 -11532313 7000688643 ywbe ywbe protein:hypothetical protein ipa-20r (db:pir2.dat) S39675 S39675 Bacillus subtilis 1423 -11532313 5000689726 ipa-20r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:21776) (re:21973) (di:complement) BSGENR X73124 g413944 Bacillus subtilis 1423 -11532313 219257 ywbe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-20r) (le:135986) (re:136183) (di:direct) BSUB0020 Z99123 g2636370 Bacillus subtilis 1423 -11532313 116662 ywbe:ipa-20r (de:hypothetical 7.3 kd protein in epr-galk intergenic region) (db:swissprot) YWBE\_BACSU P39588 BACILLUS SUBTILIS 1423 -11532313 170109 ywbe hypothetical protein ywbe (db:pir) S39675 S39675 Bacillus subtilis 1423 -11532313

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816663	6611	28767	189	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816667	6612	28768	414	137

Description

GTC ORF with score 114 to: (or:Arabidopsis thaliana) (sr:thale cress)  
(db:genpept-pln2) (de:arabidopsis thaliana plant adhesion molecule 1 (pam1)  
mrna,complete cds.) (nt:similar to drosophila extracellular matrix adhesion)  
(le:190) (re:1260) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816690	6613	28769	744	247

Description

6500728456 ipa-19d:ywbd hypothetical protein:hypothetical 44.4 kd protein in  
epr-galk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) ywbD ywbD Bacillus subtilis 1423 -11532314  
7500952880 ywbd:ipa-19d (de:hypothetical 44.4 kd protein in epr-galk  
intergenic region) (db:swissprot) YWBD\_BACSU P39587 BACILLUS SUBTILIS 1423  
-11532314 7000688642 ywbd ywbd protein:hypothetical protein ipa-19d  
(db:pir2.dat) S39674 S39674 Bacillus subtilis 1423 -11532314 5000689725  
ipa-19d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).)  
(le:20551) (re:21741) (di:direct) BSGENR X73124 g413943 Bacillus subtilis  
1423 -11532314 219256 ywbd (fn:unknown) (db:genpept-bct1) (de:bacillus  
subtilis complete genome (section 20 of 21): from 3798401to 4010550.)  
(nt:alternate gene name: ipa-19d; similar to) (le:136218) (re:137408)  
(di:complement) BSUB0020 Z99123 g2636371 Bacillus subtilis 1423 -11532314  
116661 ywbd:ipa-19d (de:hypothetical 44.4 kd protein in epr-galk intergenic  
region) (db:swissprot) YWBD\_BACSU P39587 BACILLUS SUBTILIS 1423 -11532314  
170108 ywbd conserved hypothetical protein ywbd (db:pir) S39674 S39674  
Bacillus subtilis 1423 -11532314

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816706	6614	28770	315	104

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816707	6615	28771	1311	436

Description

6500728457 ipa-18r:ywbc hypothetical protein:hypothetical 14.4 kd protein in epr-galk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywbC ywbC Bacillus subtilis 1423 -11532315  
7500952879 ywbc:ipa-18r (de:hypothetical 14.4 kd protein in epr-galk intergenic region) (db:swissprot) YWBC\_BACSU P39586 BACILLUS SUBTILIS 1423 -11532315 7000688641 ywbc ywbc protein:protein ipa-18r (db:pir2.dat) S39673 S39673 Bacillus subtilis 1423 -11532315 5000689724 ipa-18r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:20050) (re:20430) (di:complement) BSGENR X73124 g413942 Bacillus subtilis 1423 -11532315 219255 ywbc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-18r; similar to) (le:137529) (re:137909) (di:direct) BSUB0020 Z99123 g2636372 Bacillus subtilis 1423 -11532315 116660 ywbc:ipa-18r (de:hypothetical 14.4 kd protein in epr-galk intergenic region) (db:swissprot) YWBC\_BACSU P39586 BACILLUS SUBTILIS 1423 -11532315 170107 ywbc conserved hypothetical protein ywbc (db:pir) S39673 S39673 Bacillus subtilis 1423 -11532315

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816711	6616	28772	216	71

Description

GTC ORF with score 141 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac f4i1 genomic sequence,complete sequence.) (nt:hypothetical protein) (le:23483:23745:23937) (re:23650:23856:24003) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816723	6617	28773	1191	396

Description

6500728458 ipa-17d:ywbb hypothetical protein:hypothetical 25.9 kd protein in epr-galk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywbB ywbB Bacillus subtilis 1423 -11532316 7500952878 ywbb:ipa-17d (de:hypothetical 25.9 kd protein in epr-galk intergenic region) (db:swissprot) YWBB\_BACSU P39585 BACILLUS SUBTILIS 1423 -11532316 7000688640 ywbb ywbb protein:hypothetical protein ipa-17d (db:pir2.dat) S39672 S39672 Bacillus subtilis 1423 -11532316 5000689723 ipa-17d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:19335) (re:20012) (di:direct) BSGENR X73124 g413941 Bacillus subtilis 1423 -11532316 219254 ywbb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-17d) (le:137947) (re:138624) (di:complement) BSUB0020 Z99123 g2636373 Bacillus subtilis 1423 -11532316 116659 ywbb:ipa-17d (de:hypothetical 25.9 kd protein in epr-galk intergenic region) (db:swissprot) YWBB\_BACSU P39585 BACILLUS SUBTILIS 1423 -11532316 170106 ywbb hypothetical protein ywbb (db:pir) S39672 S39672 Bacillus subtilis 1423 -11532316

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816745	6618	28774	1275	424

Description

GTC ORF with score 336 to: (fn:oxygenation of trichodiene to yield unknown) (db:genpept-pln1) (de:fusarium sporotrichioides trichodiene oxygenase (tri4) gene,complete cds.) (nt:cytochrome p450; cyp58; tri6 (u22150), tri3) (le:383:685:1702:1939) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816751	6619	28775	471	157

#### Description

6500728459 ipa-16d:ywba hypothetical protein:hypothetical 47.6 kd protein in epr-galk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywba ywba Bacillus subtilis 1423 -11532317  
7500952877 ywba:ipa-16d (de:hypothetical 47.6 kd protein in epr-galk intergenic region) (db:swissprot) YWBA\_BACSU P39584 BACILLUS SUBTILIS 1423 -11532317 7000688639 ywba phosphotransferase system enzyme ii homolog ywba:protein ipa-16d (cl:phosphotransferase system enzyme ii factor ii, phosphoenolpyruvate-dependent) (db:pir2.dat) S39671 S39671 Bacillus subtilis 1423 -11532317 5000689722 ipa-16d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:17924) (re:19258) (di:direct) BSGENR X73124 g413940 Bacillus subtilis 1423 -11532317 219253 ywba (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-16d; similar to) (le:138701) (re:140035) (di:complement) BSUB0020 Z99123 g2636374 Bacillus subtilis 1423 -11532317 116658 ywba:ipa-16d (de:hypothetical 47.6 kd protein in epr-galk intergenic region) (db:swissprot) YWBA\_BACSU P39584 BACILLUS SUBTILIS 1423 -11532317 170105 ywba phosphotransferase system enzyme ii homolog ywba (db:pir) S39671 S39671 Bacillus subtilis 1423 -11532317

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816755	6620	28776	195	64

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816761	6621	28777	1263	420

Description

6500728460 ipa-11d: ywaf hypothetical protein: hypothetical 27.3 kd protein in tyrz-sacy intergenic region: orf1 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywaf ywaf Bacillus subtilis 1423 -11532318  
 219248 ywaf: ipa-11d (de: hypothetical 27.3 kd protein in tyrz-sacy intergenic region (orf1)) (db: swissprot) YWAF\_BACSU P25149 BACILLUS SUBTILIS 1423 -11532318 7000688638 ywaf hypothetical protein ywaf: hypothetical protein 1: sacs-region (db: pir2.dat) S16424 S16424 Bacillus subtilis 1423 -11532318 7500952876 ipa-11d (db: genpept-bct1) (de: b. subtilis genomic region (325 to 333).) (le: 11322) (re: 12035) (di: direct) BSGENR X73124 g580865 Bacillus subtilis 1423 -11532318 5000689721 orf1 (db: genpept-bct1) (de: bacillus subtilis tyrs1 gene for tyrosine trna synthetase, sacx andsacy genes, and three orfs.) (le: 2256) (re: 2969) (di: complement) BSTYRS1G X52480 g580945 Bacillus subtilis 1423 -11532318 219754 ywaf (fn: unknown) (db: genpept-bct1) (de: bacillus subtilis complete genome (section 20 of 21): from 3798401 to 4010550.) (nt: alternate gene name: ipa-11d) (le: 145924) (re: 146637) (di: complement) BSUB0020 Z99123 g2636379 Bacillus subtilis 1423 -11532318 116655 ywaf: ipa-11d (de: hypothetical 27.3 kd protein in tyrz-sacy intergenic region (orf1)) (db: swissprot) YWAF\_BACSU P25149 BACILLUS SUBTILIS 1423 -11532318 170186 ywaf hypothetical protein ywaf: hypothetical protein 1: sacs-region (db: pir) S16424 S16424 Bacillus subtilis 1423 -11532318

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816794	6622	28778	2484	828

Description

GTC ORF with score 765 to: (sr: baker's yeast strain=s288c (ab972)) (db: genpept-pln1) (de: saccharomyces cerevisiae chromosome viii cosmid 9196.) (nt: member of the atp-binding transport protein family) (le: 27976) (re: 32754) (di: complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816799	6623	28779	285	94

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816802	6624	28780	675	225

Description

6500728461 ipa-10r:ywae hypothetical protein:hypothetical transcriptional regulator in tyrz-sacy intergenic region:orf3 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywaE ywaE Bacillus subtilis 1423 -11532319 219247 ywae:ipa-10r (de:(orf3)) (db:swissprot) YWAE\_BACSU P25150 BACILLUS SUBTILIS 1423 -11532319 7000688637 ywae transcription regulator marr family homolog ywae:hypothetical protein 3:sacs-region (db:pir2.dat) S16425 S16425 Bacillus subtilis 1423 -11532319 7500952875 ipa-10r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:10656) (re:11171) (di:complement) BSGENR X73124 g413934 Bacillus subtilis 1423 -11532319 5000688927 orf3 (db:genpept-bct1) (de:bacillus subtilis tyrs1 gene for tyrosine trna synthetase, sacx andsacy genes, and three orfs.) (le:3120) (re:3635) (di:direct) BSTYRS1G X52480 g40241 Bacillus subtilis 1423 -11532319 219755 ywae (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-10r; similar to) (le:146788) (re:147303) (di:direct) BSUB0020 Z99123 g2636380 Bacillus subtilis 1423 -11532319 116654 ywae:ipa-10r (de:(orf3)) (db:swissprot) YWAE\_BACSU P25150 BACILLUS SUBTILIS 1423 -11532319 170209 ywae transcriptional regulator marr family homolog ywae:hypothetical protein 3:sacs-region (db:pir) S16425 S16425 Bacillus subtilis 1423 -11532319

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816803	6625	28781	435	144

Description

6500728462 ipa-8r:ywad hypothetical protein:hypothetical 49.5 kd protein in dae-tyrz intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywad ywad Bacillus subtilis 1423 -11532320 7500952874 ywad:ipa-8r (de:hypothetical 49.5 kd protein in dae-tyrz intergenic region precursor) (db:swissprot) YWAD\_BACSU P25152 BACILLUS SUBTILIS 1423 -11532320 7000688636 ywad aminopeptidase homolog ywad (db:pir2.dat) S39663 S39663 Bacillus subtilis 1423 -11532320 5000689720 ipa-8r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:7643) (re:9010) (di:complement) BSGENR X73124 g413932 Bacillus subtilis 1423 -11532320 219245 ywad (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-8r; similar to) (le:148949) (re:150316) (di:direct) BSUB0020 Z99123 g2636382 Bacillus subtilis 1423 -11532320 116653 ywad:ipa-8r (de:hypothetical 49.5 kd protein in dae-tyrz intergenic region precursor) (db:swissprot) YWAD\_BACSU P25152 BACILLUS SUBTILIS 1423 -11532320 170104 ywad aminopeptidase homolog ywad (db:pir) S39663 S39663 Bacillus subtilis 1423 -11532320

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816804	6626	28782	708	235

Description

6500728463 ipa-7d:ywac hypothetical protein:hypothetical 24.6 kd protein in dae-tyrz intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywac ywac Bacillus subtilis 1423 -11532321  
7500952873 ywac:ipa-7d (de:hypothetical 24.6 kd protein in dae-tyrz intergenic region) (db:swissprot) YWAC\_BACSU P39583 BACILLUS SUBTILIS 1423 -11532321 7000688635 ywac gtp-pyrophosphokinase homolog ywac:protein ipa-7d (cl:gtp pyrophosphokinase related protein) (db:pir2.dat) S39662 S39662 Bacillus subtilis 1423 -11532321 5000689719 ipa-7d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:6981) (re:7613) (di:direct) BSGENR X73124 g413931 Bacillus subtilis 1423 -11532321 219244 ywac (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-7d; similar to) (le:150346) (re:150978) (di:complement) BSUB0020 Z99123 g2636383 Bacillus subtilis 1423 -11532321 116652 ywac:ipa-7d (de:hypothetical 24.6 kd protein in dae-tyrz intergenic region) (db:swissprot) YWAC\_BACSU P39583 BACILLUS SUBTILIS 1423 -11532321 170103 ywac gtp-pyrophosphokinase homolog ywac (cl:gtp pyrophosphokinase related protein) (db:pir) S39662 S39662 Bacillus subtilis 1423 -11532321

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816829	6627	28783	825	274

Description

6500728464 ipa-6d:ywab hypothetical protein:hypothetical 33.8 kd protein in dae-tyrz intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywaB ywaB Bacillus subtilis 1423 -11532322  
7500885474 mena:ipa-6d (ec:2.5.1.-) (de:(dhna-octaprenyltransferase)) (db:swissprot) MENA\_BACSU P39582 BACILLUS SUBTILIS 1423 -11532322  
7000688634 ywab menaquinone biosynthesis protein homolog ywab:protein ipa-6d (cl:quinone biosynthesis homolog ywab) (db:pir2.dat) S39661 S39661 Bacillus subtilis 1423 -11532322 5000689718 ipa-6d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:5904) (re:6839) (di:direct) BSGENR X73124 g413930 Bacillus subtilis 1423 -11532322 219243 ywab (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-6d; similar to quinone) (le:151120) (re:152055) (di:complement) BSUB0020 Z99123 g2636384 Bacillus subtilis 1423 -11532322 116651 mena:ipa-6d (ec:2.5.1.-) (de:(dhna-octaprenyltransferase)) (db:swissprot) MENA\_BACSU P39582 BACILLUS SUBTILIS 1423 -11532322 170102 ywab quinone biosynthesis homolog ywab (db:pir) S39661 S39661 Bacillus subtilis 1423 -11532322

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816849	6628	28784	564	187

Description

6500728465 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxzF yxzF Bacillus subtilis 1423 -11532323  
7000694083 yxzF hypothetical protein yxzF (db:pir2.dat) F70083 F70083 Bacillus subtilis 1423 -11532323 7500964856 yxzF (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:164484) (re:164642) (di:complement) BSUB0020 Z99123 g2636396 Bacillus subtilis 1423 -11532323

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816857	6629	28785	444	147

Description

6500728466 hypothetical protein:similar to dna-3-methyladenine glycosidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxlJ yxlJ Bacillus subtilis 1423 -11532324 7502851767 yxlj (ec:3.2.2.-) (de:putative 3-methyladenine dna glycosylase,) (db:swissprot) 3MGH\_BACSU P94378 BACILLUS SUBTILIS 1423 -11532324 7000692949 yxlj dna-3-methyladenine glycosidase homolog yxlj (db:pir2.dat) D70082 D70082 Bacillus subtilis 1423 -11532324 222890 yxlj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to dna-3-methyladenine glycosidase) (le:164671) (re:165261) (di:complement) BSUB0020 Z99123 g2636397 Bacillus subtilis 1423 -11532324 301557 yxlj (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to dna glycosylases; hypothetical) (le:59204) (re:59794) (di:direct) D83026 D83026 g1783264 Bacillus subtilis 1423 -11532324

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816858	6630	28786	1338	445

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816864	6631	28787	567	188

Description

6500728467 hypothetical protein:similar to multidrug-efflux transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxlH yxlH Bacillus subtilis 1423 -11532325 7000694260 yxlh multidrug-efflux transporter homolog yxlh (db:pir2.dat) C70082 C70082 Bacillus subtilis 1423 -11532325 222888 yxlh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to multidrug-efflux transporter) (le:167138) (re:168340) (di:direct) BSUB0020 Z99123 g2636399 Bacillus subtilis 1423 -11532325 301555 yxlh (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:56125) (re:57327) (di:complement) D83026 D83026 g1783262 Bacillus subtilis 1423 -11532325

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816873	6632	28788	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816878	6633	28789	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816879	6634	28790	924	307

Description

6500728468 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxlG yxlG Bacillus subtilis 1423 -11532326 7000694079 yxlG hypothetical protein yxlG (db:pir2.dat) B70082 B70082 Bacillus subtilis 1423 -11532326 222887 yxlG (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:168333) (re:169112) (di:complement) BSUB0020 Z99123 g2636400 Bacillus subtilis 1423 -11532326 301554 yxlG (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:55353) (re:56132) (di:direct) D83026 D83026 g1783261 Bacillus subtilis 1423 -11532326

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816897	6635	28791	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816899	6636	28792	339	112

Description

6500728469 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yx1F yx1F Bacillus subtilis 1423 -11532327 7000692108 yx1f abc transporter atp-binding protein homolog yx1f (cl:atp-binding cassette homology) (db:pir2.dat) A70082 A70082 Bacillus subtilis 1423 -11532327 222886 yx1f (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to abc transporter (atp-binding protein)) (le:169109) (re:169996) (di:complement) BSUB0020 Z99123 g2636401 Bacillus subtilis 1423 -11532327 301553 yx1f (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to many atp-binding transport proteins;) (le:54469) (re:55356) (di:direct) D83026 D83026 g1783260 Bacillus subtilis 1423 -11532327

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816900	6637	28793	567	188

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816903	6638	28794	459	152

Description

GTC ORF with score 386 to: (sr:fusarium oxysporum f24) (db:genpept-pln1) (de:transposase {impala-160 element, inverted repeats} (fusariumoxysporum, f24, transposon mutant, 1280 nt).) (nt:this sequence comes from fig. 2.) (le:133:335:680) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816904	6639	28795	543	180

Description

GTC ORF with score 457 to: (sr:fusarium oxysporum f24) (db:genpept-pln1) (de:transposase {impala-160 element, inverted repeats} (fusariumoxysporum, f24, transposon mutant, 1280 nt).) (nt:this sequence comes from fig. 2.) (le:133:335:680) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816921	6640	28796	318	105

Description

6500728470 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxlE yxlE Bacillus subtilis 1423 -11532328  
 7000694078 yxle hypothetical protein yxle (db:pir2.dat) H70081 H70081 Bacillus subtilis 1423 -11532328 222885 yxle (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:170003) (re:170191) (di:complement) BSUB0020 Z99123 g2636402  
 Bacillus subtilis 1423 -11532328 301552 yxle (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:54274) (re:54462) (di:direct) D83026 D83026 g1783259 Bacillus subtilis 1423 -11532328

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816922	6641	28797	474	157

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816928	6642	28798	753	250

Description

6500728471 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxld yxld Bacillus subtilis 1423 -11532329  
 7000694077 yxld hypothetical protein yxld (db:pir2.dat) G70081 G70081 Bacillus subtilis 1423 -11532329 222884 yxld (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:170188) (re:170394) (di:complement) BSUB0020 Z99123 g2636403  
 Bacillus subtilis 1423 -11532329 301551 yxld (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:54071) (re:54277) (di:direct) D83026 D83026 g1783258 Bacillus subtilis 1423 -11532329

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816929	6643	28799	384	127

Description

GTC ORF with score 143 to: (sr:burkholderia pickettii (strain:ntp0602) dna) (db:genpept-bct1) (de:burkholderia pickettii dna for hydroxyquinol-1, 2-dioxygenase andchlorophenol-4-hydroxylase,complete cds.) (le:2659) (re:3606) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816937	6644	28800	714	237

#### Description

6500728472 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxlC yxlC Bacillus subtilis 1423 -11532330  
 7000694076 yxlC hypothetical protein yxlC (db:pir2.dat) F70081 F70081 Bacillus subtilis 1423 -11532330 222883 yxlC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:170391) (re:170711) (di:complement) BSUB0020 Z99123 g2636404 Bacillus subtilis 1423 -11532330 301550 yxlC (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:53754) (re:54074) (di:direct) D83026 D83026 g1783257 Bacillus subtilis 1423 -11532330

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816941	6645	28801	261	86

#### Description

6500728473 hypothetical protein:similar to purine-cytosine permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxlA yxlA Bacillus subtilis 1423 -11532331 7000694476 yxlA purine-cytosine permease homolog yxlA (db:pir2.dat) E70081 E70081 Bacillus subtilis 1423 -11532331 222881 yxlA (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to purine-cytosine permease) (le:171452) (re:172825) (di:direct) BSUB0020 Z99123 g2636406 Bacillus subtilis 1423 -11532331 301548 yxlA (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to purine-cytosine permease) (le:51640) (re:53013) (di:complement) D83026 D83026 g1783255 Bacillus subtilis 1423 -11532331

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816944	6646	28802	402	133

#### Description

GTC ORF with score 106 to: (db:genpept-bct2) (de:mycobacterium smegmatis exochelin gene cluster, exit (exit) andfxbb (fxbb) genes, complete cds; and fxbc (fxbc) gene, partial cds.) (nt:abc transporter; this abc transporter probably) (le:489) (re:3857) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816947	6647	28803	642	213

Description

6500728474 hypothetical protein:hypothetical 29.9 kd protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxkO yxkO Bacillus subtilis 1423 -11532332 5500686692 yxko (de:hypothetical 29.9 kd protein in sigy-cydd intergenic region) (db:swissprot) YXKO\_BACSU P94368 BACILLUS SUBTILIS 1423 -11532332 7000688783 yxko conserved hypothetical protein yxko (db:pir2.dat) D70081 D70081 Bacillus subtilis 1423 -11532332 222880 yxko (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to hypothetical proteins) (le:172840) (re:173670) (di:complement) BSUB0020 Z99123 g2636407 Bacillus subtilis 1423 -11532332 301547 yxko (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to hypothetical proteins (pir:s41739;) (le:50795) (re:51625) (di:direct) D83026 D83026 g1783254 Bacillus subtilis 1423 -11532332

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501816962	6648	28804	411	136

Description

6500728475 hypothetical protein:similar to metabolite-sodium symport (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxkJ yxkJ Bacillus subtilis 1423 -11532333 7000694209 yxkj metabolite-sodium symport homolog yxkj (cl:citrate transport protein citc) (db:pir2.dat) C70081 C70081 Bacillus subtilis 1423 -11532333 222875 yxkj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to metabolite-sodium symport) (le:180145) (re:181497) (di:direct) BSUB0020 Z99123 g2636412 Bacillus subtilis 1423 -11532333 301542 yxkj (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to citrate-sodium symport (citrate) (le:42968) (re:44320) (di:complement) D83026 D83026 g1783249 Bacillus subtilis 1423 -11532333



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816963	6649	28805	741	246

Description

6500728476 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxkI yxkI Bacillus subtilis 1423 -11532334  
 7000694075 yxki hypothetical protein yxki (db:pir2.dat) B70081 B70081 Bacillus subtilis 1423 -11532334 222874 yxki (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:181619) (re:183307) (di:direct) BSUB0020 Z99123 g2636413 Bacillus subtilis 1423 -11532334 301541 yxki (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:41158) (re:42846) (di:complement) D83026 D83026 g1783248 Bacillus subtilis 1423 -11532334

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816964	6650	28806	582	193

Description

GTC ORF with score 169 to: (sr:schizosaccharomyces pombe (strain 972 h-) dna) (db:genpept-pln1) (de:schizosaccharomyces pombe dna polymerase delta (pold) gene,complete cds.) (nt:putative) (le:341:622) (re:569:3653) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501816985	6651	28807	192	63

Description

6500728477 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxzE yxzE Bacillus subtilis 1423 -11532335  
 7000694082 yxze hypothetical protein yxze (db:pir2.dat) E70083 E70083 Bacillus subtilis 1423 -11532335 7500964855 yxze (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:183365) (re:183565) (di:direct) BSUB0020 Z99123 g2636414 Bacillus subtilis 1423 -11532335

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817000	6652	28808	402	133

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817004	6653	28809	465	154

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817008	6654	28810	2028	675

Description

6500728478 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxkH yxkH Bacillus subtilis 1423 -11532336 7000692875 yxkh conserved hypothetical protein yxkh (db:pir2.dat) A70081 A70081 Bacillus subtilis 1423 -11532336 222873 yxkh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to hypothetical proteins) (le:183579) (re:184418) (di:complement) BSUB0020 Z99123 g2636415 Bacillus subtilis 1423 -11532336 301540 yxkh (sr:bacillus subtilis (strain:bgsclal) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to swissprot:yade\_ecoli; hypothetical) (le:40047) (re:40886) (di:direct) D83026 D83026 g1783247 Bacillus subtilis 1423 -11532336

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817022	6655	28811	315	104

Description

GTC ORF with score 121 to: (fn:second multifunctional cytochrome p450 in the) (sr:sorghum) (db:genpept-pln2) (de:sorghum bicolor cytochrome p450 cyp71e1 (cyp71e1) mrna, completecds.) (nt:no est#s identified.) (le:81) (re:1676) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817025	6656	28812	531	177

Description

6500728479 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxkF yxkF Bacillus subtilis 1423 -11532337 7000692874 yxkf conserved hypothetical protein yxkf (db:pir2.dat) H70080 H70080 Bacillus subtilis 1423 -11532337 222871 yxkf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to hypothetical proteins) (le:185743) (re:186636) (di:complement) BSUB0020 Z99123 g2636417 Bacillus subtilis 1423 -11532337 301538 yxkf (sr:bacillus subtilis (strain:bgsclal) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to leucine rich protein (pir:s39972);) (le:37829) (re:38722) (di:direct) D83026 D83026 g1783245 Bacillus subtilis 1423 -11532337

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817027	6657	28813	393	130
<u>Description</u>				

6500728480 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxkD yxkD Bacillus subtilis 1423 -11532338 7000692873 yxkd conserved hypothetical protein yxkd (cl:conserved hypothetical protein yitt) (db:pir2.dat) G70080 G70080 Bacillus subtilis 1423 -11532338 222869 yxkd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to hypothetical proteins) (le:188319) (re:189155) (di:complement) BSUB0020 Z99123 g2636419 Bacillus subtilis 1423 -11532338 301536 yxkd (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to jojc gene product (b. subtilis;)) (le:35310) (re:36146) (di:direct) D83026 D83026 g1783243 Bacillus subtilis 1423 -11532338

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817031	6658	28814	609	202
<u>Description</u>				

6500728481 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxkC yxkC Bacillus subtilis 1423 -11532339 7000694074 yxkc hypothetical protein yxkc (db:pir2.dat) F70080 F70080 Bacillus subtilis 1423 -11532339 222868 yxkc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:189624) (re:190265) (di:direct) BSUB0020 Z99123 g2636420 Bacillus subtilis 1423 -11532339 301535 yxkc (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:34200) (re:34841) (di:complement) D83026 D83026 g1783242 Bacillus subtilis 1423 -11532339

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817038	6659	28815	357	118

Description

6500728482 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxkA yxkA Bacillus subtilis 1423 -11532340 7000692872 yxka conserved hypothetical protein yxka (db:pir2.dat) E70080 E70080 Bacillus subtilis 1423 -11532340 222866 yxka (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to hypothetical proteins) (le:191474) (re:191980) (di:complement) BSUB0020 Z99123 g2636422 Bacillus subtilis 1423 -11532340 301533 yxka (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:32485) (re:32991) (di:direct) D83026 D83026 g1783240 Bacillus subtilis 1423 -11532340

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817041	6660	28816	1068	355

Description

5000689426 hypothetical protein:hypothetical transcriptional regulator in gale-pept intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxjO yxjO Bacillus subtilis 1423 -11532341 116848 yxjo (de:hypothetical transcriptional regulator in gale-pept intergenic region) (db:swissprot) YXJO\_BACSU P55181 BACILLUS SUBTILIS 1423 -11532341 7000688782 yxjo transcription regulator lysr family homolog yxjo (cl:bacillus subtilis transcription repressor of citrate synthase i citr) (db:pir2.dat) D70080 D70080 Bacillus subtilis 1423 -11532341 303671 (fn:bacterial regulator of lysr family by homology) (db:genpept-bct1) (de:b.subtilis orfs 1,2,3,4, pept and gale genes.) (nt:putative; orf1) (le:1910) (re:2785) (di:direct) BSGALE X99339 g1429255 Bacillus subtilis 1423 -11532341 222865 yxjo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to transcriptional regulator (lysr family)) (le:192110) (re:192985) (di:direct) BSUB0020 Z99123 g2636423 Bacillus subtilis 1423 -11532341 301532 yxjo (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to transcriptional regulatory proteins;) (le:31480) (re:32355) (di:complement) D83026 D83026 g1783239 Bacillus subtilis 1423 -11532341 219219 (fn:bacterial regulator of lysr family by homology) (db:genpept-bct1) (de:b.subtilis orfs 1,2,3,4, pept and gale genes.) (nt:putative; orf1) (le:1910) (re:2785) (di:direct) BSGALE X99339 g1429255 Bacillus subtilis 1423 -11532341 6500728483 hypothetical protein:hypothetical transcriptional regulator in gale-pept intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxjO yxjO Bacillus subtilis 1423 -11532341

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817046	6661	28817	1167	389

Description

5000689425 hypothetical protein:hypothetical 17.4 kd protein in gale-pept intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxjN yxjN Bacillus subtilis 1423 -11532342 116847 yxjn (de:hypothetical 17.4 kd protein in gale-pept intergenic region) (db:swissprot) YXJN\_BACSU P55182 BACILLUS SUBTILIS 1423 -11532342 7000688781 yxjn conserved hypothetical protein yxjn (db:pir2.dat) C70080 C70080 Bacillus subtilis 1423 -11532342 303672 (db:genpept-bct1) (de:b.subtilis orfs 1,2,3,4, pept and gale genes.) (nt:orf2; putative) (le:2863) (re:3336) (di:direct) BSGALE X99339 g1429256 Bacillus subtilis 1423 -11532342 222864 yxjn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to hypothetical proteins from b. subtilis) (le:193063) (re:193536) (di:direct) BSUB0020 Z99123 g2636424 Bacillus subtilis 1423 -11532342 301531 yxjn (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:30929) (re:31402) (di:complement) D83026 D83026 g1783238 Bacillus subtilis 1423 -11532342 219220 (db:genpept-bct1) (de:b.subtilis orfs 1,2,3,4, pept and gale genes.) (nt:orf2; putative) (le:2863) (re:3336) (di:direct) BSGALE X99339 g1429256 Bacillus subtilis 1423 -11532342 6500728484 hypothetical protein:hypothetical 17.4 kd protein in gale-pept intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxjN yxjN Bacillus subtilis 1423 -11532342

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817086	6662	28818	183	60

Description

6500728485 hypothetical protein:hypothetical sensor-like histidine kinase in gale-pept intergenic region (gtcfc:14.1) (ec:2.7.3.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxjM yxjM Bacillus subtilis 1423 -11532343 116846 yxjm (ec:2.7.3.-) (de:region,) (db:swissprot) YXJM\_BACSU P55183 BACILLUS SUBTILIS 1423 -11532343 7000688780 yxjm two-component sensor histidine kinase homolog yxjm (db:pir2.dat) B70080 B70080 Bacillus subtilis 1423 -11532343 303673 (fn:bacterial sensor kinase by homology) (db:genpept-bct1) (de:b.subtilis orfs 1,2,3,4, pept and gale genes.) (nt:orf3; putative) (le:3354) (re:4574) (di:direct) BSGALE X99339 g1429257 Bacillus subtilis 1423 -11532343 222863 yxjm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to two-component sensor histidine kinase) (le:193554) (re:194774) (di:direct) BSUB0020 Z99123 g2636425 Bacillus subtilis 1423 -11532343 301530 yxjm (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to sensor protein uhpB) (le:29691) (re:30911) (di:complement) D83026 D83026 g1783237 Bacillus subtilis 1423 -11532343 219221 (fn:bacterial sensor kinase by homology) (db:genpept-bct1) (de:b.subtilis orfs 1,2,3,4, pept and gale genes.) (nt:orf3; putative) (le:3354) (re:4574) (di:direct) BSGALE X99339 g1429257 Bacillus subtilis 1423 -11532343 5000689451 (de:(yxjm) (pn:hypothetical sensor-like histidine kinase in gale-pept intergenic region) (gtcfc:13.07) (ec:2.7.3.-) (yxjm\_bacsu) (keggfc:11.1) (db:gtc-bacillus subtilis)) yxjM yxjM Bacillus subtilis 1423 10058571

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817087	6663	28819	243	80

Description

6500728486 hypothetical protein:hypothetical transcriptional regulator in gale-pept intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxjL yxjL Bacillus subtilis 1423 -11532344 7000694858 yxjl two-component response regulator yxjm homolog yxjl) (cl:regulatory protein coma:response regulator homology) (db:pir2.dat) A70080 A70080 Bacillus subtilis 1423 -11532344 222862 yxjl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to two-component response regulator (yxjm)) (le:194761) (re:195417) (di:direct) BSUB0020 Z99123 g2636426 Bacillus subtilis 1423 -11532344 301529 yxjl (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to many transcriptional activator) (le:29048) (re:29704) (di:complement) D83026 D83026 g1783236 Bacillus subtilis 1423 -11532344

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817088	6664	28820	327	108

Description

6500728487 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxjJ yxjJ Bacillus subtilis 1423 -11532345 7000694073 yxjJ hypothetical protein yxjJ (db:pir2.dat) H70079 H70079 Bacillus subtilis 1423 -11532345 222860 yxjJ (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:197221) (re:197484) (di:direct) BSUB0020 Z99123 g2636428 Bacillus subtilis 1423 -11532345 301527 yxjJ (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:26981) (re:27244) (di:complement) D83026 D83026 g1783234 Bacillus subtilis 1423 -11532345

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817090	6665	28821	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817093	6666	28822	183	60

Description

6500728488 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxjI yxjI Bacillus subtilis 1423 -11532346 7000694072 yxjI hypothetical protein yxjI (db:pir2.dat) G70079 G70079 Bacillus subtilis 1423 -11532346 222859 yxjI (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:197613) (re:198101) (di:direct) BSUB0020 Z99123 g2636429 Bacillus subtilis 1423 -11532346 301526 yxjI (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:26364) (re:26852) (di:complement) D83026 D83026 g1783233 Bacillus subtilis 1423 -11532346

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817099	6667	28823	255	84

Description

6500728489 n15or:yxjh hypothetical protein:hypothetical 38.3 kd protein in katb 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxjH yxjH Bacillus subtilis 1423 -11532347 116844 yxjh:n15or (de:hypothetical 38.3 kd protein in pept-katb intergenic region) (db:swissprot) YXJH\_BACSU P42319 BACILLUS SUBTILIS 1423 -11532347 7000688779 yxjh conserved hypothetical protein yxjh (db:pir2.dat) F70079 F70079 Bacillus subtilis 1423 -11532347 222858 yxjh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to hypothetical proteins from b. subtilis) (le:198356) (re:199378) (di:direct) BSUB0020 Z99123 g2636430 Bacillus subtilis 1423 -11532347 301525 yxjh (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:25087) (re:26109) (di:complement) D83026 D83026 g1783232 Bacillus subtilis 1423 -11532347

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817100	6668	28824	957	318

Description

6500728490 n15nr:yxjg hypothetical protein:hypothetical 38.0 kd protein in katb 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxjG yxjG Bacillus subtilis 1423 -11532348 116843 yxjg:n15nr (de:hypothetical 38.0 kd protein in katb 3'region) (db:swissprot) YXJG\_BACSU P42318 BACILLUS SUBTILIS 1423 -11532348 7000688778 yxjg conserved hypothetical protein yxjg (db:pir2.dat) E70079 E70079 Bacillus subtilis 1423 -11532348 222857 yxjg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to hypothetical proteins from b. subtilis) (le:199741) (re:200745) (di:direct) BSUB0020 Z99123 g2636431 Bacillus subtilis 1423 -11532348 301524 yxjg (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:23720) (re:24724) (di:complement) D83026 D83026 g666005 Bacillus subtilis 1423 -11532348 5000689840 (de:(yxjg) (pn:hypothetical 38) (gn:n15nr) (gtcfc:13.07) (ec:) (yxjg\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxjG yxjG Bacillus subtilis 1423 10058568



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817118	6669	28825	933	310
<u>Description</u>				
6500728491 n15m:yxjf hypothetical protein:hypothetical oxidoreductase in katb 3region (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxjF yxjF Bacillus subtilis 1423 -11532349 116842 yxjf:n15m (ec:1.-.-.-) (de:(ec 1.-.-.-)) (db:swissprot) YXJF_BACSU P42317 BACILLUS SUBTILIS 1423 -11532349 7000688777 yxjf gluconate 5-dehydrogenase homolog yxjf (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) D70079 D70079 Bacillus subtilis 1423 -11532349 222856 yxjf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to gluconate 5-dehydrogenase) (le:200927) (re:201700) (di:complement) BSUB0020 Z99123 g2636432 Bacillus subtilis 1423 -11532349 301523 yxjf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to gluconate 5-dehydrogenase) (le:47) (re:820) (di:complement) BSUB0021 Z99124 g2636443 Bacillus subtilis 1423 -11532349 6000685983 yxjf (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to many ketoreductases and steroid) (le:22765) (re:23538) (di:direct) D83026 D83026 g666004 Bacillus subtilis 1423 -11532349 5000689839 (de:(yxjf) (pn:hypothetical oxidoreductase in katb 3"region) (gn:n15m) (gtcfc:13.07) (ec:1.-.-.-) (yxjf_bacsu) (keggfc:11.1) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxjF yxjF Bacillus subtilis 1423 10058567				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817121	6670	28826	798	265

Description

6500728492 n15j:yxjc hypothetical protein:hypothetical 48.3 kd protein in katb 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxjc yxjc Bacillus subtilis 1423 -11532350 116841 yxjc:n15j (de:hypothetical 48.3 kd protein in katb 3'region) (db:swissprot) YXJC\_BACSU P42314 BACILLUS SUBTILIS 1423 -11532350 7000688776 yxjc conserved hypothetical protein yxjc (db:pir2.dat) A70079 A70079 Bacillus subtilis 1423 -11532350 222853 yxjc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to hypothetical proteins from b. subtilis) (le:203159) (re:204523) (di:complement) BSUB0020 Z99123 g2636435 Bacillus subtilis 1423 -11532350 301520 yxjc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins from b. subtilis) (le:2279) (re:3643) (di:complement) BSUB0021 Z99124 g2636446 Bacillus subtilis 1423 -11532350 6000685981 yxjc (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:19942) (re:21306) (di:direct) D83026 D83026 g666001 Bacillus subtilis 1423 -11532350 5000689838 (de:(yxjc) (pn:hypothetical 48) (gn:n15j) (gtcfc:13.07) (ec:) (yxjc\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxjc yxjc Bacillus subtilis 1423 10058566

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817126	6671	28827	360	119

Description

GTC ORF with score 143 to: (db:genpept-bct2) (de:pasteurella haemolytica putative coproporphyrinogen iii oxidase(hemn') gene, partial cds, leukotoxin transcriptional activator andrestriction modification methylase subunit (alxa-hsdm), (hsds) and(hsdr) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817145	6672	28828	1815	605

Description

GTC ORF with score 155 to: (fn:involved in heterokaryon incompatibility) (sr:podospora anserina dna) (db:genpept-vr1) (de:podospora anserina beta transducin-like protein (het-e1) gene,complete cds.) (nt:putative) (le:810:3142) (re:3092:4929) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817147	6673	28829	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817176	6674	28830	822	273

Description

6500728493 n15i:yxjb hypothetical protein: hypothetical 31.5 kd protein in katb 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxjB yxjB Bacillus subtilis 1423 -11532351 116840 yxjb:n15i (de: hypothetical 31.5 kd protein in katb 3'region) (db:swissprot) YXJB\_BACSU P42313 BACILLUS SUBTILIS 1423 -11532351 7000688775 yxjb conserved hypothetical protein yxjb (cl:bioc homology) (db:pir2.dat) H70078 H70078 Bacillus subtilis 1423 -11532351 222852 yxjb (fn:unknown) (db:genpept-bct1) (de: bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to hypothetical proteins) (le:204677) (re:205525) (di:complement) BSUB0020 Z99123 g2636436 Bacillus subtilis 1423 -11532351 301519 yxjb (fn:unknown) (db:genpept-bct1) (de: bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:3797) (re:4645) (di:complement) BSUB0021 Z99124 g2636447 Bacillus subtilis 1423 -11532351 6000685979 yxjb (sr:bacillus subtilis (strain: bgsclal) dna) (db:genpept-bct1) (de: bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to swissprot:yebh\_ecoli hypothetical) (le:18940) (re:19788) (di:direct) D83026 D83026 g666000 Bacillus subtilis 1423 -11532351 5000689837 (de: (yxjb) (pn:hypothetical 31) (gn:n15i) (gtcfc:13.07) (ec:) (yxjb\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxjB yxjB Bacillus subtilis 1423 10058565

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817179	6675	28831	282	93

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817194	6676	28832	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817198	6677	28833	966	321

Description

6500728494 n15hr:yxja hypothetical protein:hypothetical 43.7 kd protein in katb 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxjA yxjA Bacillus subtilis 1423 -11532352 116839 yxja:n15hr (de:hypothetical 43.7 kd protein in katb 3'region) (db:swissprot) YXJA\_BACSU P42312 BACILLUS SUBTILIS 1423 -11532352 7000688774 yxja pyrimidine nucleoside transport homolog yxja (cl:pyrimidine nucleoside transport protein nupc) (db:pir2.dat) G70078 G70078 Bacillus subtilis 1423 -11532352 222851 yxja (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to pyrimidine nucleoside transport) (le:206141) (re:207334) (di:direct) BSUB0020 Z99123 g2636437 Bacillus subtilis 1423 -11532352 301518 yxja (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to pyrimidine nucleoside transport) (le:5261) (re:6454) (di:direct) BSUB0021 Z99124 g2636448 Bacillus subtilis 1423 -11532352 6000685977 yxja (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to pyrimidine nucleoside transport) (le:17131) (re:18324) (di:complement) D83026 D83026 g665999 Bacillus subtilis 1423 -11532352 5000689836 (de:(yxja) (pn:hypothetical 43) (gn:n15hr) (gtcfc:13.07) (ec:) (yxja\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxjA yxjA Bacillus subtilis 1423 10058564

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817207	6678	28834	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817209	6679	28835	1137	378

Description

6500728495 n15g:yxit hypothetical protein:hypothetical 9.1 kd protein in katb 3region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxiT yxiT Bacillus subtilis 1423 -11532353 116838 yxit:n15g (de:hypothetical 9.1 kd protein in katb 3'region precursor) (db:swissprot) YXIT\_BACSU P42311 BACILLUS SUBTILIS 1423 -11532353 7000688773 yxit hypothetical protein yxit (db:pir2.dat) F70078 F70078 Bacillus subtilis 1423 -11532353 222850 yxit (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:207805) (re:208047) (di:complement) BSUB0020 Z99123 g2636438 Bacillus subtilis 1423 -11532353 301517 yxit (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:6925) (re:7167) (di:complement) BSUB0021 Z99124 g2636449 Bacillus subtilis 1423 -11532353 6000685975 yxit (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:16418) (re:16660) (di:direct) D83026 D83026 g665998 Bacillus subtilis 1423 -11532353 5000689835 (de:(yxit) (pn:hypothetical 9) (gn:n15g) (gtcfc:13.07) (ec:)) (yxit\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxiT yxiT Bacillus subtilis 1423 10058563

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817213	6680	28836	1695	565

Description

6500728496 n15f:yxis hypothetical protein:hypothetical 11.1 kd protein in katb 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxiS yxiS Bacillus subtilis 1423 -11532354 116836 yxis:n15f (de:hypothetical 11.1 kd protein in katb 3'region) (db:swissprot) YXIS\_BACSU P42310 BACILLUS SUBTILIS 1423 -11532354 7000688772 yxis hypothetical protein yxis (db:pir2.dat) E70078 E70078 Bacillus subtilis 1423 -11532354 222849 yxis (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:208192) (re:208482) (di:complement) BSUB0020 Z99123 g2636439 Bacillus subtilis 1423 -11532354 301516 yxis (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:7312) (re:7602) (di:complement) BSUB0021 Z99124 g2636450 Bacillus subtilis 1423 -11532354 6000685973 yxis (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:15983) (re:16273) (di:direct) D83026 D83026 g665997 Bacillus subtilis 1423 -11532354 5000689834 (de:(yxis) (pn:hypothetical 11) (gn:n15f) (gtcfc:13.07) (ec:)) (yxis\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxiS yxiS Bacillus subtilis 1423 10058561

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817221	6681	28837	1254	417

Description

6500728497 n15cr:yxiq hypothetical protein:hypothetical 45.5 kd protein in bgls-katb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxiQ yxiQ Bacillus subtilis 1423 -11532355 116835 yxiq:n15cr (de:hypothetical 45.5 kd protein in bgls-katb intergenic region) (db:swissprot) YXIQ\_BACSU P42308 BACILLUS SUBTILIS 1423 -11532355 7000688771 yxiq mg2+/citrate complex transporter homolog yxiq (db:pir2.dat) D70078 D70078 Bacillus subtilis 1423 -11532355 222847 yxiq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to mg2+/citrate complex transporter) (le:210793) (re:212073) (di:direct) BSUB0020 Z99123 g2636441 Bacillus subtilis 1423 -11532355 301514 yxiq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to mg2+/citrate complex transporter) (le:9913) (re:11193) (di:direct) BSUB0021 Z99124 g2636452 Bacillus subtilis 1423 -11532355 6000685971 yxiq (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:12392) (re:13672) (di:complement) D83026 D83026 g665994 Bacillus subtilis 1423 -11532355 5000689833 (de:(yxiq) (pn:hypothetical 45) (gn:n15cr) (gtcfc:13.07) (ec:) (yxiq\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxiQ yxiQ Bacillus subtilis 1423 10058560

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817223	6682	28838	204	67

Description

GTC ORF with score 160 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome 1 bac f9k20 sequence, completesequence.) (nt:similar to gb|x16648 pathogenesis related protein) (le:54730:55515:55679:55892) (re:54900:55586:55811:56190) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817226	6683	28839	312	103

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817243	6684	28840	255	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817282	6685	28841	345	114

Description

6500728498 s3b:yxip hypothetical protein:hypothetical 25.7 kd protein in wapa-lict intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxiP yxiP Bacillus subtilis 1423 -11532356 116834 yxip:s3b (de:hypothetical 25.7 kd protein in wapa-lict intergenic region precursor) (db:swissprot) YXIP\_BACSU P42307 BACILLUS SUBTILIS 1423 -11532356 7000688770 yxip hypothetical protein yxip (db:pir2.dat) C70078 C70078 Bacillus subtilis 1423 -11532356 222844 yxip (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:13304) (re:13984) (di:complement) BSUB0021 Z99124 g2636455 Bacillus subtilis 1423 -11532356 301511 yxip (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:9601) (re:10281) (di:direct) D83026 D83026 g665991 Bacillus subtilis 1423 -11532356 5000689832 (de:(yxip) (pn:hypothetical 25) (gn:s3b) (gtcfc:13.07) (ec:) (yxip\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxiP yxiP Bacillus subtilis 1423 10058559

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817283	6686	28842	987	329

Description

6500728499 s3ar:yxio hypothetical protein:hypothetical 47.3 kd protein in wapa-lict intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxiO yxiO Bacillus subtilis 1423 -11532357 116833 yxio:s3ar (de:hypothetical 47.3 kd protein in wapa-lict intergenic region) (db:swissprot) YXIO\_BACSU P42306 BACILLUS SUBTILIS 1423 -11532357 7000688769 yxio conserved hypothetical protein yxio (db:pir2.dat) B70078 B70078 Bacillus subtilis 1423 -11532357 222843 yxio (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:14191) (re:15477) (di:direct) BSUB0021 Z99124 g2636456 Bacillus subtilis 1423 -11532357 301510 yxio (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to swissprot:yed8\_yeast hypothetical) (le:8108) (re:9394) (di:complement) D83026 D83026 g665990 Bacillus subtilis 1423 -11532357 5000689831 (de:(yxio) (pn:hypothetical 47) (gn:s3ar) (gtcfc:13.07) (ec:) (yxio\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxiO yxiO Bacillus subtilis 1423 10058558

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817302	6687	28843	2115	705

Description

6500728500 ss8d:yxim hypothetical protein:hypothetical 41.8 kd protein in wapa-lict intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxiM yxiM Bacillus subtilis 1423 -11532358 116831 yxim:ss8d (de:hypothetical 41.8 kd protein in wapa-lict intergenic region precursor) (db:swissprot) YXIM\_BACSU P42304 BACILLUS SUBTILIS 1423 -11532358 7000688767 yxim conserved hypothetical protein yxim (cl:hypothetical protein yxim) (db:pir2.dat) A70078 A70078 Bacillus subtilis 1423 -11532358 222841 yxim (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins from b. subtilis) (le:17017) (re:18165) (di:complement) BSUB0021 Z99124 g2636458 Bacillus subtilis 1423 -11532358 301508 yxim (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:5420) (re:6568) (di:direct) D83026 D83026 g665988 Bacillus subtilis 1423 -11532358 5000689829 (de:(yxim) (pn:hypothetical 41) (gn:ss8d) (gtcfc:13.07) (ec:) (yxim\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxiM yxiM Bacillus subtilis 1423 10058556

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817339	6688	28844	315	104

Description

GTC ORF with score 111 to: (sr:human) (db:genpept-pril) (de:homo sapiens chromosome x region from filamin (fln) gene toglucose-6-phosphate dehydrogenase (g6pd) gene, complete cds's.) (le:<116240:116844:118913) (re:116340:116989:118989) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817364	6689	28845	327	108

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817380	6690	28846	372	123

Description

6500728501 ss8c:yxil hypothetical protein:hypothetical 7.8 kd protein in wapa-lict intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxiL yxiL Bacillus subtilis 1423 -11532359 116830 yxil:ss8c (de:hypothetical 7.8 kd protein in wapa-lict intergenic region) (db:swissprot) YXIL\_BACSU P42303 BACILLUS SUBTILIS 1423 -11532359 7000688766 yxil hypothetical protein yxil (db:pir2.dat) H70077 H70077 Bacillus subtilis 1423 -11532359 222840 yxil (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:18348) (re:18548) (di:complement) BSUB0021 Z99124 g2636459 Bacillus subtilis 1423 -11532359 301507 yxil (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:5037) (re:5237) (di:direct) D83026 D83026 g665987 Bacillus subtilis 1423 -11532359 5000689828 (de:(yxil) (pn:hypothetical 7) (gn:ss8c) (gtcfc:13.07) (ec:) (yxil\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxiL yxiL Bacillus subtilis 1423 10058555

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817381	6691	28847	276	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817385	6692	28848	447	148

Description

6500728502 ss8b:yxik hypothetical protein:hypothetical 17.6 kd protein in wapa-lict intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxiK yxiK Bacillus subtilis 1423 -11532360 116829 yxik:ss8b (de:hypothetical 17.6 kd protein in wapa-lict intergenic region) (db:swissprot) YXIK\_BACSU P42302 BACILLUS SUBTILIS 1423 -11532360 7000688765 yxik hypothetical protein yxik (db:pir2.dat) G70077 G70077 Bacillus subtilis 1423 -11532360 222839 yxik (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:18657) (re:19118) (di:complement) BSUB0021 Z99124 g2636460 Bacillus subtilis 1423 -11532360 301506 yxik (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:4467) (re:4928) (di:direct) D83026 D83026 g665986 Bacillus subtilis 1423 -11532360 5000689827 (de:(yxik) (pn:hypothetical 17) (gn:ss8b) (gtcfc:13.07) (ec:) (yxik\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxiK yxiK Bacillus subtilis 1423 10058554

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817387	6693	28849	1548	516

Description

GTC ORF with score 97 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac f12a24 genomic sequence,complete sequence.) (nt:unknown protein) (le:41767:42098:42501) (re:42021:42409:42640) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817392	6694	28850	261	86

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817403	6695	28851	588	195

Description

6500728503 ss8a:yxij hypothetical protein:hypothetical 11.9 kd protein in wapa-lict intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxiJ yxiJ Bacillus subtilis 1423 -11532361 116828 yxij:ss8a (de:hypothetical 11.9 kd protein in wapa-lict intergenic region) (db:swissprot) YXIJ\_BACSU P42320 BACILLUS SUBTILIS 1423 -11532361 7000688764 yxij hypothetical protein yxij (db:pir2.dat) F70077 F70077 Bacillus subtilis 1423 -11532361 222838 yxij (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:19134) (re:19430) (di:complement) BSUB0021 Z99124 g2636461 Bacillus subtilis 1423 -11532361 301505 yxij (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:4155) (re:4451) (di:direct) D83026 D83026 g665985 Bacillus subtilis 1423 -11532361 5000689826 (de:(yxij) (pn:hypothetical 11) (gn:ss8a) (gtcfc:13.07) (ec:)) (yxij\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxiJ yxiJ Bacillus subtilis 1423 10058553

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817410	6696	28852	510	169

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817412	6697	28853	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817428	6698	28854	195	64

Description

6500728504 n17l:yxii hypothetical protein:hypothetical 18.7 kd protein in wapa-lict intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxiI yxiI Bacillus subtilis 1423 -11532362 116827 yxii:n17l (de:hypothetical 18.7 kd protein in wapa-lict intergenic region) (db:swissprot) YXII\_BACSU P42301 BACILLUS SUBTILIS 1423 -11532362 7000688763 yxii hypothetical protein yxii (db:pir2.dat) E70077 E70077 Bacillus subtilis 1423 -11532362 222837 yxii (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:19458) (re:19946) (di:complement) BSUB0021 Z99124 g2636462 Bacillus subtilis 1423 -11532362 301504 yxii::n17l (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:3639) (re:4127) (di:direct) D83026 D83026 g665984 Bacillus subtilis 1423 -11532362 5000689825 (de:(yxii) (pn:hypothetical 18) (gn:n17l) (gtcfc:13.07) (ec:) (yxii\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxiI yxiI Bacillus subtilis 1423 10058552

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817429	6699	28855	1647	549

Description

6500728505 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxzG yxzG Bacillus subtilis 1423 -11532363 7000694084 yxzg hypothetical protein yxzg (db:pir2.dat) G70083 G70083 Bacillus subtilis 1423 -11532363 7500964857 yxzg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:19964) (re:20416) (di:complement) BSUB0021 Z99124 g2636463 Bacillus subtilis 1423 -11532363

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817452	6700	28856	1182	394

Description

6500728506 n17k:yxih hypothetical protein:hypothetical 12.4 kd protein in wapa-lict intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxiH yxiH Bacillus subtilis 1423 -11532364  
 116826 yxih:n17k (de:hypothetical 12.4 kd protein in wapa-lict intergenic region) (db:swissprot) YXIH\_BACSU P42300 BACILLUS SUBTILIS 1423 -11532364  
 7000688762 yxih hypothetical protein yxih (db:pir2.dat) D70077 D70077 Bacillus subtilis 1423 -11532364 215880 n17k hypothetical protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome containing the hut and wapa loci.) (le:28020) (re:28349) (di:direct) BACHUTWAPA D31856 g603786 Bacillus subtilis 1423 -11532364  
 215895 hypothetical 12.4-kda protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis wapa and orf genes for wall-associated proteinand hypothetical proteins.) (le:16123) (re:16452) (di:direct) BACHYPTP D29985 g849033 Bacillus subtilis 1423 -11532364  
 7500953006 yxih (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:20486) (re:20815) (di:complement) BSUB0021 Z99124 g2636464 Bacillus subtilis 1423 -11532364 5000689824 (de:(yxih) (pn:hypothetical 12) (gn:n17k) (gtcfc:13.07) (ec:) (yxih\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxiH yxiH Bacillus subtilis 1423 10058551

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817456	6701	28857	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817475	6702	28858	1362	453

Description

6500728507 n17j:yxig hypothetical protein:hypothetical 16.2 kd protein in wapa-lict intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxiG yxiG Bacillus subtilis 1423 -11532365 116825 yxig:n17j (de:hypothetical 16.2 kd protein in wapa-lict intergenic region) (db:swissprot) YXIG\_BACSU P42299 BACILLUS SUBTILIS 1423 -11532365 7000688761 yxig hypothetical protein yxig (db:pir2.dat) C70077 C70077 Bacillus subtilis 1423 -11532365 215879 n17j hypothetical protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome containing the hut and wapa loci.) (le:27481) (re:27897) (di:direct) BACHUTWAPA D31856 g603785 Bacillus subtilis 1423 -11532365 215894 hypothetical 16.2-kda protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis wapa and orf genes for wall-associated proteinand hypothetical proteins.) (le:15584) (re:16000) (di:direct) BACHYPTP D29985 g849032 Bacillus subtilis 1423 -11532365 222835 yxig (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:20938) (re:21354) (di:complement) BSUB0021 Z99124 g2636465 Bacillus subtilis 1423 -11532365 301502 yxig::n17j (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:2231) (re:2647) (di:direct) D83026 D83026 g665982 Bacillus subtilis 1423 -11532365 5000689823 (de:(yxig) (pn:hypothetical 16) (gn:n17j) (gtcfc:13.07) (ec:) (yxig\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxiG yxiG Bacillus subtilis 1423 10058550

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817490	6703	28859	555	185

Description

6500728508 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxzC yxzC Bacillus subtilis 1423 -11532366 7000694081 yxzc hypothetical protein yxzc (db:pir2.dat) D70083 D70083 Bacillus subtilis 1423 -11532366 7500964854 yxzc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:21405) (re:21773) (di:complement) BSUB0021 Z99124 g2636466 Bacillus subtilis 1423 -11532366

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817492	6704	28860	615	204

Description

6500728509 n17i:yxif hypothetical protein:hypothetical 18.1 kd protein in wapa-lict intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxiF yxiF Bacillus subtilis 1423 -11532367 116824 yxif:n17i (de:hypothetical 18.1 kd protein in wapa-lict intergenic region) (db:swissprot) YXIF\_BACSU P42298 BACILLUS SUBTILIS 1423 -11532367 7000688760 yxif hypothetical protein yxif (db:pir2.dat) B70077 B70077 Bacillus subtilis 1423 -11532367 215878 n17i hypothetical protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome containing the hut and wapa loci.) (le:26598) (re:27068) (di:direct) BACHUTWAPA D31856 g603784 Bacillus subtilis 1423 -11532367 215893 hypothetical 18.1-kda protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis wapa and orf genes for wall-associated proteinand hypothetical proteins.) (le:14701) (re:15171) (di:direct) BACHYTP D29985 g849031 Bacillus subtilis 1423 -11532367 222834 yxif (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:21767) (re:22237) (di:complement) BSUB0021 Z99124 g2636467 Bacillus subtilis 1423 -11532367 301501 yxif::n17i (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:1348) (re:1818) (di:direct) D83026 D83026 g665981 Bacillus subtilis 1423 -11532367 5000689822 (de:(yxif) (pn:hypothetical 18) (gn:n17i) (gtcfc:13.07) (ec:) (yxif\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxiF yxiF Bacillus subtilis 1423 10058549

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817504	6705	28861	1158	385

Description

GTC ORF with score 144 to: (sr:baker's yeast) (db:genpept-pln1) (de:saccharomyces cerevisiae profilin synthetic lethal (psl1) gene,complete cds.) (nt:psl1=sec3; the psl1 product contains a region of) (le:549) (re:4559) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817505	6706	28862	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817509	6707	28863	306	102

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817515	6708	28864	552	183

Description

6500728510 n17h:yxg hypothetical protein:hypothetical 16.4 kd protein in wapa-lict intergenic region:orf3 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxxG yxxG Bacillus subtilis 1423 -11532368 116857 yxxg:n17h (de:hypothetical 16.4 kd protein in wapa-lict intergenic region (orf3)) (db:swissprot) YXXG\_BACSU Q07836 BACILLUS SUBTILIS 1423 -11532368 7000688788 yxxg hypothetical protein yxxg:hypothetical protein wapa 3 region (db:pir2.dat) S32921 S32921 Bacillus subtilis 1423 -11532368 7500953013 n17h hypothetical protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome containing the hut and wapa loci.) (le:25844) (re:26272) (di:direct) BACHUTWAPA D31856 g603783 Bacillus subtilis 1423 -11532368 215877 orf3 hypothetical 16.4-kda protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis wapa and orf genes for wall-associated proteinand hypothetical proteins.) (le:13947) (re:14375) (di:direct) BACHYTP D29985 g849030 Bacillus subtilis 1423 -11532368 215892 (sr:bacillus subtilis (strain w168) (library: lambda gt11) dna) (db:genpept-bct1) (de:bacillus subtilis orf1, 3' end; wall-associated protein (wala)gene, complete cds; complete orf3.) (nt:orf3) (le:7772) (re:8200) (di:direct) BACWAPAX L05634 g304180 Bacillus subtilis 1423 -11532368 217052 yxxg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:22563) (re:22991) (di:complement) BSUB0021 Z99124 g2636468 Bacillus subtilis 1423 -11532368 301500 yxxg:n17h (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:594) (re:1022) (di:direct) D83026 D83026 g665980 Bacillus subtilis 1423 -11532368 170092 yxxg hypothetical protein yxxg:hypothetical protein wapa 3 region (db:pir) S32921 S32921 Bacillus subtilis 1423 -11532368 222833 yxxg:n17h (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:hypothetical) (le:594) (re:1022) (di:direct) D83026 D83026 g665980 Bacillus subtilis 1423 -11532368 5000689846 (de:(yxxg) (pn:hypothetical 16) (gn:n17h) (gtcfc:13.07) (ec:) (yxxg\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxxG yxxG Bacillus subtilis 1423 10058582

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817516	6709	28865	819	276
<u>Description</u>				

GTC ORF with score 368 to: (db:genpept-bct1) (de:bacillus licheniformis) bacitracin synthetase operon including bacitracin synthetase 1 (baca), (bacb) and 3 (bacc) genes, complete cds.) (nt:peptide synthetase; ba3; bacc) (le:24119) (re:43198) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817524	6710	28866	525	174
<u>Description</u>				

6500728511 n17f:yxxf hypothetical protein:hypothetical 34.3 kd protein in bglh-wapa intergenic region:orf1 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxxF yxxF Bacillus subtilis 1423 -11532369 116856 yxxf:n17f (de:hypothetical 34.3 kd protein in bglh-wapa intergenic region (orf1)) (db:swissprot) YXXF\_BACSU Q07835 BACILLUS SUBTILIS 1423 -11532369 7000688787 yxxf hypothetical protein yxxf:hypothetical protein wapa 5 region (db:pir2.dat) B70083 B70083 Bacillus subtilis 1423 -11532369 215875 n17f hypothetical protein (sr:bacillus subtilis (strain:bgsclal) dna) (db:genpept-bct1) (de:bacillus subtilis genome containing the hut and wapa loci.) (le:17681) (re:18616) (di:direct) BACHUTWAPA D31856 g603781 Bacillus subtilis 1423 -11532369 215890 orf1 hypothetical 34.3-kda protein (sr:bacillus subtilis (strain:bgsclal) dna) (db:genpept-bct1) (de:bacillus subtilis wapa and orf genes for wall-associated protein and hypothetical proteins.) (le:5785) (re:6720) (di:direct) BACHYPTP D29985 g849028 Bacillus subtilis 1423 -11532369 7500953012 yxxf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814.) (le:30219) (re:31154) (di:complement) BSUB0021 Z99124 g2636470 Bacillus subtilis 1423 -11532369 5000689845 (de:(yxxf) (pn:hypothetical 34) (gn:n17f) (gtcfc:13.07) (ec:) (yxxf\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxxF yxxF Bacillus subtilis 1423 10058581

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817528	6711	28867	240	79
<u>Description</u>				

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817535	6712	28868	561	186

Description

6500728512 n17e:yxie hypothetical protein:hypothetical 15.9 kd protein in bglh-wapa intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxiE yxiE Bacillus subtilis 1423 -11532370 116823 yxie:n17e (de:hypothetical 15.9 kd protein in bglh-wapa intergenic region precursor) (db:swissprot) YXIE\_BACSU P42297 BACILLUS SUBTILIS 1423 -11532370 7000688759 yxie conserved hypothetical protein yxie (cl:escherichia coli ybdq protein) (db:pir2.dat) A70077 A70077 Bacillus subtilis 1423 -11532370 215874 n17e hypothetical protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome containing the hut and wapa loci.) (le:17083) (re:17529) (di:direct) BACHUTWAPA D31856 g603780 Bacillus subtilis 1423 -11532370 215889 hypothetical 15.9-kda protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis wapa and orf genes for wall-associated proteinand hypothetical proteins.) (le:5187) (re:5633) (di:direct) BACHYPTP D29985 g849027 Bacillus subtilis 1423 -11532370 7500953005 yxie (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:31306) (re:31752) (di:complement) BSUB0021 Z99124 g2636471 Bacillus subtilis 1423 -11532370 5000689821 (de:(yxie) (pn:hypothetical 15) (gn:n17e) (gtcfc:13.07) (ec:) (yxie\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxiE yxiE Bacillus subtilis 1423 10058548

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817538	6713	28869	594	197
<u>Description</u>				
6500728513 n17b:yxxe hypothetical protein:hypothetical 11.9 kd protein in hutp-bglp intergenic region:orf2 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxxE yxxE Bacillus subtilis 1423 -11532371 215886 yxxe:n17b (de:hypothetical 11.9 kd protein in hutp-bglp intergenic region (orf2)) (db:swissprot) YXXE_BACSU P40738 BACILLUS SUBTILIS 1423 -11532371 7000688786 yxxe hypothetical protein yxxe (db:pir2.dat) I40405 I40405 Bacillus subtilis 1423 -11532371 7500953011 n17b hypothetical protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome containing the hut and wapa loci.) (le:13028) (re:13336) (di:direct) BACHUTWAPA D31856 g603777 Bacillus subtilis 1423 -11532371 215871 hypothetical 11.9-kda protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis wapa and orf genes for wall-associated proteinand hypothetical proteins.) (le:1132) (re:1440) (di:direct) BACHYPTP D29985 g849024 Bacillus subtilis 1423 -11532371 5000689844 hypothetical protein (fn:unknown) (db:genpept-bct1) (de:b.subtilis (marburg 168) genes for beta-glucoside permease andbeta-glucosidase.) (nt:orf2) (le:311) (re:619) (di:direct) BSGBGLUC Z34526 g505575 Bacillus subtilis 1423 -11532371 219226 yxxe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:35499) (re:35807) (di:complement) BSUB0021 Z99124 g2636474 Bacillus subtilis 1423 -11532371 116855 yxxe:n17b (de:hypothetical 11.9 kd protein in hutp-bglp intergenic region (orf2)) (db:swissprot) YXXE_BACSU P40738 BACILLUS SUBTILIS 1423 -11532371 170194 yxxe hypothetical protein yxxe (db:pir) I40405 I40405 Bacillus subtilis 1423 -11532371				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817540	6714	28870	594	197

Description

6500728514 n17a:yyxd hypothetical protein:hypothetical 17.7 kd protein in hutp-bglp intergenic region:orf1 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyxD yyxD Bacillus subtilis 1423 -11532372  
304131 yyxd:n17a (de:hypothetical 17.7 kd protein in hutp-bglp intergenic region (orf1)) (db:swissprot) YXXD\_BACSU P40737 BACILLUS SUBTILIS 1423 -11532372 7000688785 yyxd hypothetical protein yyxd (db:pir2.dat) S65579 S65579 Bacillus subtilis 1423 -11532372 7500953010 n17a hypothetical protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome containing the hut and wapa loci.) (le:12539) (re:12982) (di:direct) BACHUTWAPA D31856 g603776 Bacillus subtilis 1423 -11532372 215870 hypothetical 17.7-kda protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis wapa and orf genes for wall-associated proteinand hypothetical proteins.) (le:643) (re:1086) (di:direct) BACHYPTP D29985 g849023 Bacillus subtilis 1423 -11532372 5000689843 orf1 (fn:unknown) (db:genpept-bct1) (de:b.subtilllis dna for ribonucleic antiterminator and bglp gene.) (nt:putative protein of 147 aminoacids) (le:441) (re:884) (di:direct) BSRABGLP X85408 g1037170 Bacillus subtilis 1423 -11532372 219563 yyxd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:35853) (re:36296) (di:complement) BSUB0021 Z99124 g2636475 Bacillus subtilis 1423 -11532372 116854 yyxd:n17a (de:hypothetical 17.7 kd protein in hutp-bglp intergenic region (orf1)) (db:swissprot) YXXD\_BACSU P40737 BACILLUS SUBTILIS 1423 -11532372 206173 yyxd hypothetical protein yyxd (db:pir) S65579 S65579 Bacillus subtilis 1423 -11532372 215885 orf1 (fn:unknown) (db:genpept-bct1) (de:b.subtilllis dna for ribonucleic antiterminator and bglp gene.) (nt:putative protein of 147 aminoacids) (le:441) (re:884) (di:direct) BSRABGLP X85408 g1037170 Bacillus subtilis 1423 -11532372

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817543	6715	28871	633	210

Description

6500728515 j3d:yxid hypothetical protein:hypothetical 64.3 kd protein in hutp-bglp intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxiD yxiD Bacillus subtilis 1423 -11532373  
 116822 yxid:j3d (de:hypothetical 64.3 kd protein in hutp-bglp intergenic region) (db:swissprot) YXID\_BACSU P42296 BACILLUS SUBTILIS 1423 -11532373  
 7000688758 yxid hypothetical protein yxid (db:pir2.dat) H70076 H70076 Bacillus subtilis 1423 -11532373 215869 j3d hypothetical protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome containing the hut and wapa loci.) (le:10833) (re:12542) (di:direct) BACHUTWAPA D31856 g603775 Bacillus subtilis 1423 -11532373  
 7500953004 yxid (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:36293) (re:38002) (di:complement) BSUB0021 Z99124 g2636476 Bacillus subtilis 1423 -11532373 5000689820 (de:(yxid) (pn:hypothetical 64) (gn:j3d) (gtcfc:13.07) (ec:) (yxid\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxiD yxiD Bacillus subtilis 1423 10058547

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817555	6716	28872	669	223

Description

6500728516 j3c:yxic hypothetical protein:hypothetical 9.8 kd protein in hutp-bglp intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxiC yxiC Bacillus subtilis 1423 -11532374  
 116821 yxic:j3c (de:hypothetical 9.8 kd protein in hutp-bglp intergenic region) (db:swissprot) YXIC\_BACSU P42295 BACILLUS SUBTILIS 1423 -11532374  
 7000688757 yxic conserved hypothetical protein yxic (db:pir2.dat) G70076 G70076 Bacillus subtilis 1423 -11532374 215868 j3c hypothetical protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome containing the hut and wapa loci.) (le:10544) (re:10813) (di:direct) BACHUTWAPA D31856 g603774 Bacillus subtilis 1423 -11532374  
 7500953003 yxic (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins from b. subtilis) (le:38022) (re:38291) (di:complement) BSUB0021 Z99124 g2636477 Bacillus subtilis 1423 -11532374  
 5000689819 (de:(yxic) (pn:hypothetical 9) (gn:j3c) (gtcfc:13.07) (ec:) (yxic\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxiC yxiC Bacillus subtilis 1423 10058546

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817556	6717	28873	540	179

Description

GTC ORF with score 250 to: (sr:fruit fly) (db:genpept-inv) (de:drosophila melanogaster gp150 protein and putative type iii alcoholdehydrogenase (t3dh) genes, partial cds.) (nt:gene predicted by genefinder, no cdna clones) (le:1920:2976:3507) ...

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817557	6718	28874	768	256

Description

6500728517 j3b:yxib hypothetical protein:hypothetical 14.5 kd protein in hutp-bglp intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxiB yxiB Bacillus subtilis 1423 -11532375 116820 yxib:j3b (de:hypothetical 14.5 kd protein in hutp-bglp intergenic region) (db:swissprot) YXIB\_BACSU P42294 BACILLUS SUBTILIS 1423 -11532375 7000688756 yxib conserved hypothetical protein yxib (db:pir2.dat) F70076 F70076 Bacillus subtilis 1423 -11532375 215867 j3b hypothetical protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome containing the hut and wapa loci.) (le:10167) (re:10532) (di:direct) BACHUTWAPA D31856 g603773 Bacillus subtilis 1423 -11532375 7500953002 yxib (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins from b. subtilis) (le:38303) (re:38668) (di:complement) BSUB0021 Z99124 g2636478 Bacillus subtilis 1423 -11532375 5000689818 (de:(yxib) (pn:hypothetical 14) (gn:j3b) (gtcfc:13.07) (ec:) (yxib\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxiB yxiB Bacillus subtilis 1423 10058545

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817559	6719	28875	612	204

Description

6500728518 j3a:yxia hypothetical protein:hypothetical 52.5 kd protein in hutp-bglp intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxiA yxiA Bacillus subtilis 1423 -11532376 116819 yxia:j3a (de:hypothetical 52.5 kd protein in hutp-bglp intergenic region precursor) (db:swissprot) YXIA\_BACSU P42293 BACILLUS SUBTILIS 1423 -11532376 7000688755 yxia arabinan endo-1:5-alpha-l-arabinosidase homolog yxia:hypothetical protein hutp 5 region (db:pir2.dat) E70076 E70076 Bacillus subtilis 1423 -11532376 215866 j3a hypothetical protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome containing the hut and wapa loci.) (nt:homologous to endo-1,5-alpha-l-arabinase of) (le:8451) (re:9860) (di:direct) BACHUTWAPA D31856 g603772 Bacillus subtilis 1423 -11532376 7500953001 yxia (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to arabinan endo-1,5-alpha-l-arabinosidase) (le:38975) (re:40384) (di:complement) BSUB0021 Z99124 g2636479 Bacillus subtilis 1423 -11532376 5000689817 (de:(yxia) (pn:hypothetical 52) (gn:j3a) (gtcfc:13.07) (ec:)) (yxia\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxiA yxiA Bacillus subtilis 1423 10058544

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817571	6720	28876	657	218

Description

6500728519 lp6b:yxxb hypothetical protein:hypothetical 31.8 kd protein in deor 5'region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxxB yxxB Bacillus subtilis 1423 -11532377 116853 yxxb:lp6b (de:hypothetical 31.8 kd protein in deor 5'region) (db:swissprot) YXXB\_BACSU P39139 BACILLUS SUBTILIS 1423 -11532377 7000688784 yxxb yxxb protein (db:pir2.dat) G70082 G70082 Bacillus subtilis 1423 -11532377 222536 yxxb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:52922) (re:53791) (di:complement) BSUB0021 Z99124 g2636490 Bacillus subtilis 1423 -11532377 7500953009 yxxb (sr:bacillus subtilis (strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (le:17685) (re:18554) (di:direct) D45912 D45912 g1408504 Bacillus subtilis 1423 -11532377 5000689842 (de:(yxxb) (pn:hypothetical 31:hypothetical protein in dra 5"region:fragment) (gn:lp6b) (gtcfc:13.07) (ec:)) (yxxb\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxxB yxxB Bacillus subtilis 1423 10058578

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817572	6721	28877	369	122

Description

6500728520 lp6a:yxer hypothetical protein:hypothetical 38.4 kd protein in idh-deor intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxeR yxeR Bacillus subtilis 1423 -11532378 116816 yxeR:lp6a (de:hypothetical 38.4 kd protein in idh-deor intergenic region) (db:swissprot) YXER\_BACSU P54957 BACILLUS SUBTILIS 1423 -11532378 7000688754 yxeR ethanolamine transporter homolog yxeR (db:pir2.dat) D70076 D70076 Bacillus subtilis 1423 -11532378 222535 yxeR (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to ethanolamine transporter) (le:53864) (re:54976) (di:complement) BSUB0021 Z99124 g2636491 Bacillus subtilis 1423 -11532378 7500952998 yxeR (sr:bacillus subtilis (strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (le:16500) (re:17612) (di:direct) D45912 D45912 g1408503 Bacillus subtilis 1423 -11532378 5000689423 (de:(yxer) (pn:hypothetical 38) (gn:lp6a) (gtcfc:13.07) (ec:) (yxer\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yxeR yxeR Bacillus subtilis 1423 10058541

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817577	6722	28878	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817589	6723	28879	672	224

Description

GTC ORF with score 154 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome xii cosmid 8083.) (nt:similar to kluyveromyces lactis deoxyribonucleic) (le:23775) (re:26219) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817591	6724	28880	777	258

Description

6500728521 lp9i:yxex hypothetical protein:hypothetical 47.8 kd protein in idh-deor intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxex yxex Bacillus subtilis 1423 -11532379 116815 yxex:lp9i (de:hypothetical 47.8 kd protein in idh-deor intergenic region) (db:swissprot) YXEX\_BACSU P54956 BACILLUS SUBTILIS 1423 -11532379 7000688753 yxex hypothetical protein yxex (db:pir2.dat) C70076 C70076 Bacillus subtilis 1423 -11532379 222534 yxex (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:55046) (re:56383) (di:complement) BSUB0021 Z99124 g2636492 Bacillus subtilis 1423 -11532379 7500952997 yxex (sr:bacillus subtilis (strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (le:15093) (re:16430) (di:direct) D45912 D45912 g1408502 Bacillus subtilis 1423 -11532379 5000689422 (de:(yxex) (pn:hypothetical 47) (gn:lp9i) (gtcfc:13.07) (ec:) (yxex\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yxex yxex Bacillus subtilis 1423 10058540

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817592	6725	28881	201	66

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817596	6726	28882	510	169

Description

6500728522 lp9h:yxep hypothetical protein:hypothetical 41.6 kd protein in idh-deor intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxep yxep Bacillus subtilis 1423 -11532380 116814 yxep:lp9h (de:hypothetical 41.6 kd protein in idh-deor intergenic region) (db:swissprot) YXEP\_BACSU P54955 BACILLUS SUBTILIS 1423 -11532380 7000688752 yxep aminoacylase homolog yxep (cl:hippurate hydrolase) (db:pir2.dat) B70076 Bacillus subtilis 1423 -11532380 222533 yxep (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to aminoacylase) (le:56380) (re:57522) (di:complement) BSUB0021 Z99124 g2636493 Bacillus subtilis 1423 -11532380 7500952996 yxep (sr:bacillus subtilis (strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (nt:homologous to n-acyl-l-amino acid amidohydrolase of) (le:13954) (re:... D45912 D45912 g1408501 Bacillus subtilis 1423 -11532380 5000689421 (de:(yxep) (pn:hypothetical 41) (gn:lp9h) (gtcfc:13.07) (ec:) (yxep\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yxep yxep Bacillus subtilis 1423 10058539

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817597	6727	28883	486	161

Description

6500728523 lp9g:yxeo hypothetical protein:probable amino-acid abc transporter atp-binding protein in idh-deor intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxeO yxeO Bacillus subtilis 1423 -11532381 116813 yxeo:lp9g (de:intergenic region) (db:swissprot) YXEO\_BACSU P54954 BACILLUS SUBTILIS 1423 -11532381 7000688751 yxeo abc-type transport protein yxeo (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) A70076 Bacillus subtilis 1423 -11532381 222532 yxeo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to amino acid abc transporter (atp-binding) (le:57539) (re:58288) (di:complement) BSUB0021 Z99124 g2636494 Bacillus subtilis 1423 -11532381 7500952995 yxeo (sr:bacillus subtilis (strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (nt:homologous to glng glutamine transport atp-binding) (le:13188) (re:1... D45912 D45912 g1408500 Bacillus subtilis 1423 -11532381 5000689420 (de:(yxeo) (pn:probable amino-acid abc transporter atp-binding protein in idh- deor intergenic region) (gn:lp9g) (gtcfc:13.07) (ec:) (yxeo\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yxeO yxeO Bacillus subtilis 1423 10058538

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817601	6728	28884	813	270

Description

6500728524 lp9f:yxen hypothetical protein:probable amino-acid abc transporter permease protein in idh-deor intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxeN yxeN Bacillus subtilis 1423 -11532382 116812 yxen:lp9f (de:intergenic region) (db:swissprot) YXEN\_BACSU P54953 BACILLUS SUBTILIS 1423 -11532382 7000688750 yxen amino acid abc transporter permease homolog yxen (cl:histidine permease protein m) (db:pir2.dat) H70075 H70075 Bacillus subtilis 1423 -11532382 222531 yxen (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to amino acid abc transporter (permease)) (le:58301) (re:58975) (di:complement) BSUB0021 Z99124 g2636495 Bacillus subtilis 1423 -11532382 7500952994 yxen (sr:bacillus subtilis (strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (nt:homologous to gln transport system permease) (le:12501) (re:13175) (... D45912 D45912 g1408499 Bacillus subtilis 1423 -11532382 5000689419 (de:(yxen) (pn:probable amino-acid abc transporter permease protein in idh-deor intergenic region) (gn:lp9f) (gtcfc:13.07) (ec:) (yxen\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yxeN yxeN Bacillus subtilis 1423 10058537

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817629	6729	28885	276	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817630	6730	28886	393	130

Description

6500728525 lp9e:yxem hypothetical protein:probable amino-acid abc transporter binding protein in idh-deor intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxeM yxeM Bacillus subtilis 1423 -11532383 116811 yxem:lp9e (de:intergenic region precursor) (db:swissprot) YXEM\_BACSU P54952 BACILLUS SUBTILIS 1423 -11532383 7000688749 yxem amino acid abc transporter binding protei homolog yxem (cl:lysine-arginine-ornithine-binding protein) (db:pir2.dat) G70075 G70075 Bacillus subtilis 1423 -11532383 222530 yxem (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to amino acid abc transporter (binding) (le:58998) (re:59792) (di:complement) BSUB0021 Z99124 g2636496 Bacillus subtilis 1423 -11532383 7500952993 yxem (sr:bacillus subtilis (strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (nt:homologous to gln-binding periplasmic proteins) (le:11684) (re:12478... D45912 D45912 g1408498 Bacillus subtilis 1423 -11532383 5000689418 (de:(yxem) (pn:probable amino-acid abc transporter binding protein in idh-deor intergenic region precursor) (gn:lp9e) (gtcfc:13.07) (ec:) (yxem\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yxeM yxeM Bacillus subtilis 1423 10058536

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817631	6731	28887	294	97

Description

6500728526 lp9d:yxel hypothetical protein:hypothetical 19.0 kd protein in idh-deor intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxeL yxeL Bacillus subtilis 1423 -11532384 116810 yxel:lp9d (de:hypothetical 19.0 kd protein in idh-deor intergenic region) (db:swissprot) YXEL\_BACSU P54951 BACILLUS SUBTILIS 1423 -11532384 7000688748 yxel conserved hypothetical protein yxel (db:pir2.dat) F70075 F70075 Bacillus subtilis 1423 -11532384 222529 yxel (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins from b. subtilis) (le:59817) (re:60314) (di:complement) BSUB0021 Z99124 g2636497 Bacillus subtilis 1423 -11532384 7500952992 yxel (sr:bacillus subtilis (strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (le:11162) (re:11659) (di:direct) D45912 D45912 g1408497 Bacillus subtilis 1423 -11532384 5000689417 (de:(yxel) (pn:hypothetical 19) (gn:lp9d) (gtcfc:13.07) (ec:) (yxel\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yxeL yxeL Bacillus subtilis 1423 10058535

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817635	6732	28888	522	173

Description

6500728527 lp9c:yxeK hypothetical protein:hypothetical 49.3 kd protein in idh-deor intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxeK yxeK Bacillus subtilis 1423 -11532385  
 116809 yxeK:lp9c (de:hypothetical 49.3 kd protein in idh-deor intergenic region) (db:swissprot) YXEK\_BACSU P54950 BACILLUS SUBTILIS 1423 -11532385  
 7000688747 yxeK monooxygenase homolog yxeK (cl:nitrilotriacetate monooxygenase) (db:pir2.dat) E70075 E70075 Bacillus subtilis 1423 -11532385  
 222528 yxeK (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to monooxygenase) (le:60328) (re:61653) (di:complement) BSUB0021 Z99124 g2636498 Bacillus subtilis 1423 -11532385 7500952991 yxeK (sr:bacillus subtilis (strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (nt:homologous to dsza gene product of rhodococcus sp.) (le:9823) (re:11... D45912 D45912 g1408496 Bacillus subtilis 1423 -11532385 5000689416 (de:(yxeK) (pn:hypothetical 49) (gn:lp9c) (gtcfc:13.07) (ec:)(yxeK\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yxeK yxeK Bacillus subtilis 1423 10058534

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817636	6733	28889	399	132

Description

6500728528 lp9b:yxeJ hypothetical protein:hypothetical 8.4 kd protein in idh-deor intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxeJ yxeJ Bacillus subtilis 1423 -11532386  
 116808 yxeJ:lp9b (de:hypothetical 8.4 kd protein in idh-deor intergenic region) (db:swissprot) YXEJ\_BACSU P54949 BACILLUS SUBTILIS 1423 -11532386  
 7000688746 yxeJ hypothetical protein yxeJ (db:pir2.dat) D70075 D70075 Bacillus subtilis 1423 -11532386 222527 yxeJ (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:61839) (re:62066) (di:complement) BSUB0021 Z99124 g2636499 Bacillus subtilis 1423 -11532386 7500952990 yxeJ (sr:bacillus subtilis (strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (le:9410) (re:9637) (di:direct) D45912 D45912 g1408495 Bacillus subtilis 1423 -11532386 5000689415 (de:(yxeJ) (pn:hypothetical 8) (gn:lp9b) (gtcfc:13.07) (ec:)(yxeJ\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yxeJ yxeJ Bacillus subtilis 1423 10058533

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817637	6734	28890	231	76

Description

6500728529 lp9a:yxai hypothetical protein:hypothetical 37.2 kd protein in idh-deor intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxeI yxeI Bacillus subtilis 1423 -11532387  
 116807 yxai:lp9a (de:hypothetical 37.2 kd protein in idh-deor intergenic region) (db:swissprot) YXEI\_BACSU P54948 BACILLUS SUBTILIS 1423 -11532387  
 7000688745 yxai penicillin amidase homolog yxai (cl:choloylglycine hydrolase) (db:pir2.dat) C70075 C70075 Bacillus subtilis 1423 -11532387  
 222526 yxai (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to penicillin amidase) (le:62053) (re:63039) (di:complement) BSUB0021 Z99124 g2636500 Bacillus subtilis 1423 -11532387 7500952989 yxai (sr:bacillus subtilis (strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (nt:homologous to penicillin acylase) (le:8437) (re:9423) (di:direct) D45912 D45912 g1408494 Bacillus subtilis 1423 -11532387  
 5000689414 (de:(yxai) (pn:hypothetical 37) (gn:lp9a) (gtcfc:13.07) (ec:)(yxai\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yxeI yxeI Bacillus subtilis 1423 10058532

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817638	6735	28891	525	174

Description

6500728530 ip1b:yxeh hypothetical protein:hypothetical 30.2 kd protein in idh-deor intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxeH yxeH Bacillus subtilis 1423 -11532388  
 116806 yxeh:ip1b (de:hypothetical 30.2 kd protein in idh-deor intergenic region) (db:swissprot) YXEH\_BACSU P54947 BACILLUS SUBTILIS 1423 -11532388  
 7000688744 yxeh conserved hypothetical protein yxeh (cl:methanobacterium thermoautotrophicum conserved hypothetical protein mth1071) (db:pir2.dat) B70075 B70075 Bacillus subtilis 1423 -11532388 222525 yxeh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:63194) (re:64006) (di:complement) BSUB0021 Z99124 g2636501 Bacillus subtilis 1423 -11532388 7500952988 yxeh (sr:bacillus subtilis (strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (nt:homologous to swissprot:yida\_ecoli hypothetical) (le:7470) (re:8282)... D45912 D45912 g1408493 Bacillus subtilis 1423 -11532388 5000689413 (de:(yxeh) (pn:hypothetical 30) (gn:ip1b) (gtcfc:13.07) (ec:)(yxeh\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yxeH yxeH Bacillus subtilis 1423 10058531

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817639	6736	28892	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817640	6737	28893	327	108

Description

6500728531 ip1a:yxeg hypothetical protein:hypothetical 21.4 kd protein in idh-deor intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxeG yxeG Bacillus subtilis 1423 -11532389 116805 yxeg:ip1a (de:hypothetical 21.4 kd protein in idh-deor intergenic region) (db:swissprot) YXEG\_BACSU P54946 BACILLUS SUBTILIS 1423 -11532389 7000688743 yxeg hypothetical protein yxeg (db:pir2.dat) A70075 A70075 Bacillus subtilis 1423 -11532389 222524 yxeg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:64046) (re:64603) (di:complement) BSUB0021 Z99124 g2636502 Bacillus subtilis 1423 -11532389 7500952987 yxeg (sr:bacillus subtilis (strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (le:6873) (re:7430) (di:direct) D45912 D45912 g1408492 Bacillus subtilis 1423 -11532389 5000689412 (de:(yxeg) (pn:hypothetical 21) (gn:ip1a) (gtcfc:13.07) (ec:) (yxeg\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yxeG yxeG Bacillus subtilis 1423 10058530

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817661	6738	28894	582	193

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817677	6739	28895	1125	374

Description

6500728532 hs74f:yxef hypothetical protein:hypothetical 16.3 kd protein in idh-deor intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxeF yxeF Bacillus subtilis 1423 -11532390 116804 yxef:hs74f (de:hypothetical 16.3 kd protein in idh-deor intergenic region precursor) (db:swissprot) YXEF\_BACSU P54945 BACILLUS SUBTILIS 1423 -11532390 7000688742 yxef hypothetical protein yxef (db:pir2.dat) H70074 H70074 Bacillus subtilis 1423 -11532390 222523 yxef (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:64584) (re:65018) (di:complement) BSUB0021 Z99124 g2636503 Bacillus subtilis 1423 -11532390 7500952986 yxef (sr:bacillus subtilis (strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (le:6458) (re:6892) (di:direct) D45912 D45912 g1408491 Bacillus subtilis 1423 -11532390 5000689411 (de:(yxef) (pn:hypothetical 16) (gn:hs74f) (gtcfc:13.07) (ec:) (yxef\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yxeF yxeF Bacillus subtilis 1423 10058529

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817688	6740	28896	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817707	6741	28897	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817715	6742	28898	1992	663

Description

6500728533 hs74er:yxee hypothetical protein:hypothetical 14.7 kd protein in idh-deor intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxeE yxeE Bacillus subtilis 1423 -11532391 116803 yxee:hs74er (de:hypothetical 14.7 kd protein in idh-deor intergenic region) (db:swissprot) YXEE\_BACSU P54944 BACILLUS SUBTILIS 1423 -11532391 7000688741 yxee hypothetical protein yxee (db:pir2.dat) G70074 G70074 Bacillus subtilis 1423 -11532391 222522 yxee (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:65106) (re:65471) (di:direct) BSUB0021 Z99124 g2636504 Bacillus subtilis 1423 -11532391 7500952985 yxee (sr:bacillus subtilis (strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (le:6005) (re:6370) (di:complement) D45912 D45912 g1408490 Bacillus subtilis 1423 -11532391 5000689410 (de:(yxee) (pn:hypothetical 14) (gn:hs74er) (gtcfc:13.07) (ec:) (yxee\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yxeE yxeE Bacillus subtilis 1423 10058528

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817726	6743	28899	549	183

Description

6500728534 hs74dr:yxed hypothetical protein:hypothetical 13.6 kd protein in idh-deor intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxeD yxeD Bacillus subtilis 1423 -11532392 116802 yxed:hs74dr (de:hypothetical 13.6 kd protein in idh-deor intergenic region) (db:swissprot) YXED\_BACSU P54943 BACILLUS SUBTILIS 1423 -11532392 7000688740 yxed hypothetical protein yxed (db:pir2.dat) F70074 F70074 Bacillus subtilis 1423 -11532392 222521 yxed (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:65719) (re:66072) (di:direct) BSUB0021 Z99124 g2636505 Bacillus subtilis 1423 -11532392 7500952984 yxed (sr:bacillus subtilis (strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (nt:gln rich protein) (le:5404) (re:5757) (di:complement) D45912 D45912 g1408489 Bacillus subtilis 1423 -11532392 5000689409 (de:(yxed) (pn:hypothetical 13) (gn:hs74dr) (gtcfc:13.07) (ec:) (yxed\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yxeD yxeD Bacillus subtilis 1423 10058527



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817736	6744	28900	768	255

Description

6500728535 hs74c:yxec hypothetical protein:hypothetical 15.7 kd protein in idh-deor intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxeC yxeC Bacillus subtilis 1423 -11532393 116801 yxec:hs74c (de:hypothetical 15.7 kd protein in idh-deor intergenic region) (db:swissprot) YXEC\_BACSU P54942 BACILLUS SUBTILIS 1423 -11532393 7000688739 yxec hypothetical protein yxec (db:pir2.dat) E70074 E70074 Bacillus subtilis 1423 -11532393 222520 yxec (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:66116) (re:66514) (di:complement) BSUB0021 Z99124 g2636506 Bacillus subtilis 1423 -11532393 7500952983 yxec (sr:bacillus subtilis (strain:bgsc 1al (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (le:4962) (re:5360) (di:direct) D45912 D45912 g1408488 Bacillus subtilis 1423 -11532393 5000689408 (de:(yxec) (pn:hypothetical 15) (gn:hs74c) (gtcfc:13.07) (ec:) (yxec\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yxeC yxeC Bacillus subtilis 1423 10058526

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817737	6745	28901	846	281

Description

6500728536 hs74br:yxeb hypothetical protein:probable abc transporter binding protein in idh-deor intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxeB yxeB Bacillus subtilis 1423 -11532394 116800 yxeb:hs74br (de:precursor) (db:swissprot) YXEB\_BACSU P54941 BACILLUS SUBTILIS 1423 -11532394 7000688738 yxeb abc transporter binding protein homolog yxeb (cl:bacillus subtilis ferrichrome abc transporter fhud) (db:pir2.dat) D70074 D70074 Bacillus subtilis 1423 -11532394 222519 yxeb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to abc transporter (binding protein)) (le:66692) (re:67651) (di:direct) BSUB0021 Z99124 g2636507 Bacillus subtilis 1423 -11532394 7500952982 yxeb (sr:bacillus subtilis (strain:bgsc 1al (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (nt:homologous to fhud protein of bacillus subtilis) (le:3825) (re:4784)... D45912 D45912 g1408487 Bacillus subtilis 1423 -11532394 5000689407 (de:(yxeb) (pn:probable abc transporter binding protein in idh-deor intergenic region precursor) (gn:hs74br) (gtcfc:13.07) (ec:) (yxeb\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yxeB yxeB Bacillus subtilis 1423 10058525

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817757	6746	28902	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817763	6747	28903	1104	368

Description

6500728537 hs74a:yxea hypothetical protein:hypothetical 13.0 kd protein in idh-deor intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxeA yxeA Bacillus subtilis 1423 -11532395 116799 yxea:hs74a (de:hypothetical 13.0 kd protein in idh-deor intergenic region precursor) (db:swissprot) YXEA BACSU P54940 BACILLUS SUBTILIS 1423 -11532395 7000688737 yxea hypothetical protein yxea (db:pir2.dat) C70074 C70074 Bacillus subtilis 1423 -11532395 222518 yxea (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:67698) (re:68045) (di:complement) BSUB0021 Z99124 g2636508 Bacillus subtilis 1423 -11532395 7500952981 yxea (sr:bacillus subtilis (strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (le:3431) (re:3778) (di:direct) D45912 D45912 g1408486 Bacillus subtilis 1423 -11532395 5000689406 (de:(yxea) (pn:hypothetical 13) (gn:hs74a) (gtcfc:13.07) (ec:)(yxea\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yxeA yxeA Bacillus subtilis 1423 10058524

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817776	6748	28904	960	319

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817787	6749	28905	870	289

Description

6500728538 b65g:yxdm hypothetical protein:hypothetical 70.5 kd protein in idh 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxdm yxdm Bacillus subtilis 1423 -11532396 116798 yxdm:b65g (de:hypothetical 70.5 kd protein in idh 3'region) (db:swissprot) YXDM\_BACSU P42424 BACILLUS SUBTILIS 1423 -11532396 7000688736 yxdm abc transporter permease homolog yxdm (db:pir2.dat) B70074 B70074 Bacillus subtilis 1423 -11532396 222517 yxdm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to abc transporter (permease)) (le:68059) (re:69927) (di:complement) BSUB0021 Z99124 g2636509 Bacillus subtilis 1423 -11532396 7500952980 yxdm (sr:bacillus subtilis (strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (le:1549) (re:3417) (di:direct) D45912 D45912 g1408485 Bacillus subtilis 1423 -11532396 5000689816 (de:(yxdm) (pn:hypothetical 70:hypothetical protein in idh 3"region:fragment) (gn:b65g) (gtcfc:13.07) (ec:) (yxdm\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxdm yxdm Bacillus subtilis 1423 10058523

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817789	6750	28906	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817825	6751	28907	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817827	6752	28908	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817830	6753	28909	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817831	6754	28910	297	98

Description

6500728539 b65f:yxdL hypothetical protein:hypothetical abc transporter  
atp-binding protein in idh 3region (gtcfc:14.1) (keggfc:14.2)  
(bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxdL yxdL Bacillus subtilis 1423  
-11532397 116797 yxdL:b65f (de:hypothetical abc transporter atp-binding  
protein in idh 3'region) (db:swissprot) YXDL\_BACSU P42423 BACILLUS SUBTILIS  
1423 -11532397 7000688735 yxdL abc transporter atp-binding protein homolog  
yxdL (cl:atp-binding cassette homology) (db:pir2.dat) A70074 A70074 Bacillus  
subtilis 1423 -11532397 215922 b65f hypothetical protein (sr:bacillus  
subtilis (strain:bgsc 1a1 (168 trpc2)) dna) (db:genpept-bct1) (de:bacillus  
subtilis 15 kb chromosome segment contains the iol operon.) (nt:homologous  
to cell division protein ftse of e.) (le:13014) (re:13787) (di:direct)  
BACIOLO D14399 g709993 Bacillus subtilis 1423 -11532397 222516 yxdL  
(fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome  
(section 21 of 21): from 3999281to 4214814.) (nt:similar to abc transporter  
(atp-binding protein)) (le:69902) (re:70675) (di:complement) BSUB0021 Z99124  
g2636510 Bacillus subtilis 1423 -11532397 303054 yxdL (sr:bacillus subtilis  
(strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus  
subtilis genome sequence between the iol and hut operon,partial and complete  
cds.) (nt:homologous to ftse protein of e. coli, belonging to) (le:801)  
(re:15... D45912 D45912 g1408484 Bacillus subtilis 1423 -11532397  
5000688781 (de:(yxdL) (pn:hypothetical abc transporter atp-binding protein  
in idh 3"region:hypothetical abc transporter in idh 3"region) (gn:b65f)  
(gtcfc:12.01:12.02:12.03) (ec:) (yxdL\_bacsu) (keggfc:11.2) (bsorffc:1.0.0)  
(db:gtc-bacillus) yxdL yxdL Bacillus subtilis 1423 10058522

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817833	6755	28911	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817836	6756	28912	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817852	6757	28913	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817853	6758	28914	264	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817854	6759	28915	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817865	6760	28916	366	121

Description

GTC ORF with score 204 to: (gtcfc:2.1:12.13:12.16:12.5:12.6) (ec:3.6.1.34) (keggfc:2.1) (sgdfc:1.8.2:7.2.2:7.8.0:8.5.0:9.10.0) (db:gtc-saccharomyces cerevisiae) (gtcfc:energy metabolism-oxidative phosphorylation:cell processes-metabolic regulators ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817868	6761	28917	396	131

Description

GTC ORF with score 192 to: (sr:neurospora crassa (strain 74a) dna) (db:genpept-pln1) (de:neurospora crassa proteolipid subunit of vacuolar atpase (vma3)gene, complete cds.) (le:800:1036:1182:1392:1713) (re:813:1048:1311:1655:1777) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817899	6762	28918	252	83

Description

6500728540 b65e:yxdk hypothetical protein:hypothetical sensor-like histidine kinase in idh 3region (gtcfc:14.1) (ec:2.7.3.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxdK yxdK Bacillus subtilis 1423 -11532398 116796 yxdk:b65e (ec:2.7.3.-) (de:(ec 2.7.3.-)) (db:swissprot) YXDK\_BACSU P42422 BACILLUS SUBTILIS 1423 -11532398 7000688734 yxdk two-component sensor histidine kinase homolog yxdk (db:pir2.dat) H70073 H70073 Bacillus subtilis 1423 -11532398 215921 b65e hypothetical protein (sr:bacillus subtilis (strain:bgsc 1a1 (168 trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis 15 kb chromosome segment contains the iol operon.) (nt:homologous to sensor protein bvgc, his protein) (le:11893) (re:12870) (di:direct) BACIOLO D14399 g709992 Bacillus subtilis 1423 -11532398 303053 yxdk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to two-component sensor histidine kinase) (le:70819) (re:71796) (di:complement) BSUB0021 Z99124 g2636511 Bacillus subtilis 1423 -11532398 5000688861 (de:(yxdk) (pn:hypothetical sensor-like histidine kinase in idh 3"region) (gn:b65e) (gtcfc:12.13) (ec:2.7.3.-) (yxdk\_bacsu) (keggfc:11.1) (bsorffc:6.1.2) (db:gtc-bacillus subtilis)) yxdK yxdK Bacillus subtilis 1423 10058521

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817906	6763	28919	1512	504

Description

GTC ORF with score 173 to: (sr:fruit fly) (db:genpept-inv) (de:drosophila melanogaster rga and atu genes, complete cds.) (nt:contains arg-ser and ser-arg dipeptides; c-terminal) (le:78:1474:2325) (re:1373:2260:2388) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817925	6764	28920	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817926	6765	28921	237	78

Description

6500728541 b65d:yxdj hypothetical protein:hypothetical 26.6 kd sensory transduction protein in idh 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxdJ yxdJ Bacillus subtilis 1423 -11532399 116795 yxdj:b65d (de:hypothetical 26.6 kd sensory transduction protein in idh 3'region) (db:swissprot) YXDJ\_BACSU P42421 BACILLUS SUBTILIS 1423 -11532399 7000688733 yxdj two-component response regulator yxdk homolog yxdj) (cl:ompr protein:response regulator homology) (db:pir2.dat) G70073 G70073 Bacillus subtilis 1423 -11532399 215920 b65d hypothetical protein (sr:bacillus subtilis (strain:bgsc 1a1 (168 trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis 15 kb chromosome segment contains the iol operon.) (nt:homologous to phosphate regulon regulatory protein) (le:11207) (re:11896) (di:direct) BACIOLO D14399 g709991 Bacillus subtilis 1423 -11532399 303052 yxdj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to two-component response regulator (yxdk)) (le:71793) (re:72482) (di:complement) BSUB0021 Z99124 g2636512 Bacillus subtilis 1423 -11532399 5000688860 (de:(yxdj) (pn:hypothetical 26) (gn:b65d) (gtcfc:12.13) (ec:) (yxdj\_bacsu) (keggfc:11.2) (bsorffc:6.1.2) (db:gtc-bacillus subtilis)) yxdJ yxdJ Bacillus subtilis 1423 10058520

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817927	6766	28922	255	84

Description

5000689815 yxdh:b65b:ioli hypothetical protein:hypothetical 31.7 kd protein in idh 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) iolI iolI Bacillus subtilis 1423 -11532400 116794 ioli:b65b (de:ioli protein) (db:swissprot) IOLI\_BACSU P42419 BACILLUS SUBTILIS 1423 -11532400 7000688732 ioli myo-inositol catabolism ioli (db:pir2.dat) A69646 A69646 Bacillus subtilis 1423 -11532400 215918 b65b hypothetical protein (sr:bacillus subtilis (strain:bgsc 1a1 (168 trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis 15 kb chromosome segment contains the iol operon.) (le:9369) (re:10205) (di:direct) BACIOLO D14399 g709989 Bacillus subtilis 1423 -11532400 303050 ioli (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yxdh; myo-inositol catabolism) (le:73484) (re:74320) (di:complement) BSUB0021 Z99124 g2636514 Bacillus subtilis 1423 -11532400 6500728542 yxdh:b65b hypothetical protein:hypothetical 31.7 kd protein in idh 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) iolI iolI Bacillus subtilis 1423 -11532400

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817928	6767	28923	549	182

Description

5000689814 yxdg:b65a:iolh hypothetical protein:hypothetical 33.5 kd protein in idh 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) iolH iolH Bacillus subtilis 1423 -11532401 116793 yxdg:b65a (de:hypothetical 33.5 kd protein in idh 3'region) (db:swissprot) YXDG\_BACSU P42418 BACILLUS SUBTILIS 1423 -11532401 7000688731 iolh myo-inositol catabolism iolh (db:pir2.dat) H69645 H69645 Bacillus subtilis 1423 -11532401 215917 b65a hypothetical protein (sr:bacillus subtilis (strain:bgsc 1a1 (168 trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis 15 kb chromosome segment contains the iol operon.) (le:8414) (re:9283) (di:direct) BACIOLO D14399 g709988 Bacillus subtilis 1423 -11532401 303049 iolh (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yxdg; myo-inositol catabolism) (le:74406) (re:75275) (di:complement) BSUB0021 Z99124 g2636515 Bacillus subtilis 1423 -11532401 6500728543 yxdg:b65a hypothetical protein:hypothetical 33.5 kd protein in idh 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) iolH iolH Bacillus subtilis 1423 -11532401

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501817938	6768	28924	891	296

Description

5000689813 yxde:e83e:iole hypothetical protein:hypothetical 33.6 kd protein in idh 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) iolE iolE Bacillus subtilis 1423 -11532402 116791 iole:e83e (de:iole protein) (db:swissprot) IOLE\_BACSU P42416 BACILLUS SUBTILIS 1423 -11532402 7000688729 iole myo-inositol catabolism iole (cl:rhizobium meliloti mocc protein) (db:pir2.dat) E69645 E69645 Bacillus subtilis 1423 -11532402 215914 e83e hypothetical protein (sr:bacillus subtilis (strain:bgsc 1a1 (168 trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis 15 kb chromosome segment contains the iol operon.) (le:5110) (re:6003) (di:direct) BACIOLO D14399 g709985 Bacillus subtilis 1423 -11532402 303046 iole (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yxde; myo-inositol catabolism) (le:77686) (re:78579) (di:complement) BSUB0021 Z99124 g2636518 Bacillus subtilis 1423 -11532402 6500728544 yxde:e83e hypothetical protein:hypothetical 33.6 kd protein in idh 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) iole iole Bacillus subtilis 1423 -11532402



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817961	6769	28925	396	131

Description

5000689812 yxdd:e83d:iold hypothetical protein:hypothetical 64.1 kd protein in idh 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) iold iold Bacillus subtilis 1423 -11532403 116790 iold:e83d (de:iold protein) (db:swissprot) IOLD\_BACSU P42415 BACILLUS SUBTILIS 1423 -11532403 7000688728 iold myo-inositol catabolism iold (db:pir2.dat) D69645 D69645 Bacillus subtilis 1423 -11532403 215913 e83d hypothetical protein (sr:bacillus subtilis (strain:bgsc 1al (168 trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis 15 kb chromosome segment contains the iol operon.) (nt:homologous to acetolactate synthases) (le:3351) (re:5093) (di:direct) BACIOLO D14399 g709984 Bacillus subtilis 1423 -11532403 303045 iold (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yxdd; myo-inositol catabolism) (le:78596) (re:80338) (di:complement) BSUB0021 Z99124 g2636519 Bacillus subtilis 1423 -11532403 6500728545 yxdd:e83d hypothetical protein:hypothetical 64.1 kd protein in idh 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) iold iold Bacillus subtilis 1423 -11532403

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817965	6770	28926	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817967	6771	28927	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501817968	6772	28928	207	68

#### Description

5000689811 yxdc:e83c:iolc hypothetical protein:hypothetical 35.6 kd protein in idh 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) iolC iolC Bacillus subtilis 1423 -11532404 116789 iolc:e83c (de:iolc protein) (db:swissprot) IOLC\_BACSU P42414 BACILLUS SUBTILIS 1423 -11532404 7000688727 iolc myo-inositol catabolism iolc (db:pir2.dat) C69645 C69645 Bacillus subtilis 1423 -11532404 215912 e83c hypothetical protein (sr:bacillus subtilis (strain:bgsc 1a1 (168 trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis 15 kb chromosome segment contains the iol operon.) (nt:homologous to fructokinases) (le:2170) (re:3147) (di:direct) BACIOLO D14399 g709983 Bacillus subtilis 1423 -11532404 303044 iolc (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yxdc; myo-inositol catabolism) (le:80542) (re:81519) (di:complement) BSUB0021 Z99124 g2636520 Bacillus subtilis 1423 -11532404 6500728546 yxdc:e83c hypothetical protein:hypothetical 35.6 kd protein in idh 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) iolC iolC Bacillus subtilis 1423 -11532404

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501817972	6773	28929	375	124

#### Description

5000689810 yxdb:e83b:iolb hypothetical protein:hypothetical 30.8 kd protein in idh 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) iolB iolB Bacillus subtilis 1423 -11532405 116788 iolb:e83b (de:iolb protein) (db:swissprot) IOLB\_BACSU P42413 BACILLUS SUBTILIS 1423 -11532405 7000688726 iolb myo-inositol catabolism iolb (db:pir2.dat) B69645 B69645 Bacillus subtilis 1423 -11532405 215911 e83b hypothetical protein (sr:bacillus subtilis (strain:bgsc 1a1 (168 trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis 15 kb chromosome segment contains the iol operon.) (le:1331) (re:2146) (di:direct) BACIOLO D14399 g709982 Bacillus subtilis 1423 -11532405 303043 iolb (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yxdb; myo-inositol catabolism) (le:81543) (re:82358) (di:complement) BSUB0021 Z99124 g2636521 Bacillus subtilis 1423 -11532405 6500728547 yxdb:e83b hypothetical protein:hypothetical 30.8 kd protein in idh 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) iolB iolB Bacillus subtilis 1423 -11532405

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501817995	6774	28930	363	120

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501817998	6775	28931	201	66

Description

6500728548 yxbf:ss92er:iols hypothetical protein:iols protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) iols iols Bacillus subtilis 1423 -11532406 79609 iols:ss92er (de:iols protein (vegetative protein 147) (veg147)) (db:swissprot) IOLS\_BACSU P46336 BACILLUS SUBTILIS 1423 -11532406 7000685640 iols myo-inositol catabolism iols (cl:conserved hypothetical protein ypl088w) (db:pir2.dat) D69646 D69646 Bacillus subtilis 1423 -11532406 215756 iols (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:plausibly involved in inositol catabolism) (le:32539) (re:33471) (di:complement) AB005554 AB005554 g904205 Bacillus subtilis 1423 -11532406 7500884197 iols (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yxbf; myo-inositol catabolism) (le:85121) (re:86053) (di:direct) BSUB0021 Z99124 g2636524 Bacillus subtilis 1423 -11532406 5000689088 (de:(iols) (pn:iols protein) (gn:ss92er) (gtcfc:13.07) (ec:) (iols\_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) iols iols Bacillus subtilis 1423 10021924

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818003	6776	28932	504	167

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818007	6777	28933	705	234

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818012	6778	28934	237	78

Description

5000689809 yxbe:ss92dr:yxce hypothetical protein:hypothetical 23.1 kd protein in htpg-iolr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxcE yxcE Bacillus subtilis 1423 -11532407 116784 yxbe:ss92dr (de:hypothetical 23.1 kd protein in htpg-iolr intergenic region) (db:swissprot) YXBE\_BACSU P46335 BACILLUS SUBTILIS 1423 -11532407 7000688725 yxce hypothetical protein yxce (db:pir2.dat) F70073 F70073 Bacillus subtilis 1423 -11532407 215755 yxce (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (le:31627) (re:32277) (di:complement) AB005554 AB005554 g904204 Bacillus subtilis 1423 -11532407 7500952977 yxce (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:86315) (re:86965) (di:direct) BSUB0021 Z99124 g2636525 Bacillus subtilis 1423 -11532407 6500728549 yxbe:ss92dr hypothetical protein:hypothetical 23.1 kd protein in htpg-iolr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxcE yxcE Bacillus subtilis 1423 -11532407

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818013	6779	28935	237	78

Description

5000689808 yxbd:ss92cr:yxcd hypothetical protein:hypothetical 11.9 kd protein in htpg-iolr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxcD yxcD Bacillus subtilis 1423 -11532408 116783 yxbd:ss92cr (de:hypothetical 11.9 kd protein in htpg-iolr intergenic region) (db:swissprot) YXBD\_BACSU P46334 BACILLUS SUBTILIS 1423 -11532408 7000688724 yxcd hypothetical protein yxcd (db:pir2.dat) E70073 E70073 Bacillus subtilis 1423 -11532408 215754 yxcd (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (le:31315) (re:31623) (di:complement) AB005554 AB005554 g904203 Bacillus subtilis 1423 -11532408 7500952976 yxcd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:86969) (re:87277) (di:direct) BSUB0021 Z99124 g2636526 Bacillus subtilis 1423 -11532408 6500728550 yxbd:ss92cr hypothetical protein:hypothetical 11.9 kd protein in htpg-iolr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxcD yxcD Bacillus subtilis 1423 -11532408

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818018	6780	28936	204	67

Description

6500728551 hypothetical protein:similar to metabolite transport protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxC Bacillus subtilis 1423 -11532409 7000694207 yxcc metabolite transport protein homolog yxcc (cl:glucose transport protein) (db:pir2.dat) D70073 D70073 Bacillus subtilis 1423 -11532409 7500964934 yxcc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to metabolite transport protein) (le:87516) (re:88901) (di:direct) BSUB0021 Z99124 g2636527 Bacillus subtilis 1423 -11532409

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818020	6781	28937	315	104

Description

5000689807 yxba:e3c:yxca hypothetical protein:hypothetical 9.8 kd protein in gntr-htpg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxcA yxcA Bacillus subtilis 1423 -11532410 116781 yxba:e3c (de:hypothetical 9.8 kd protein in gntr-htpg intergenic region) (db:swissprot) YXBA\_BACSU P46332 BACILLUS SUBTILIS 1423 -11532410 7000688723 yxca hypothetical protein yxca (db:pir2.dat) C70073 C70073 Bacillus subtilis 1423 -11532410 215751 yxca (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (le:27351) (re:27602) (di:direct) AB005554 AB005554 g904200 Bacillus subtilis 1423 -11532410 7500952975 yxca (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:90991) (re:91242) (di:complement) BSUB0021 Z99124 g2636529 Bacillus subtilis 1423 -11532410 6500728552 yxba:e3c hypothetical protein:hypothetical 9.8 kd protein in gntr-htpg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxcA yxcA Bacillus subtilis 1423 -11532410

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818032	6782	28938	642	213

Description

5000689806 yxau:e3br:xybg hypothetical protein:hypothetical oxidoreductase in gntr-htpg intergenic region (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxbG yxbG Bacillus subtilis 1423 -11532411 116780 yxbg:e3br (ec:1.-.-.-) (de:(ec 1.-.-.-)) (db:swissprot) YXBG\_BACSU P46331 BACILLUS SUBTILIS 1423 -11532411 7000688722 yxbg glucose 1-dehydrogenase homolog yxbg (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) B70073 B70073 Bacillus subtilis 1423 -11532411 215750 yxbg probable oxidoreductase (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (ec:1.1.1.47) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:conserved universally) (le:26446) (re:27234) (di:complement) AB005554 AB005554 g904199 Bacillus subtilis 1423 -11532411 7500952979 yxbg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yxau; similar to glucose) (le:91359) (re:92147) (di:direct) BSUB0021 Z99124 g2636530 Bacillus subtilis 1423 -11532411 6500728553 yxau:e3br hypothetical protein:hypothetical oxidoreductase in gntr-htpg intergenic region (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxbG yxbG Bacillus subtilis 1423 -11532411

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818033	6783	28939	198	66

Description

5000689805 yxat:e3a:yxbf hypothetical protein:hypothetical 44.3 kd protein in gntr-htpg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxbF yxbF Bacillus subtilis 1423 -11532412 116779 yxbf:e3a (de:hypothetical 44.3 kd protein in htpg-aldx intergenic region) (db:swissprot) YXBF\_BACSU P46330 BACILLUS SUBTILIS 1423 -11532412 7000688721 yxbf hypothetical protein yxbf (db:pir2.dat) A70073 A70073 Bacillus subtilis 1423 -11532412 215749 yxbf (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (le:25243) (re:26385) (di:direct) AB005554 AB005554 g904198 Bacillus subtilis 1423 -11532412 7500952978 yxbf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yxat) (le:92208) (re:93350) (di:complement) BSUB0021 Z99124 g2636531 Bacillus subtilis 1423 -11532412 6500728554 yxat:e3a hypothetical protein:hypothetical 44.3 kd protein in gntr-htpg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxbF yxbF Bacillus subtilis 1423 -11532412

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818035	6784	28940	444	147

Description

5000689804 yxar:ve7e:yxbd hypothetical protein:hypothetical 18.1 kd protein in gntr-htpg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxbd yxbd Bacillus subtilis 1423 -11532413  
 116778 yxar:ve7e (de:hypothetical 18.1 kd protein in gntr-htpg intergenic region) (db:swissprot) YXAR\_BACSU P46328 BACILLUS SUBTILIS 1423 -11532413  
 7000688720 yxbd conserved hypothetical protein yxbd (db:pir2.dat) H70072 H70072 Bacillus subtilis 1423 -11532413 215747 yxbd (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:see swiss\_prot acc#: p46334) (le:23245) (re:23724) (di:direct) AB005554 AB005554 g904196 Bacillus subtilis 1423 -11532413 7500952974 yxbd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yxar; similar to hypothetical) (le:94869) (re:95348) (di:complement) BSUB0021 Z99124 g2636533 Bacillus subtilis 1423 -11532413 6500728555 yxar:ve7e hypothetical protein:hypothetical 18.1 kd protein in gntr-htpg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxbd yxbd Bacillus subtilis 1423 -11532413

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818036	6785	28941	237	78

Description

5000689803 yxaq:ve7d:yxbc hypothetical protein:hypothetical 37.5 kd protein in gntr-htpg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxbc yxbc Bacillus subtilis 1423 -11532414  
 116777 yxaq:ve7d (de:hypothetical 37.5 kd protein in gntr-htpg intergenic region) (db:swissprot) YXAQ\_BACSU P46327 BACILLUS SUBTILIS 1423 -11532414  
 7000688719 yxbc hypothetical protein yxbc (db:pir2.dat) G70072 G70072 Bacillus subtilis 1423 -11532414 215746 yxbc (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:see swiss\_prot acc#: p46333) (le:22173) (re:23165) (di:direct) AB005554 AB005554 g904195 Bacillus subtilis 1423 -11532414 7500952973 yxbc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yxaq) (le:95428) (re:96420) (di:complement) BSUB0021 Z99124 g2636534 Bacillus subtilis 1423 -11532414  
 6500728556 yxaq:ve7d hypothetical protein:hypothetical 37.5 kd protein in gntr-htpg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxbc yxbc Bacillus subtilis 1423 -11532414

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818060	6786	28942	312	103

Description

5000689802 yxap:ve7cr:yxbb hypothetical protein:hypothetical 28.2 kd protein in gntr-htpg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxbB yxbB Bacillus subtilis 1423 -11532415  
 116776 yxap:ve7cr (de:hypothetical 28.2 kd protein in gntr-htpg intergenic region) (db:swissprot) YXAP\_BACSU P46326 BACILLUS SUBTILIS 1423 -11532415  
 7000688718 yxbb conserved hypothetical protein yxbb (cl:bioc homology) (db:pir2.dat) F70072 F70072 Bacillus subtilis 1423 -11532415 215745 yxbb (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (le:20930) (re:21664) (di:complement) AB005554 AB005554 g904194 Bacillus subtilis 1423 -11532415 7500952972 yxbb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yxap; similar to hypothetical) (le:96929) (re:97663) (di:direct) BSUB0021 Z99124 g2636535 Bacillus subtilis 1423 -11532415 6500728557 yxap:ve7cr hypothetical protein:hypothetical 28.2 kd protein in gntr-htpg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxbB yxbB Bacillus subtilis 1423 -11532415

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818062	6787	28943	186	61

Description

5000689801 yxao:ve7br:yxba hypothetical protein:hypothetical 10.1 kd protein in gntr-htpg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxbA yxbA Bacillus subtilis 1423 -11532416  
 116775 yxao:ve7br (de:hypothetical 10.1 kd protein in gntr-htpg intergenic region) (db:swissprot) YXAO\_BACSU P46325 BACILLUS SUBTILIS 1423 -11532416  
 7000688717 yxba hypothetical protein yxba (db:pir2.dat) E70072 E70072 Bacillus subtilis 1423 -11532416 215744 yxba (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:see swiss\_prot acc#: p46332) (le:20661) (re:20930) (di:complement) AB005554 AB005554 g904193 Bacillus subtilis 1423 -11532416 7500952971 yxba (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yxao) (le:97663) (re:97932) (di:direct) BSUB0021 Z99124 g2636536 Bacillus subtilis 1423 -11532416 6500728558 yxao:ve7br hypothetical protein:hypothetical 10.1 kd protein in gntr-htpg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxbA yxbA Bacillus subtilis 1423 -11532416



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818063	6788	28944	246	81

Description

6500728559 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxnB yxnB Bacillus subtilis 1423 -11532417  
7000694080 yxnb hypothetical protein yxnb (db:pir2.dat) F70082 F70082 Bacillus subtilis 1423 -11532417 4000713631 yxnb (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (le:20175) (re:20657) (di:complement) AB005554 AB005554 g2280499 Bacillus subtilis 1423 -11532417 7500964853 yxnb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:97936) (re:98418) (di:direct) BSUB0021 Z99124 g2636537 Bacillus subtilis 1423 -11532417

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818064	6789	28945	636	212

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818079	6790	28946	534	178

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818097	6791	28947	867	288

Description

6500728560 hypothetical protein:similar to antibiotic resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxaM yxaM Bacillus subtilis 1423 -11532418 7500952967 yxam:s14mr (de:hypothetical 44.7 kd protein in gntr-htpg intergenic region) (db:swissprot) YXAM\_BACSU P42112 BACILLUS SUBTILIS 1423 -11532418 7000692218 yxam antibiotic resistance protein homolog yxam (db:pir2.dat) D70072 D70072 Bacillus subtilis 1423 -11532418 4000713630 yxam probable transporter (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:similar to tetracycline resistance protein (c.) (le:16715) (re:17914) (di:complement) AB005554 AB005554 g2280498 Bacillus subtilis 1423 -11532418 7500952970 yxam (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to antibiotic resistance protein) (le:100679) (re:101878) (di:direct) BSUB0021 Z99124 g2636539 Bacillus subtilis 1423 -11532418

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818101	6792	28948	831	277

Description

6500728561 s14l:yxal hypothetical protein:hypothetical 38.5 kd protein in gntr-htpg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxaL yxaL Bacillus subtilis 1423 -11532419 7000694581 yxal serine/threonine protein kinase homolog yxal (db:pir2.dat) C70072 C70072 Bacillus subtilis 1423 -11532419 7500965180 yxal (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to serine/threonine protein kinase) (le:101942) (re:102994) (di:complement) BSUB0021 Z99124 g2636540 Bacillus subtilis 1423 -11532419

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818106	6793	28949	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818107	6794	28950	192	63

Description

6500728562 s14k:yxak hypothetical protein:hypothetical 19.5 kd protein in gntr-htpg intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxaK yxaK Bacillus subtilis 1423 -11532420 116772 yxak:s14k (de:hypothetical 19.5 kd protein in gntr-htpg intergenic region precursor) (db:swissprot) YXAK\_BACSU P42110 BACILLUS SUBTILIS 1423 -11532420 7000688716 yxak conserved hypothetical protein yxak (db:pir2.dat) B70072 B70072 Bacillus subtilis 1423 -11532420 215740 yxak (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:see swiss\_prot acc#: p42110) (le:15008) (re:15565) (di:direct) AB005554 AB005554 g563944 Bacillus subtilis 1423 -11532420 7500952966 yxak (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins from b. subtilis) (le:103027) (re:103584) (di:complement) BSUB0021 Z99124 g2636541 Bacillus subtilis 1423 -11532420 5000689798 (de:(yxak) (pn:hypothetical 19) (gn:s14k) (gtcfc:13.07) (ec:) (yxak\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxaK yxaK Bacillus subtilis 1423 10058497

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818120	6795	28951	405	134

Description

6500728563 s14j:yxaj hypothetical protein:hypothetical 15.0 kd protein in gntr-htpg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxaJ yxaJ Bacillus subtilis 1423 -11532421 116771 yxaj:s14j (de:hypothetical 15.0 kd protein in gntr-htpg intergenic region) (db:swissprot) YXAJ\_BACSU P42109 BACILLUS SUBTILIS 1423 -11532421 7000688715 yxaj hypothetical protein yxaj (db:pir2.dat) A70072 A70072 Bacillus subtilis 1423 -11532421 215739 yxaj (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:see swiss\_prot acc#: p42109) (le:14479) (re:14907) (di:direct) AB005554 AB005554 g563943 Bacillus subtilis 1423 -11532421 7500952965 yxaj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:103685) (re:104113) (di:complement) BSUB0021 Z99124 g2636542 Bacillus subtilis 1423 -11532421 5000689797 (de:(yxaj) (pn:hypothetical 15) (gn:s14j) (gtcfc:13.07) (ec:) (yxaj\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxaJ yxaJ Bacillus subtilis 1423 10058496

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818124	6796	28952	462	153

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818129	6797	28953	273	90

Description

6500728564 s14ir:yxai hypothetical protein:hypothetical 16.9 kd protein in gntr-htpg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxaI yxaI Bacillus subtilis 1423 -11532422 116770 yxai:s14ir (de:hypothetical 16.9 kd protein in gntr-htpg intergenic region) (db:swissprot) YXAI\_BACSU P42108 BACILLUS SUBTILIS 1423 -11532422 7000688714 yxai conserved hypothetical protein yxai (db:pir2.dat) H70071 H70071 Bacillus subtilis 1423 -11532422 215738 yxai (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:see swiss\_prot acc#: p42108) (le:13767) (re:14222) (di:complement) AB005554 AB005554 g563942 Bacillus subtilis 1423 -11532422 7500952964 yxai (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:104370) (re:104825) (di:direct) BSUB0021 Z99124 g2636543 Bacillus subtilis 1423 -11532422 5000689796 (de:(yxai) (pn:hypothetical 16) (gn:s14ir) (gtcfc:13.07) (ec:) (yxai\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxaI yxaI Bacillus subtilis 1423 10058495

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818135	6798	28954	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818139	6799	28955	516	171

Description

6500728565 s14h:yxah hypothetical protein:hypothetical 46.2 kd protein in gntr-htpg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxaH yxaH Bacillus subtilis 1423 -11532423 116769 yxah:s14h (de:hypothetical 46.2 kd protein in gntr-htpg intergenic region) (db:swissprot) YXAH\_BACSU P42107 BACILLUS SUBTILIS 1423 -11532423 7000688713 yxah conserved hypothetical protein yxah (db:pir2.dat) G70071 G70071 Bacillus subtilis 1423 -11532423 215737 yxah (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:homology was found to yrko\_bacsu, yeib\_ecoli and) (le:12529) (re:13737) (di:direct) AB005554 AB005554 g563941 Bacillus subtilis 1423 -11532423 7500952963 yxah (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:104855) (re:106063) (di:complement) BSUB0021 Z99124 g2636544 Bacillus subtilis 1423 -11532423 5000689795 (de:(yxah) (pn:hypothetical 46) (gn:s14h) (gtcfc:13.07) (ec:) (yxah\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxaH yxaH Bacillus subtilis 1423 10058494

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818145	6800	28956	279	92

Description

6500728566 s14g:yxag hypothetical protein:hypothetical 37.6 kd protein in gntr-htpg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxaG yxaG Bacillus subtilis 1423 -11532424 116768 yxag:s14g (de:hypothetical 37.6 kd protein in gntr-htpg intergenic region) (db:swissprot) YXAG\_BACSU P42106 BACILLUS SUBTILIS 1423 -11532424 7000688712 yxag hypothetical protein yxag (db:pir2.dat) F70071 F70071 Bacillus subtilis 1423 -11532424 215736 yxag (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:see swiss\_prot acc#: p42106) (le:11408) (re:12421) (di:direct) AB005554 AB005554 g563940 Bacillus subtilis 1423 -11532424 7500952962 yxag (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:106171) (re:107184) (di:complement) BSUB0021 Z99124 g2636545 Bacillus subtilis 1423 -11532424 5000689794 (de:(yxag) (pn:hypothetical 37) (gn:s14g) (gtcfc:13.07) (ec:) (yxag\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxaG yxaG Bacillus subtilis 1423 10058493

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818155	6801	28957	222	73

Description

6500728567 s14f:yxaf hypothetical protein:hypothetical 21.0 kd protein in gntr-htpg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxaF yxaF Bacillus subtilis 1423 -11532425 116767 yxaf:s14f (de:hypothetical 21.0 kd protein in gntr-htpg intergenic region) (db:swissprot) YXAF\_BACSU P42105 BACILLUS SUBTILIS 1423 -11532425 7000688711 yxaf conserved hypothetical protein yxaf (db:pir2.dat) E70071 E70071 Bacillus subtilis 1423 -11532425 215735 yxaf (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:see swiss\_prot acc#: p42105) (le:10739) (re:11314) (di:direct) AB005554 AB005554 g563939 Bacillus subtilis 1423 -11532425 7500952961 yxaf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:107278) (re:107853) (di:complement) BSUB0021 Z99124 g2636546 Bacillus subtilis 1423 -11532425 5000689793 (de:(yxaf) (pn:hypothetical 21) (gn:s14f) (gtcfc:13.07) (ec:)(yxaf\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxaF yxaF Bacillus subtilis 1423 10058492

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818156	6802	28958	795	264

Description

6500728568 hypothetical protein:similar to glucose 1-dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxna yxna Bacillus subtilis 1423 -11532426 7000693038 yxna glucose 1-dehydrogenase homolog yxna (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) E70082 E70082 Bacillus subtilis 1423 -11532426 7500964018 yxna (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to glucose 1-dehydrogenase) (le:107984) (re:108907) (di:direct) BSUB0021 Z99124 g2636547 Bacillus subtilis 1423 -11532426

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818169	6803	28959	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818198	6804	28960	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818199	6805	28961	261	86
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818224	6806	28962	387	129
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818226	6807	28963	471	156
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818227	6808	28964	225	74
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818232	6809	28965	2106	701
<u>Description</u>				

6500728569 s14d:yxad hypothetical protein:hypothetical transcriptional regulator in gntr-htpg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxaD yxaD Bacillus subtilis 1423 -11532427 116765 yxad:s14d (de:hypothetical transcriptional regulator in asnh-gntr intergenic region) (db:swissprot) YXAD\_BACSU P42103 BACILLUS SUBTILIS 1423 -11532427 7000688710 yxad transcription regulator marr family homolog yxad (db:pir2.dat) D70071 D70071 Bacillus subtilis 1423 -11532427 215733 yxad probable transcriptional regulator (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:prosite; ps01117; hth\_marr\_family; see swiss\_prot) (le:9048) (re:9479) (di:direct) AB005554 AB005554 g563937 Bacillus subtilis 1423 -11532427 7500952960 yxad (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to transcriptional regulator (marr family)) (le:109112) (re:109543) (di:complement) BSUB0021 Z99124 g2636548 Bacillus subtilis 1423 -11532427 5000688930 (de:(yxad) (pn:hypothetical transcriptional regulator in gntr-htpg intergenic region) (gn:s14d) (gtcfc:12.13) (ec:) (yxad\_bacsu) (keggfc:11.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis)) yxaD yxaD Bacillus subtilis 1423 10058490

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818236	6810	28966	762	253

Description

6500728570 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxaC yxaC Bacillus subtilis 1423 -11532428 7000692871 yxac conserved hypothetical protein yxac (db:pir2.dat) C70071 C70071 Bacillus subtilis 1423 -11532428 7500963908 yxac (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:109770) (re:110675) (di:direct) BSUB0021 Z99124 g2636549 Bacillus subtilis 1423 -11532428

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818237	6811	28967	567	188

Description

6500728571 s14b:yxab hypothetical protein:hypothetical 36.6 kd protein in gntr-htpg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxaB yxaB Bacillus subtilis 1423 -11532429 7000688709 yxab conserved hypothetical protein yxab (cl:hypothetical protein yxab) (db:pir2.dat) B70071 B70071 Bacillus subtilis 1423 -11532429 7500955855 yxab (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:see swiss\_prot acc#: p42101; similar to eps1) (le:6684) (re:7637) (di:direct) AB005554 AB005554 g563935 Bacillus subtilis 1423 -11532429 215731 yxab (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:110955) (re:111908) (di:complement) BSUB0021 Z99124 g2636550 Bacillus subtilis 1423 -11532429 116763 yxab\_bacsu (de:hypothetical 36.6 kd protein in gntr-htpg intergenic region.) P42101 P42101 Bacillus subtilis 1423 -11532429 5000689790 (de:(yxab) (pn:hypothetical 36) (gn:s14b) (gtcfc:13.07) (ec:) (yxab\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxaB yxaB Bacillus subtilis 1423 10058488

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818254	6812	28968	948	315

Description

6500728572 s14a:yxaa hypothetical protein:hypothetical 39.4 kd protein in gntr-htpg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxaA yxaA Bacillus subtilis 1423 -11532430 116762 yxaa:s14a (de:hypothetical 39.4 kd protein in gntr-htpg intergenic region) (db:swissprot) YXAA\_BACSU P42100 BACILLUS SUBTILIS 1423 -11532430 7000688708 yxaa conserved hypothetical protein yxaa (cl:yhad protein) (db:pir2.dat) A70071 A70071 Bacillus subtilis 1423 -11532430 215730 yxaa (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:homologs are found in e. coli and h. influenzae;) (le:5443) (re:6591) (di:direct) AB005554 AB005554 g563934 Bacillus subtilis 1423 -11532430 7500952959 yxaa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:112001) (re:113149) (di:complement) BSUB0021 Z99124 g2636551 Bacillus subtilis 1423 -11532430 5000689789 (de:(yxaa) (pn:hypothetical 39) (gn:s14a) (gtcfc:13.07) (ec:) (yxaa\_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxaA yxaA Bacillus subtilis 1423 10058487

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818269	6813	28969	717	239

Description

6500728573 hypothetical protein:similar to phosphotransferase systeme enzyme ii (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyzE yyzE Bacillus subtilis 1423 -11532431 7000694425 yyze phosphotransferase systeme enzyme ii homolog yyze (db:pir2.dat) D70092 D70092 Bacillus subtilis 1423 -11532431 7500965081 yyze (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to phosphotransferase systeme enzyme ii) (le:122547) (re:122777) (di:complement) BSUB0021 Z99124 g2636559 Bacillus subtilis 1423 -11532431



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818270	6814	28970	261	86

Description

6500728574 hypothetical protein:similar to transcriptional regulator:gntr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yydK yydK Bacillus subtilis 1423 -11532432 7000694743 yydk transcription regulator gntr family homolog yydk (db:pir2.dat) A70092 A70092 Bacillus subtilis 1423 -11532432 7500965315 yydk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to transcriptional regulator (gntr family)) (le:123121) (re:123831) (di:direct) BSUB0021 Z99124 g2636560 Bacillus subtilis 1423 -11532432

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818277	6815	28971	1080	359

Description

6500728575 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yydJ yydJ Bacillus subtilis 1423 -11532433 7000694098 yydj hypothetical protein yydj (db:pir2.dat) H70091 H70091 Bacillus subtilis 1423 -11532433 215765 yydj (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (le:5766) (re:6488) (di:complement) BACGNTZA D78193 g1064786 Bacillus subtilis 1423 -11532433 302061 yydj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:124148) (re:124870) (di:complement) BSUB0021 Z99124 g2636561 Bacillus subtilis 1423 -11532433

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818280	6816	28972	633	210

Description

6500728576 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yydI yydI Bacillus subtilis 1423 -11532434 7000692109 yydi abc transporter atp-binding protein homolog yydi (db:pir2.dat) G70091 G70091 Bacillus subtilis 1423 -11532434 215766 yydi (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (le:6509) (re:7138) (di:complement) BACGNTZA D78193 g1064787 Bacillus subtilis 1423 -11532434 302062 yydi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to abc transporter (atp-binding protein)) (le:124891) (re:125520) (di:complement) BSUB0021 Z99124 g2636562 Bacillus subtilis 1423 -11532434

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818303	6817	28973	348	115

Description

6500728577 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yydH yydH Bacillus subtilis 1423 -11532435  
7000694097 yydh hypothetical protein yydh (db:pir2.dat) F70091 F70091 Bacillus subtilis 1423 -11532435 215767 yydh (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (le:7288) (re:8046) (di:complement) BACGNTZA D78193 g1064788 Bacillus subtilis 1423 -11532435 302063 yydh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:125670) (re:126428) (di:complement) BSUB0021 Z99124 g2636563 Bacillus subtilis 1423 -11532435

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818321	6818	28974	690	230

Description

6500728578 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yydG yydG Bacillus subtilis 1423 -11532436  
7000694096 yydg hypothetical protein yydg (db:pir2.dat) E70091 E70091 Bacillus subtilis 1423 -11532436 215768 yydg (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (le:8027) (re:8986) (di:complement) BACGNTZA D78193 g1064789 Bacillus subtilis 1423 -11532436 302064 yydg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:126409) (re:127368) (di:complement) BSUB0021 Z99124 g2636564 Bacillus subtilis 1423 -11532436

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818336	6819	28975	717	238

Description

6500728579 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yydF yydF Bacillus subtilis 1423 -11532437  
7000694095 yydf hypothetical protein yydf (db:pir2.dat) D70091 D70091 Bacillus subtilis 1423 -11532437 215769 yydf (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (le:9044) (re:9193) (di:complement) BACGNTZA D78193 g1064790 Bacillus subtilis 1423 -11532437 302065 yydf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:127426) (re:127575) (di:complement) BSUB0021 Z99124 g2636565 Bacillus subtilis 1423 -11532437

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818337	6820	28976	363	120

Description

6500728580 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yydD yydD Bacillus subtilis 1423 -11532438 7000692878 yydd conserved hypothetical protein yydd (db:pir2.dat) C70091 C70091 Bacillus subtilis 1423 -11532438 215771 yydd (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (le:12124) (re:13884) (di:complement) BACGNTZA D78193 g1064792 Bacillus subtilis 1423 -11532438 302067 yydd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:130506) (re:132266) (di:complement) BSUB0021 Z99124 g2636567 Bacillus subtilis 1423 -11532438

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818354	6821	28977	909	303

Description

6500728581 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yydC yydC Bacillus subtilis 1423 -11532439 7000694094 yydc hypothetical protein yydc (db:pir2.dat) B70091 B70091 Bacillus subtilis 1423 -11532439 215772 yydc (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (le:13884) (re:14282) (di:complement) BACGNTZA D78193 g1064793 Bacillus subtilis 1423 -11532439 302068 yydc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:132266) (re:132664) (di:complement) BSUB0021 Z99124 g2636568 Bacillus subtilis 1423 -11532439

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818380	6822	28978	618	205

Description

6500728582 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yydB yydB Bacillus subtilis 1423 -11532440 7000694093 yydb probable phosphoesterase:yydb (cl:unassigned probable phosphoesterases:phosphoesterase core homology) (ec:3.1.-.-) (db:pir2.dat) A70091 A70091 Bacillus subtilis 1423 -11532440 215773 yydb (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (le:14275) (re:15720) (di:complement) BACGNTZA D78193 g1064794 Bacillus subtilis 1423 -11532440 302069 yydb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:132657) (re:134102) (di:complement) BSUB0021 Z99124 g2636569 Bacillus subtilis 1423 -11532440

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818409	6823	28979	549	182

Description

6500728583 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yydA yydA Bacillus subtilis 1423 -11532441 7000692877 yyda conserved hypothetical protein yyda (cl:conserved hypothetical protein hi0033) (db:pir2.dat) H70090 H70090 Bacillus subtilis 1423 -11532441 215774 yyda (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (le:15982) (re:16461) (di:complement) BACGNTZA D78193 g1064795 Bacillus subtilis 1423 -11532441 302070 yyda (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:134364) (re:134843) (di:complement) BSUB0021 Z99124 g2636570 Bacillus subtilis 1423 -11532441

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818413	6824	28980	267	89

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818415	6825	28981	327	109

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818416	6826	28982	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818463	6827	28983	249	82

Description

6500728584 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yycS yycS Bacillus subtilis 1423 -11532442  
7000694092 yycs hypothetical protein yycs (db:pir2.dat) G70090 G70090 Bacillus subtilis 1423 -11532442 215776 yycs (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genes encoding 34 orfs.) (le:16898) (re:17311) (di:direct) BACGNTZA D78193 g1064797 Bacillus subtilis 1423 -11532442 302072 yycs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814.) (le:135280) (re:135693) (di:direct) BSUB0021 Z99124 g2636571 Bacillus subtilis 1423 -11532442

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818465	6828	28984	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818472	6829	28985	747	249

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818474	6830	28986	864	287

Description

GTC ORF with score 115 to: (sr:saccharomyces cerevisiae (library: lambda yes by s. elledge) cdn) (db:genpept-pln1) (de:saccharomyces cerevisiae putative malr homologue mrna, partial cds.) (nt:sequence similarity to yeast malr protein,) (le:6) (re:392) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818490	6831	28987	1425	475

Description

6500728585 hypothetical protein:similar to formaldehyde dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yycR yycR Bacillus subtilis 1423 -11532443 7000692998 yycr probable formaldehyde dehydrogenase:yycr (cl:alcohol dehydrogenase:long-chain alcohol dehydrogenase homology) (ec:1.2.1.46) (db:pir2.dat) F70090 F70090 Bacillus subtilis 1423 -11532443 215777 yycr (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (nt:homologous to psefd\_1 (formaldehyde) (le:17345) (re:18571) (di:complement) BACGNTZA D78193 g1064798 Bacillus subtilis 1423 -11532443 302073 yycr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to formaldehyde dehydrogenase) (le:135727) (re:136953) (di:complement) BSUB0021 Z99124 g2636572 Bacillus subtilis 1423 -11532443

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818515	6832	28988	231	76

Description

GTC ORF with score 98 to: (fn:required for o-glycosylation) (db:genpept-pln2) (de:candida albicans protein mannosyltransferase 1 (pmt1) gene,complete cds.) (nt:similar to saccharomyces cerevisiae pmt1p,) (le:151) (re:2784) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818516	6833	28989	855	284

Description

6500728586 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yycQ yycQ Bacillus subtilis 1423 -11532444 7000694091 yycq hypothetical protein yycq (db:pir2.dat) E70090 E70090 Bacillus subtilis 1423 -11532444 215778 yycq (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (le:18909) (re:19157) (di:complement) BACGNTZA D78193 g1064799 Bacillus subtilis 1423 -11532444 302074 yycq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:137291) (re:137539) (di:complement) BSUB0021 Z99124 g2636573 Bacillus subtilis 1423 -11532444

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818519	6834	28990	687	228

Description

GTC ORF with score 206 to: (fn:required for o-glycosylation)  
(db:genpept-pln2) (de:candida albicans protein mannosyltransferase 1 (pmt1)  
gene,complete cds.) (nt:similar to saccharomyces cerevisiae pmt1p,) (le:151)  
(re:2784) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818525	6835	28991	513	170

Description

GTC ORF with score 272 to: (fn:probable transporter of sugars across plasma)  
(sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces  
cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208)  
(re:1818) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818526	6836	28992	291	96

Description

6500728587 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yycP yycP Bacillus subtilis 1423 -11532445  
7000694090 yycp hypothetical protein yycp (db:pir2.dat) D70090 D70090  
Bacillus subtilis 1423 -11532445 215779 yycp (sr:bacillus subtilis  
(strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence  
between gntz and trny genesencoding 34 orfs.) (le:19173) (re:20336)  
(di:complement) BACGNTZA D78193 g1064800 Bacillus subtilis 1423 -11532445  
302075 yycp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete  
genome (section 21 of 21): from 3999281to 4214814.) (le:137555) (re:138718)  
(di:complement) BSUB0021 Z99124 g2636574 Bacillus subtilis 1423 -11532445

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818539	6837	28993	570	189

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818560	6838	28994	249	82

Description

6500728588 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yycO yycO Bacillus subtilis 1423 -11532446  
7000694089 yyco hypothetical protein yyco (db:pir2.dat) C70090 C70090 Bacillus subtilis 1423 -11532446 215780 yyco (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (le:20347) (re:21084) (di:complement) BACGNTZA D78193 g1064801 Bacillus subtilis 1423 -11532446 302076 yyco (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:138729) (re:139466) (di:complement) BSUB0021 Z99124 g2636575 Bacillus subtilis 1423 -11532446

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818566	6839	28995	1035	344

Description

6500728589 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yycN yycN Bacillus subtilis 1423 -11532447 7000692876 yycn conserved hypothetical protein yycn (db:pir2.dat) B70090 B70090 Bacillus subtilis 1423 -11532447 7500963909 yycn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:139608) (re:140078) (di:complement) BSUB0021 Z99124 g2636576 Bacillus subtilis 1423 -11532447



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818585	6840	28996	204	67

Description

6500728590 yyck:yyxa hypothetical protein:hypothetical protease in rocr-pura intergenic region (gtcfc:10.11:14.1) (ec:3.4.21.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyxA yyxA Bacillus subtilis 1423 -11532448 116956 yyxa:yyck (ec:3.4.21.-) (de:hypothetical protease in rocr-pura intergenic region,) (db:swissprot) YYXA\_BACSU P39668 BACILLUS SUBTILIS 1423 -11532448 7000688834 yyxa serine proteinase do homolog yyxa (cl:proteinase hhob) (db:pir2.dat) B70092 B70092 Bacillus subtilis 1423 -11532448 215788 yyck (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (nt:homologous to htra\_ecoli) (le:29111) (re:30313) (di:complement) BACGNTZA D78193 g1064809 Bacillus subtilis 1423 -11532448 302084 yyxa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yyck; similar to serine) (le:147495) (re:148697) (di:complement) BSUB0021 Z99124 g2636583 Bacillus subtilis 1423 -11532448 5000689887 (de:(yyxa) (pn:hypothetical protease in rocr-pura intergenic region:hypothetical protein in rocr 3"region:fragment) (gn:yyck) (gtcfc:13.07) (ec:3.4.21.-) (yyxa\_bacsu) (keggfc:11.1) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yyxA yyxA Bacillus subtilis 1423 10058681

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818588	6841	28997	309	102

Description

6500728591 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yycJ yycJ Bacillus subtilis 1423 -11532449 7000694088 yycj hypothetical protein yycj (db:pir2.dat) A70090 A70090 Bacillus subtilis 1423 -11532449 215789 yycj (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (le:30382) (re:31188) (di:complement) BACGNTZA D78193 g1064810 Bacillus subtilis 1423 -11532449 302085 yycj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:148766) (re:149572) (di:complement) BSUB0021 Z99124 g2636584 Bacillus subtilis 1423 -11532449

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818590	6842	28998	210	69

Description

6500728592 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yycI yycI Bacillus subtilis 1423 -11532450  
7000694087 yyci hypothetical protein yyci (db:pir2.dat) H70089 H70089 Bacillus subtilis 1423 -11532450 215790 yyci (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (le:31210) (re:32052) (di:complement) BACGNTZA D78193 g1064811 Bacillus subtilis 1423 -11532450 302086 yyci (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:149594) (re:150436) (di:complement) BSUB0021 Z99124 g2636585 Bacillus subtilis 1423 -11532450

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818605	6843	28999	666	222

Description

6500728593 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyCH yyCH Bacillus subtilis 1423 -11532451  
7000694086 yych hypothetical protein yych (db:pir2.dat) G70089 G70089 Bacillus subtilis 1423 -11532451 7500964859 yych (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:150423) (re:151790) (di:complement) BSUB0021 Z99124 g2636586 Bacillus subtilis 1423 -11532451

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818607	6844	29000	357	118

Description

6500728594 hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yycG yycG Bacillus subtilis 1423 -11532452 7000694887 yycg two-component sensor histidine kinase homolog yycg (db:pir2.dat) F70089 F70089 Bacillus subtilis 1423 -11532452 215792 yycg (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (nt:homologous to phor\_bacsu) (le:33396) (re:35231) (di:complement) BACGNTZA D78193 g1064813 Bacillus subtilis 1423 -11532452 302088 yycg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to two-component sensor histidine kinase) (le:151780) (re:153615) (di:complement) BSUB0021 Z99124 g2636587 Bacillus subtilis 1423 -11532452

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818608	6845	29001	225	74

Description

5000688935 hypothetical protein:hypothetical 27.2 kd sensory transduction protein in rocr-pura intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yycF yycF Bacillus subtilis 1423 -11532453 116950 yycf (de:intergenic region) (db:swissprot) YYCF\_BACSU P37478 BACILLUS SUBTILIS 1423 -11532453 7000688833 yycf two-component response regulator yycf (cl:ompr protein:response regulator homology) (db:pir2.dat) S65967 S65967 Bacillus subtilis 1423 -11532453 7500953063 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:1691) (re:2398) (di:complement) BAC180K D26185 g467327 Bacillus subtilis 1423 -11532453 302089 yycf (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (nt:homologous to phop\_bacsub) (le:35239) (re:35946) (di:complement) BACGNTZA D78193 g1064814 Bacillus subtilis 1423 -11532453 215793 yycf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to two-component response regulator (yycg)) (le:153623) (re:154330) (di:complement) BSUB0021 Z99124 g2636588 Bacillus subtilis 1423 -11532453 206175 yycf two-component response regulator yycf (cl:ompr protein:response regulator homology) (db:pir) S65967 S65967 Bacillus subtilis 1423 -11532453 214927 yycf (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (nt:homologous to phop\_bacsub) (le:35239) (re:35946) (di:complement) BACGNTZA D78193 g1064814 Bacillus subtilis 1423 -11532453 6500728595 hypothetical protein:hypothetical 27.2 kd sensory transduction protein in rocr-pura intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yycF yycF Bacillus subtilis 1423 -11532453

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818615	6846	29002	498	165

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818617	6847	29003	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818635	6848	29004	327	108

Description

5000689886 hypothetical protein:hypothetical 15.6 kd protein in pura-dnac intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yycE yycE Bacillus subtilis 1423 -11532454  
116949 yyce (de:hypothetical 15.6 kd protein in pura-dnac intergenic region) (db:swissprot) YYCE\_BACSU P37479 BACILLUS SUBTILIS 1423 -11532454  
7000688832 yyce hypothetical protein yyce (db:pir2.dat) S65969 S65969 Bacillus subtilis 1423 -11532454 7500953062 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:4927) (re:5346) (di:complement) BAC180K D26185 g467329 Bacillus subtilis 1423 -11532454 214929 yyce (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:156859) (re:157278) (di:complement) BSUB0021 Z99124 g2636590 Bacillus subtilis 1423 -11532454 206176 yyce hypothetical protein yyce (db:pir) S65969 S65969 Bacillus subtilis 1423 -11532454 6500728596 hypothetical protein:hypothetical 15.6 kd protein in pura-dnac intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yycE yycE Bacillus subtilis 1423 -11532454

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818636	6849	29005	204	67

Description

5000689885 hypothetical protein:hypothetical 7.5 kd protein in dnac-rpli intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yyCD yyCD Bacillus subtilis 1423 -11532455  
116948 yyCD (de:hypothetical 7.5 kd protein in dnac-rpli intergenic region) (db:swissprot) YYCD\_BACSU P37480 BACILLUS SUBTILIS 1423 -11532455  
7000688831 yyCD hypothetical protein yyCD (db:pir2.dat) S65971 S65971 Bacillus subtilis 1423 -11532455 7500953061 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:7001) (re:7201) (di:direct) BAC180K D26185 g467331 Bacillus subtilis 1423 -11532455 214931 yyCD (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:158933) (re:159133) (di:direct) BSUB0021 Z99124 g2636592 Bacillus subtilis 1423 -11532455 206177 yyCD hypothetical protein yyCD (db:pir) S65971 S65971 Bacillus subtilis 1423 -11532455 6500728597 hypothetical protein:hypothetical 7.5 kd protein in dnac-rpli intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyCD yyCD Bacillus subtilis 1423 -11532455

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818639	6850	29006	390	129

Description

6500728598 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyzB yyzB Bacillus subtilis 1423 -11532456  
 7000694099 yyzb hypothetical protein yyzb (db:pir2.dat) C70092 C70092 Bacillus subtilis 1423 -11532456 7500964860 yyzb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:159181) (re:159384) (di:complement) BSUB0021 Z99124 g2636593 Bacillus subtilis 1423 -11532456

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818650	6851	29007	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818663	6852	29008	462	153

Description

6500728599 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yycC yycC Bacillus subtilis 1423 -11532457  
 7500964858 yycC (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:159505) (re:159645) (di:direct) BSUB0021 Z99124 g2636594 Bacillus subtilis 1423 -11532457 7000694085 yycC hypothetical protein yycC (db:pir) B70089 B70089 Bacillus subtilis 1423 -11532457

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818664	6853	29009	723	240

Description

5000689883 hypothetical protein:hypothetical 43.2 kd protein in dnac-rpli intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yycB yycB Bacillus subtilis 1423 -11532458 116946 yycb (de:hypothetical 43.2 kd protein in dnac-rpli intergenic region) (db:swissprot) YYCB\_BACSU P37482 BACILLUS SUBTILIS 1423 -11532458 7000688830 yycb abc transporter permease homolog yycb (cl:cynx protein) (db:pir2.dat) S65973 S65973 Bacillus subtilis 1423 -11532458 7500953060 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:7786) (re:8994) (di:direct) BAC180K D26185 g467333 Bacillus subtilis 1423 -11532458 214933 yycb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to abc transporter (permease)) (le:159718) (re:160926) (di:direct) BSUB0021 Z99124 g2636595 Bacillus subtilis 1423 -11532458 206179 yycb abc transporter permease homolog yycb (cl:cynx protein) (db:pir) S65973 S65973 Bacillus subtilis 1423 -11532458 6500728600 hypothetical protein:hypothetical 43.2 kd protein in dnac-rpli intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yycB yycB Bacillus subtilis 1423 -11532458

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818665	6854	29010	216	71

Description

5000689882 hypothetical protein:hypothetical 73.6 kd protein in dnac-rpli intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyca yyca Bacillus subtilis 1423 -11532459 116945 yyca (de:hypothetical 73.6 kd protein in dnac-rpli intergenic region) (db:swissprot) YYCA\_BACSU P37483 BACILLUS SUBTILIS 1423 -11532459 7000688829 yyca conserved hypothetical protein yyca (db:pir2.dat) S65974 S65974 Bacillus subtilis 1423 -11532459 7500953059 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:9099) (re:11156) (di:direct) BAC180K D26185 g467334 Bacillus subtilis 1423 -11532459 214934 yyca (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins from b. subtilis) (le:161031) (re:163088) (di:direct) BSUB0021 Z99124 g2636596 Bacillus subtilis 1423 -11532459 206180 yyca conserved hypothetical protein yyca (db:pir) S65974 S65974 Bacillus subtilis 1423 -11532459 6500728601 hypothetical protein:hypothetical 73.6 kd protein in dnac-rpli intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyca yyca Bacillus subtilis 1423 -11532459

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818669	6855	29011	339	113

Description

5000689881 hypothetical protein:hypothetical 74.3 kd protein in rpli-cotf intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yybT yybT Bacillus subtilis 1423 -11532460  
116944 yybt (de:hypothetical 74.3 kd protein in rpli-cotf intergenic region) (db:swissprot) YYBT\_BACSU P37484 BACILLUS SUBTILIS 1423 -11532460  
7000688828 yybt hypothetical protein yybt (db:pir2.dat) S65976 S65976 Bacillus subtilis 1423 -11532460 7500953058 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:11639) (re:13618) (di:complement) BAC180K D26185 g467336 Bacillus subtilis 1423 -11532460  
214936 yybt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:163571) (re:165550) (di:complement) BSUB0021 Z99124 g2636598 Bacillus subtilis 1423 -11532460  
206181 yybt hypothetical protein yybt (db:pir) S65976 S65976 Bacillus subtilis 1423 -11532460 6500728602 hypothetical protein:hypothetical 74.3 kd protein in rpli-cotf intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybT yybT Bacillus subtilis 1423 -11532460

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818676	6856	29012	750	249

Description

5000689880 hypothetical protein:hypothetical 34.5 kd protein in rpli-cotf intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yybS yybS Bacillus subtilis 1423 -11532461  
116943 yybs (de:hypothetical 34.5 kd protein in rpli-cotf intergenic region) (db:swissprot) YYBS\_BACSU P37485 BACILLUS SUBTILIS 1423 -11532461  
7000688827 yybs hypothetical protein yybs (db:pir2.dat) S65977 S65977 Bacillus subtilis 1423 -11532461 7500953057 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:13655) (re:14584) (di:complement) BAC180K D26185 g467337 Bacillus subtilis 1423 -11532461  
214937 yybs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:165587) (re:166516) (di:complement) BSUB0021 Z99124 g2636599 Bacillus subtilis 1423 -11532461  
206182 yybs hypothetical protein yybs (db:pir) S65977 S65977 Bacillus subtilis 1423 -11532461 6500728603 hypothetical protein:hypothetical 34.5 kd protein in rpli-cotf intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybS yybS Bacillus subtilis 1423 -11532461

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818682	6857	29013	660	220

Description

5000689879 hypothetical protein:hypothetical 14.7 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybR yybR Bacillus subtilis 1423 -11532462 116942 yybr (de:hypothetical 14.7 kd protein in cotf-tetb intergenic region) (db:swissprot) YYBR\_BACSU P37486 BACILLUS SUBTILIS 1423 -11532462 7000688826 yybr conserved hypothetical protein yybr (cl:conserved hypothetical protein mth1285) (db:pir2.dat) S65979 S65979 Bacillus subtilis 1423 -11532462 7500953056 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:15618) (re:15995) (di:complement) BAC180K D26185 g467339 Bacillus subtilis 1423 -11532462 214939 yybr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:167550) (re:167927) (di:complement) BSUB0021 Z99124 g2636601 Bacillus subtilis 1423 -11532462 206183 yybr conserved hypothetical protein yybr (db:pir) S65979 S65979 Bacillus subtilis 1423 -11532462 6500728604 hypothetical protein:hypothetical 14.7 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybR yybR Bacillus subtilis 1423 -11532462

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818685	6858	29014	273	90

Description

5000689878 hypothetical protein:hypothetical 34.0 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybQ yybQ Bacillus subtilis 1423 -11532463 116941 yybq (de:hypothetical 34.0 kd protein in cotf-tetb intergenic region) (db:swissprot) YYBQ\_BACSU P37487 BACILLUS SUBTILIS 1423 -11532463 7000688825 yybq conserved hypothetical protein yybq (cl:conserved hypothetical protein mj0608) (db:pir2.dat) S65980 S65980 Bacillus subtilis 1423 -11532463 7500953055 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:16200) (re:17129) (di:direct) BAC180K D26185 g467340 Bacillus subtilis 1423 -11532463 214940 yybq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:168132) (re:169061) (di:direct) BSUB0021 Z99124 g2636602 Bacillus subtilis 1423 -11532463 206184 yybq conserved hypothetical protein yybq (db:pir) S65980 S65980 Bacillus subtilis 1423 -11532463 6500728605 hypothetical protein:hypothetical 34.0 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybQ yybQ Bacillus subtilis 1423 -11532463



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818690	6859	29015	210	69

Description

5000689877 hypothetical protein:hypothetical 16.0 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yybP yybP Bacillus subtilis 1423 -11532464  
116940 yybp (de:hypothetical 16.0 kd protein in cotf-tetb intergenic region) (db:swissprot) YYBP\_BACSU P37488 BACILLUS SUBTILIS 1423 -11532464  
7000688824 yybp hypothetical protein yybp (db:pir2.dat) S65981 S65981  
Bacillus subtilis 1423 -11532464 7500953054 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:17162) (re:17608)  
(di:complement) BAC180K D26185 g467341 Bacillus subtilis 1423 -11532464  
214941 yybp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:169094) (re:169540)  
(di:complement) BSUB0021 Z99124 g2636603 Bacillus subtilis 1423 -11532464  
206185 yybp hypothetical protein yybp (db:pir) S65981 S65981 Bacillus subtilis 1423 -11532464 6500728606 hypothetical protein:hypothetical 16.0 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybP yybP Bacillus subtilis 1423 -11532464

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818695	6860	29016	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818697	6861	29017	885	294

Description

GTC ORF with score 798 to: (sr:baker's yeast strain=s288c (ab972))  
(db:genpept-pln1) (de:saccharomyces cerevisiae chromosome iv cosmid 9819.)  
(nt:similar to glutamate decarboxylase (swiss prot.) (le:22916) (re:24685)  
(di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818711	6862	29018	1854	617

#### Description

5000689876 hypothetical protein:hypothetical 48.2 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
 (db:gtc-bacillus subtilis) yybO yybO Bacillus subtilis 1423 -11532465  
 116939 yybo (de:hypothetical 48.2 kd protein in cotf-tetb intergenic region) (db:swissprot) YYBO\_BACSU P37489 BACILLUS SUBTILIS 1423 -11532465  
 7000688823 yybo abc transporter permease homolog yybo (cl:hexuronate transporter) (db:pir2.dat) S65982 S65982 Bacillus subtilis 1423 -11532465  
 7500953053 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:18041) (re:19348) (di:direct) BAC180K D26185  
 g467342 Bacillus subtilis 1423 -11532465 214942 yybo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to abc transporter (permease)) (le:169973) (re:171280) (di:direct) BSUB0021 Z99124 g2636604 Bacillus subtilis 1423 -11532465 206186 yybo abc transporter permease homolog yybo (cl:hexuronate transporter) (db:pir) S65982 S65982 Bacillus subtilis 1423 -11532465 6500728607 hypothetical protein:hypothetical 48.2 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybO yybO Bacillus subtilis 1423 -11532465

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818717	6863	29019	219	72

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818735	6864	29020	300	99

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818742	6865	29021	819	272

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818770	6866	29022	276	91

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818771	6867	29023	747	248

Description

5000689875 hypothetical protein:hypothetical 16.2 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybN yybN Bacillus subtilis 1423 -11532466 116938 yybn (de:hypothetical 16.2 kd protein in cotf-tetb intergenic region) (db:swissprot) YYBN\_BACSU P37490 BACILLUS SUBTILIS 1423 -11532466 7000688822 yybn hypothetical protein yybn (db:pir2.dat) S65983 S65983 Bacillus subtilis 1423 -11532466 7500953052 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:21110) (re:21547) (di:direct) BAC180K D26185 g467343 Bacillus subtilis 1423 -11532466 214943 yybn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:173042) (re:173479) (di:direct) BSUB0021 Z99124 g2636605 Bacillus subtilis 1423 -11532466 206187 yybn hypothetical protein yybn (db:pir) S65983 S65983 Bacillus subtilis 1423 -11532466 6500728608 hypothetical protein:hypothetical 16.2 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybN yybN Bacillus subtilis 1423 -11532466

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818774	6868	29024	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818787	6869	29025	528	175

Description

5000689874 hypothetical protein:hypothetical 29.1 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybM yybM Bacillus subtilis 1423 -11532467 116937 yybm (de:hypothetical 29.1 kd protein in cotf-tetb intergenic region) (db:swissprot) YYBM\_BACSU P37491 BACILLUS SUBTILIS 1423 -11532467 7000688821 yybm hypothetical protein yybm (db:pir2.dat) S65984 S65984 Bacillus subtilis 1423 -11532467 7500953051 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:21661) (re:22416) (di:direct) BAC180K D26185 g467344 Bacillus subtilis 1423 -11532467 214944 yybm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:173593) (re:174348) (di:direct) BSUB0021 Z99124 g2636606 Bacillus subtilis 1423 -11532467 206188 yybm hypothetical protein yybm (db:pir) S65984 S65984 Bacillus subtilis 1423 -11532467 6500728609 hypothetical protein:hypothetical 29.1 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybM yybM Bacillus subtilis 1423 -11532467

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818809	6870	29026	717	238

Description

5000689873 hypothetical protein:hypothetical 27.9 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybL yybL Bacillus subtilis 1423 -11532468 116936 yybl (de:hypothetical 27.9 kd protein in cotf-tetb intergenic region) (db:swissprot) YYBL\_BACSU P37492 BACILLUS SUBTILIS 1423 -11532468 7000688820 yybl abc transporter permease homolog yybl (db:pir2.dat) S65985 S65985 Bacillus subtilis 1423 -11532468 7500953050 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:22406) (re:23116) (di:direct) BAC180K D26185 g467345 Bacillus subtilis 1423 -11532468 214945 yybl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to abc transporter (permease)) (le:174338) (re:175048) (di:direct) BSUB0021 Z99124 g2636607 Bacillus subtilis 1423 -11532468 206189 yybl abc transporter permease homolog yybl (db:pir) S65985 S65985 Bacillus subtilis 1423 -11532468 6500728610 hypothetical protein:hypothetical 27.9 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybL yybL Bacillus subtilis 1423 -11532468

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818810	6871	29027	252	83

Description

5000689872 hypothetical protein:hypothetical 29.0 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybK yybK Bacillus subtilis 1423 -11532469 116935 yybk (de:hypothetical 29.0 kd protein in cotf-tetb intergenic region) (db:swissprot) YYBK\_BACSU P37493 BACILLUS SUBTILIS 1423 -11532469 7000688819 yybk hypothetical protein yybk (db:pir2.dat) E41666 E41666 Bacillus subtilis 1423 -11532469 7500953049 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:23113) (re:23868) (di:direct) BAC180K D26185 g467346 Bacillus subtilis 1423 -11532469 214946 type-ii membrane binding region (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis type ii-membrane binding region (orf i-v) gene,complete cds; type ii-membrane binding region (orf vi) gene,partial cds.) (nt:orf v) (le:1695) (re:2450) (di:direct) BACMBR M77837 g143172 Bacillus subtilis 1423 -11532469 216316 yybk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:175045) (re:175800) (di:direct) BSUB0021 Z99124 g2636608 Bacillus subtilis 1423 -11532469 170058 yybk hypothetical protein yybk (db:pir) E41666 E41666 Bacillus subtilis 1423 -11532469 6500728611 hypothetical protein:hypothetical 29.0 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybK yybK Bacillus subtilis 1423 -11532469

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818822	6872	29028	207	68

Description

5000689871 hypothetical protein:hypothetical abc transporter atp-binding protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybJ yybJ Bacillus subtilis 1423 -11532470 116934 yybj (de:intergenic region) (db:swissprot) YYBJ\_BACSU P37494 BACILLUS SUBTILIS 1423 -11532470 7000688818 yybj abc transporter atp-binding protein homolog yybj (cl:atp-binding cassette homology) (db:pir2.dat) S65987 S65987 Bacillus subtilis 1423 -11532470 7500953048 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:23865) (re:24521) (di:direct) BAC180K D26185 g467347 Bacillus subtilis 1423 -11532470 214947 yybj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to abc transporter (atp-binding protein)) (le:175797) (re:176453) (di:direct) BSUB0021 Z99124 g2636609 Bacillus subtilis 1423 -11532470 206190 yybj abc transporter atp-binding protein homolog yybj (cl:atp-binding cassette homology) (db:pir) S65987 S65987 Bacillus subtilis 1423 -11532470 6500728612 hypothetical protein:hypothetical abc transporter atp-binding protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybJ yybJ Bacillus subtilis 1423 -11532470

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818833	6873	29029	975	324

Description

5000689870 hypothetical protein:hypothetical 30.1 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybI yybI Bacillus subtilis 1423 -11532471 116933 yybi (de:hypothetical 30.1 kd protein in cotf-tetb intergenic region) (db:swissprot) YYBI\_BACSU P37495 BACILLUS SUBTILIS 1423 -11532471 7000688817 yybi hypothetical protein yybi (db:pir2.dat) S65988 S65988 Bacillus subtilis 1423 -11532471 7500953047 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:24896) (re:25684) (di:complement) BAC180K D26185 g467348 Bacillus subtilis 1423 -11532471 214948 yybi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:176828) (re:177616) (di:complement) BSUB0021 Z99124 g2636610 Bacillus subtilis 1423 -11532471 206191 yybi hypothetical protein yybi (db:pir) S65988 S65988 Bacillus subtilis 1423 -11532471 6500728613 hypothetical protein:hypothetical 30.1 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybI yybI Bacillus subtilis 1423 -11532471

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818835	6874	29030	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818838	6875	29031	198	65

Description

5000689869 hypothetical protein: hypothetical 14.6 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybH yybH Bacillus subtilis 1423 -11532472 116932 yybh (de: hypothetical 14.6 kd protein in cotf-tetb intergenic region) (db:swissprot) YYBH\_BACSU P37496 BACILLUS SUBTILIS 1423 -11532472 7000688816 yybh hypothetical protein yybh (db:pir2.dat) S65989 S65989 Bacillus subtilis 1423 -11532472 7500953046 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:25752) (re:26141) (di:complement) BAC180K D26185 g467349 Bacillus subtilis 1423 -11532472 214949 yybh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814.) (le:177684) (re:178073) (di:complement) BSUB0021 Z99124 g2636611 Bacillus subtilis 1423 -11532472 206192 yybh hypothetical protein yybh (db:pir) S65989 S65989 Bacillus subtilis 1423 -11532472 6500728614 hypothetical protein: hypothetical 14.6 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybH yybH Bacillus subtilis 1423 -11532472

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818843	6876	29032	291	96

Description

GTC ORF with score 189 to: (sr:schizosaccharomyces pombe (strain 972h-) dna) (db:genpept-pln1) (de:schizosaccharomyces pombe small phosphorylated subunit common torna polymerases i, ii and iii (rpb6) gene, complete cds.) (nt:common to rna polymerases ...)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818853	6877	29033	750	249

Description

5000689868 hypothetical protein:hypothetical 31.3 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybG yybG Bacillus subtilis 1423 -11532473 116931 yybg (de:hypothetical 31.3 kd protein in cotf-tetb intergenic region) (db:swissprot) YBGB\_BACSU P37497 BACILLUS SUBTILIS 1423 -11532473 7000688815 yybg conserved hypothetical protein yybg (db:pir2.dat) S65990 S65990 Bacillus subtilis 1423 -11532473 7500953045 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:26287) (re:27126) (di:direct) BAC180K D26185 g467350 Bacillus subtilis 1423 -11532473 214950 yybg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:178219) (re:179058) (di:direct) BSUB0021 Z99124 g2636612 Bacillus subtilis 1423 -11532473 206193 yybg conserved hypothetical protein yybg (db:pir) S65990 S65990 Bacillus subtilis 1423 -11532473 6500728615 hypothetical protein:hypothetical 31.3 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybG yybG Bacillus subtilis 1423 -11532473

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818866	6878	29034	300	100

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818875	6879	29035	186	61

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818890	6880	29036	489	162

Description

5000689867 hypothetical protein:hypothetical 44.2 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybF yybF Bacillus subtilis 1423 -11532474 116930 yybf (de:hypothetical 44.2 kd protein in cotf-tetb intergenic region) (db:swissprot) YYBF\_BACSU P37498 BACILLUS SUBTILIS 1423 -11532474 7000688814 yybf antibiotic resistance protein homolog yybf (cl:probable antibiotic resistance protein yybf) (db:pir2.dat) S65991 S65991 Bacillus subtilis 1423 -11532474 7500953044 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:27159) (re:28373) (di:complement) BAC180K D26185 g467351 Bacillus subtilis 1423 -11532474 214951 yybf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to antibiotic resistance protein) (le:179091) (re:180305) (di:complement) BSUB0021 Z99124 g2636613 Bacillus subtilis 1423 -11532474 206194 yybf antibiotic resistance protein homolog yybf (db:pir) S65991 S65991 Bacillus subtilis 1423 -11532474 6500728616 hypothetical protein:hypothetical 44.2 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybF yybF Bacillus subtilis 1423 -11532474

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818904	6881	29037	489	162

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818912	6882	29038	927	308

Description

GTC ORF with score 1003 to: (sr:baker's yeast) (db:genpept-pln1) (de:saccharomyces cerevisiae splicing factor prp43p (prp43) gene, complete cds.) (nt:proposed function in spliceosome disassembly; deah) (le:379) (re:2682) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818918	6883	29039	315	104

Description

5000688934 hypothetical protein:hypothetical transcriptional regulator in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybE yybE Bacillus subtilis 1423 -11532475  
 116929 yybe (de:hypothetical transcriptional regulator in cotf-tetb intergenic region) (db:swissprot) YYBE\_BACSU P37499 BACILLUS SUBTILIS 1423 -11532475 7000688813 yybe transcription regulator lysr family homolog yybe (cl:probable transcription regulator lysr) (db:pir2.dat) S65992 S65992 Bacillus subtilis 1423 -11532475 7500953043 lysr family of transcriptional regulator (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:28602) (re:29438) (di:direct) BAC180K D26185 g467352 Bacillus subtilis 1423 -11532475 214952 yybe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to transcriptional regulator (lysr family)) (le:180534) (re:181370) (di:direct) BSUB0021 Z99124 g2636614 Bacillus subtilis 1423 -11532475 206294 yybe transcriptional regulator lysr family homolog yybe (db:pir) S65992 S65992 Bacillus subtilis 1423 -11532475  
 6500728617 hypothetical protein:hypothetical transcriptional regulator in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybE yybE Bacillus subtilis 1423 -11532475

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818919	6884	29040	1233	410

Description

5000689866 hypothetical protein:hypothetical 16.6 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybD yybD Bacillus subtilis 1423 -11532476  
 116928 yybd (de:hypothetical 16.6 kd protein in cotf-tetb intergenic region) (db:swissprot) YYBD\_BACSU P37500 BACILLUS SUBTILIS 1423 -11532476 7000688812 yybd conserved hypothetical protein yybd (cl:hypothetical protein yjcf) (db:pir2.dat) S65993 S65993 Bacillus subtilis 1423 -11532476 7500953042 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:29452) (re:29895) (di:direct) BAC180K D26185 g467353 Bacillus subtilis 1423 -11532476 214953 yybd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:181384) (re:181827) (di:direct) BSUB0021 Z99124 g2636615 Bacillus subtilis 1423 -11532476 206195 yybd conserved hypothetical protein yybd (cl:hypothetical protein yjcf) (db:pir) S65993 S65993 Bacillus subtilis 1423 -11532476  
 6500728618 hypothetical protein:hypothetical 16.6 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybD yybD Bacillus subtilis 1423 -11532476

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818924	6885	29041	282	93

Description

5000689865 hypothetical protein:hypothetical 17.6 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybC yybC Bacillus subtilis 1423 -11532477  
 116927 yybc (de:hypothetical 17.6 kd protein in cotf-tetb intergenic region) (db:swissprot) YYBC\_BACSU P37501 BACILLUS SUBTILIS 1423 -11532477  
 7000688811 yybc hypothetical protein yybc (db:pir2.dat) S65994 S65994 Bacillus subtilis 1423 -11532477 7500953041 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:29978) (re:30457) (di:direct) BAC180K D26185 g467354 Bacillus subtilis 1423 -11532477 214954 yybc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:181910) (re:182389) (di:direct) BSUB0021 Z99124 g2636616 Bacillus subtilis 1423 -11532477  
 206196 yybc hypothetical protein yybc (db:pir) S65994 S65994 Bacillus subtilis 1423 -11532477 6500728619 hypothetical protein:hypothetical 17.6 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybC yybC Bacillus subtilis 1423 -11532477

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818932	6886	29042	225	74

Description

5000689864 hypothetical protein:hypothetical 25.3 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybB yybB Bacillus subtilis 1423 -11532478  
 116926 yybb (de:hypothetical 25.3 kd protein in cotf-tetb intergenic region) (db:swissprot) YYBB\_BACSU P37502 BACILLUS SUBTILIS 1423 -11532478  
 7000688810 yybb conserved hypothetical protein yybb (db:pir2.dat) S65995 S65995 Bacillus subtilis 1423 -11532478 7500953040 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:30632) (re:31294) (di:complement) BAC180K D26185 g467355 Bacillus subtilis 1423 -11532478 214955 yybb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:182564) (re:183226) (di:complement) BSUB0021 Z99124 g2636617 Bacillus subtilis 1423 -11532478 206197 yybb conserved hypothetical protein yybb (db:pir) S65995 S65995 Bacillus subtilis 1423 -11532478 6500728620 hypothetical protein:hypothetical 25.3 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybB yybB Bacillus subtilis 1423 -11532478

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818933	6887	29043	990	330

Description

5000688933 hypothetical protein:hypothetical transcriptional regulator in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybA yybA Bacillus subtilis 1423 -11532479 116925 yyba (de:hypothetical transcriptional regulator in cotf-tetb intergenic region) (db:swissprot) YYBA\_BACSU P37503 BACILLUS SUBTILIS 1423 -11532479 7000688809 yyba transcription regulator marr family homolog yyba (db:pir2.dat) S65996 S65996 Bacillus subtilis 1423 -11532479 7500953039 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:31441) (re:31893) (di:complement) BAC180K D26185 g467356 Bacillus subtilis 1423 -11532479 214956 yyba (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to transcriptional regulator (marr family)) (le:183373) (re:183825) (di:complement) BSUB0021 Z99124 g2636618 Bacillus subtilis 1423 -11532479 206198 yyba transcriptional regulator marr family homolog yyba (db:pir) S65996 S65996 Bacillus subtilis 1423 -11532479 6500728621 hypothetical protein:hypothetical transcriptional regulator in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yybA yybA Bacillus subtilis 1423 -11532479

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818943	6888	29044	423	140

Description

5000689863 hypothetical protein:hypothetical 17.0 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaT yyaT Bacillus subtilis 1423 -11532480 116924 yyat (de:hypothetical 17.0 kd protein in cotf-tetb intergenic region) (db:swissprot) YYAT\_BACSU P37504 BACILLUS SUBTILIS 1423 -11532480 7000688808 yyat conserved hypothetical protein yyat (cl:hypothetical protein yjcf) (db:pir2.dat) S65997 S65997 Bacillus subtilis 1423 -11532480 7500953038 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:32013) (re:32459) (di:direct) BAC180K D26185 g467357 Bacillus subtilis 1423 -11532480 214957 yyat (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:183945) (re:184391) (di:direct) BSUB0021 Z99124 g2636619 Bacillus subtilis 1423 -11532480 206199 yyat conserved hypothetical protein yyat (cl:hypothetical protein yjcf) (db:pir) S65997 S65997 Bacillus subtilis 1423 -11532480 6500728622 hypothetical protein:hypothetical 17.0 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaT yyaT Bacillus subtilis 1423 -11532480

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818944	6889	29045	342	113

Description

5000689862 hypothetical protein:hypothetical 22.0 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaS yyaS Bacillus subtilis 1423 -11532481 116923 yyas (de:hypothetical 22.0 kd protein in cotf-tetb intergenic region) (db:swissprot) YYAS\_BACSU P37505 BACILLUS SUBTILIS 1423 -11532481 7000688807 yyas conserved hypothetical protein yyas (db:pir2.dat) S65998 S65998 Bacillus subtilis 1423 -11532481 7500953037 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:32456) (re:33061) (di:direct) BAC180K D26185 g467358 Bacillus subtilis 1423 -11532481 214958 yyas (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:184388) (re:184993) (di:direct) BSUB0021 Z99124 g2636620 Bacillus subtilis 1423 -11532481 206200 yyas conserved hypothetical protein yyas (db:pir) S65998 S65998 Bacillus subtilis 1423 -11532481 6500728623 hypothetical protein:hypothetical 22.0 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaS yyaS Bacillus subtilis 1423 -11532481

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818948	6890	29046	1473	490

Description

5000689861 hypothetical protein:hypothetical 20.4 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaR yyaR Bacillus subtilis 1423 -11532482 116922 yyar (de:hypothetical 20.4 kd protein in cotf-tetb intergenic region) (db:swissprot) YYAR\_BACSU P37506 BACILLUS SUBTILIS 1423 -11532482 7000688806 yyar streptothricine acetyl-transferase homolog yyar (db:pir2.dat) S65999 S65999 Bacillus subtilis 1423 -11532482 7500953036 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:33156) (re:33677) (di:complement) BAC180K D26185 g467359 Bacillus subtilis 1423 -11532482 214959 yyar (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to streptothricine acetyl-transferase) (le:185088) (re:185609) (di:complement) BSUB0021 Z99124 g2636621 Bacillus subtilis 1423 -11532482 206201 yyar streptothricine acetyl-transferase homolog yyar (db:pir) S65999 S65999 Bacillus subtilis 1423 -11532482 6500728624 hypothetical protein:hypothetical 20.4 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaR yyaR Bacillus subtilis 1423 -11532482

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818954	6891	29047	1119	372

Description

5000689860 hypothetical protein:hypothetical 13.9 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaQ yyaQ Bacillus subtilis 1423 -11532483  
 116921 yyaq (de:hypothetical 13.9 kd protein in cotf-tetb intergenic region) (db:swissprot) YYAQ\_BACSU P37507 BACILLUS SUBTILIS 1423 -11532483  
 7000688805 yyaq hypothetical protein yyaq (db:pir2.dat) S66000 S66000 Bacillus subtilis 1423 -11532483 7500953035 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:34088) (re:34444) (di:direct) BAC180K D26185 g467360 Bacillus subtilis 1423 -11532483 214960 yyaq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:186020) (re:186376) (di:direct) BSUB0021 Z99124 g2636622 Bacillus subtilis 1423 -11532483  
 206202 yyaq hypothetical protein yyaq (db:pir) S66000 S66000 Bacillus subtilis 1423 -11532483 6500728625 hypothetical protein:hypothetical 13.9 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaQ yyaQ Bacillus subtilis 1423 -11532483

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818967	6892	29048	210	69

Description

5000689859 hypothetical protein:hypothetical 21.7 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaP yyaP Bacillus subtilis 1423 -11532484  
 116920 yyap (de:hypothetical 21.7 kd protein in cotf-tetb intergenic region) (db:swissprot) YYAP\_BACSU P37508 BACILLUS SUBTILIS 1423 -11532484  
 7000688804 yyap conserved hypothetical protein yyap (db:pir2.dat) S66001 S66001 Bacillus subtilis 1423 -11532484 7500953034 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:34604) (re:35170) (di:direct) BAC180K D26185 g467361 Bacillus subtilis 1423 -11532484 214961 yyap (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins from b. subtilis) (le:186536) (re:187102) (di:direct) BSUB0021 Z99124 g2636623 Bacillus subtilis 1423 -11532484 206203 yyap conserved hypothetical protein yyap (db:pir) S66001 S66001 Bacillus subtilis 1423 -11532484 6500728626 hypothetical protein:hypothetical 21.7 kd protein in cotf-tetb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaP yyaP Bacillus subtilis 1423 -11532484

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818969	6893	29049	393	130

Description

5000689858 hypothetical protein:hypothetical 9.1 kd protein in tetb-exoa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaO yyaO Bacillus subtilis 1423 -11532485 116919 yyao (de:hypothetical 9.1 kd protein in tetb-exoa intergenic region) (db:swissprot) YYAO\_BACSU P37509 BACILLUS SUBTILIS 1423 -11532485 7000688803 yyao conserved hypothetical protein yyao (db:pir2.dat) F70085 F70085 Bacillus subtilis 1423 -11532485 7500953033 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:37402) (re:37641) (di:direct) BAC180K D26185 g467363 Bacillus subtilis 1423 -11532485 214963 yyao (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:189334) (re:189573) (di:direct) BSUB0021 Z99124 g2636626 Bacillus subtilis 1423 -11532485 206204 yyao conserved hypothetical protein yyao (db:pir) F70085 F70085 Bacillus subtilis 1423 -11532485 6500728627 hypothetical protein:hypothetical 9.1 kd protein in tetb-exoa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaO yyaO Bacillus subtilis 1423 -11532485

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501818974	6894	29050	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818978	6895	29051	822	274

Description

5000688932 hypothetical protein:hypothetical transcriptional regulator in tetb-exoa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaN yyaN Bacillus subtilis 1423 -11532486 116918 yyan (de:hypothetical transcriptional regulator in tetl-exoa intergenic region) (db:swissprot) YYAN\_BACSU P37510 BACILLUS SUBTILIS 1423 -11532486 7000688802 yyan transcription regulator merr family homolog yyan:probable dna binding protein yyan (cl:transcription repressor glnr) (db:pir2.dat) S66004 S66004 Bacillus subtilis 1423 -11532486 7500953032 dna binding protein probale (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:37792) (re:38208) (di:direct) BAC180K D26185 g467364 Bacillus subtilis 1423 -11532486 214964 yyan (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to transcriptional regulator (merr family)) (le:189724) (re:190140) (di:direct) BSUB0021 Z99124 g2636627 Bacillus subtilis 1423 -11532486 206271 yyan transcriptional regulator merr family homolog yyan:probable dna binding protein yyan (db:pir) S66004 S66004 Bacillus subtilis 1423 -11532486 6500728628 hypothetical protein:hypothetical transcriptional regulator in tetb-exoa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaN yyaN Bacillus subtilis 1423 -11532486

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501818982	6896	29052	312	103

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819001	6897	29053	480	159

Description

GTC ORF with score 92 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome iv cosmid 9819.) (nt:small region of similarity to nadh-ubiquinone) (le:3007) (re:3876) (di:complement)



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819002	6898	29054	705	234

Description

GTC ORF with score 209 to: (sr:baker's yeast strain=s288c (ab972))  
(db:genpept-pln1) (de:saccharomyces cerevisiae chromosome iv cosmid 9819.)  
(nt:small region of similarity to nadh-ubiquinone) (le:3007) (re:3876)  
(di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819013	6899	29055	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819018	6900	29056	579	192

Description

GTC ORF with score 609 to: (sr:gibberella zeae (sub\_species:graminearum, strain:f15) dna) (db:genpept-pln2) (de:gibberella zeae genes for trichothecene 3-o-acetyltransferase,utp-ammonia ligase and phosphate permease, complete cds.) (le:6588:7075:7622) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819023	6901	29057	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819027	6902	29058	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819029	6903	29059	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819031	6904	29060	663	220

Description

5000689857 hypothetical protein:hypothetical 32.9 kd protein in tetb-exoa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaM yyaM Bacillus subtilis 1423 -11532487 116917 yyam (de:hypothetical 32.9 kd protein in tetb-exoa intergenic region) (db:swissprot) YYAM\_BACSU P37511 BACILLUS SUBTILIS 1423 -11532487 7000688801 yyam conserved hypothetical protein yyam (db:pir2.dat) S66005 S66005 Bacillus subtilis 1423 -11532487 7500953031 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:38205) (re:39122) (di:direct) BAC180K D26185 g467365 Bacillus subtilis 1423 -11532487 214965 yyam (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:190137) (re:191054) (di:direct) BSUB0021 Z99124 g2636628 Bacillus subtilis 1423 -11532487 206205 yyam conserved hypothetical protein yyam (db:pir) S66005 S66005 Bacillus subtilis 1423 -11532487 6500728629 hypothetical protein:hypothetical 32.9 kd protein in tetb-exoa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaM yyaM Bacillus subtilis 1423 -11532487

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819059	6905	29061	261	86

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819066	6906	29062	846	282

Description

5000689856 hypothetical protein:hypothetical 78.8 kd protein in tetb-exoa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaL yyaL Bacillus subtilis 1423 -11532488 116916 yyaL (de:hypothetical 78.8 kd protein in tetb-exoa intergenic region) (db:swissprot) YYAL\_BACSU P37512 BACILLUS SUBTILIS 1423 -11532488 7000688800 yyaL conserved hypothetical protein yyaL (cl:conserved hypothetical protein yyaL) (db:pir2.dat) S66006 S66006 Bacillus subtilis 1423 -11532488 7500953030 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:39194) (re:41263) (di:direct) BAC180K D26185 g467366 Bacillus subtilis 1423 -11532488 214966 yyaL (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:191126) (re:193195) (di:direct) BSUB0021 Z99124 g2636629 Bacillus subtilis 1423 -11532488 206206 yyaL conserved hypothetical protein yyaL (db:pir) S66006 S66006 Bacillus subtilis 1423 -11532488 6500728630 hypothetical protein:hypothetical 78.8 kd protein in tetb-exoa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaL yyaL Bacillus subtilis 1423 -11532488

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819068	6907	29063	381	126

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819080	6908	29064	657	218

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819088	6909	29065	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819096	6910	29066	291	96

Description

5000689855 hypothetical protein:hypothetical 34.0 kd protein in tetb-exoa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaK yyaK Bacillus subtilis 1423 -11532489  
 116915 yyak (de:hypothetical 34.0 kd protein in tetb-exoa intergenic region) (db:swissprot) YYAK\_BACSU P37513 BACILLUS SUBTILIS 1423 -11532489  
 7000688799 yyak hypothetical protein yyak (db:pir2.dat) S66007 S66007 Bacillus subtilis 1423 -11532489 7500953029 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:41260) (re:42159) (di:complement) BAC180K D26185 g467367 Bacillus subtilis 1423 -11532489  
 214967 yyak (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:193192) (re:194091) (di:complement) BSUB0021 Z99124 g2636630 Bacillus subtilis 1423 -11532489  
 206207 yyak hypothetical protein yyak (db:pir) S66007 S66007 Bacillus subtilis 1423 -11532489 6500728631 hypothetical protein:hypothetical 34.0 kd protein in tetb-exoa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaK yyaK Bacillus subtilis 1423 -11532489

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819104	6911	29067	573	190

Description

5000689854 hypothetical protein:hypothetical 49.7 kd protein in tetb-exoa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaJ yyaJ Bacillus subtilis 1423 -11532490  
 116914 yyaj (de:hypothetical 49.7 kd protein in tetb-exoa intergenic region) (db:swissprot) YYAJ\_BACSU P37514 BACILLUS SUBTILIS 1423 -11532490  
 7000688798 yyaj transporter homolog yyaj (db:pir2.dat) S66008 S66008 Bacillus subtilis 1423 -11532490 7500953028 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:42385) (re:43740) (di:direct) BAC180K D26185 g467368 Bacillus subtilis 1423 -11532490 214968 yyaj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to transporter) (le:194317) (re:195672) (di:direct) BSUB0021 Z99124 g2636631 Bacillus subtilis 1423 -11532490 206208 yyaj transporter homolog yyaj (db:pir) S66008 S66008 Bacillus subtilis 1423 -11532490 6500728632 hypothetical protein:hypothetical 49.7 kd protein in tetb-exoa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaJ yyaJ Bacillus subtilis 1423 -11532490

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819105	6912	29068	774	258

Description

GTC ORF with score 456 to: (fn:conversion of o-methylsterigmatocystin to) (db:genpept-pln2) (de:aspergillus flavus omst-oxidoreductase (ord1) mrna, complete cds.) (nt:cytochrome p450 monooxygenase (cyp64)) (le:235) (re:1821) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819129	6913	29069	606	202

Description

6500728633 hypothetical protein:hypothetical 20.2 kd protein in tetb-exoa intergenic region:orfg (gtcfc:14.1) (ec:2.3.1.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaI yyaI Bacillus subtilis 1423 -11532491 116913 maa (ec:2.3.1.79) (de:transacetylase)) (db:swissprot) MAA\_BACSU P37515 BACILLUS SUBTILIS 1423 -11532491 7000688797 yyai probable o-acetyltransferase:yyai (cl:galactoside acetyltransferase) (ec:2.3.1.-) (db:pir2.dat) I39920 I39920 Bacillus subtilis 1423 -11532491 7500885252 acetyltransferase of cyce\_laca\_nodI family (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:43774) (re:44328) (di:complement) BAC180K D26185 g467369 Bacillus subtilis 1423 -11532491 214969 (sr:bacillus subtilis (strain bd99) dna) (db:genpept-bct1) (de:bacillus subtilis membrane transport protein homologue (orfd), acetyltransferase homologue (orfg), orff, purr repressor homologue(orfe), complete cds's.) (nt:probable operon with orff. possi... BACORFDEFG L16865 g438465 Bacillus subtilis 1423 -11532491 216412 yyai (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to galactoside acetyltransferase) (le:195706) (re:196260) (di:complement) BSUB0021 Z99124 g2636632 Bacillus subtilis 1423 -11532491 169844 yyai galactoside acetyltransferase homolog yyai (db:pir) I39920 I39920 Bacillus subtilis 1423 -11532491 5000688487 (de:(yyai) (pn:hypothetical 20) (gtcfc:7.01) (ec:)(yyai\_bacsu) (keggfc:11.2) (bsorffc:2.1.0) (db:gtc-bacillus subtilis)) yyai yyai Bacillus subtilis 1423 10058638

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819139	6914	29070	270	89

Description

5000689853 hypothetical protein:hypothetical 14.4 kd protein in tetb-exoa intergenic region:orff (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaH yyaH Bacillus subtilis 1423 -11532492 116912 yyah (de:hypothetical 14.4 kd protein in tetb-exoa intergenic region (orff)) (db:swissprot) YYAH\_BACSU P37516 BACILLUS SUBTILIS 1423 -11532492 7000688796 yyah hypothetical protein yyah (db:pir2.dat) I39921 I39921 Bacillus subtilis 1423 -11532492 7500953027 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:44346) (re:44726) (di:complement) BAC180K D26185 g467370 Bacillus subtilis 1423 -11532492 214970 (sr:bacillus subtilis (strain bd99) dna) (db:genpept-bct1) (de:bacillus subtilis membrane transport protein homologue (orfd), acetyltransferase homologue (orfg), orff, purr repressor homologue(orfe), complete cds's.) (nt:possible operon with orfg. hydro... BACORFDEFG L16865 g438466 Bacillus subtilis 1423 -11532492 216413 yyah (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:196278) (re:196658) (di:complement) BSUB0021 Z99124 g2636633 Bacillus subtilis 1423 -11532492 170250 yyah hypothetical protein yyah (db:pir) I39921 I39921 Bacillus subtilis 1423 -11532492 6500728634 hypothetical protein:hypothetical 14.4 kd protein in tetb-exoa intergenic region:orff (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaH yyaH Bacillus subtilis 1423 -11532492

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819147	6915	29071	585	195

Description

5000688931 hypothetical protein:hypothetical transcriptional regulator in tetb-exoa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaG yyaG Bacillus subtilis 1423 -11532493  
 116911 yyag (de:hypothetical transcriptional regulator in tetl-exoa intergenic region) (db:swissprot) YYAG\_BACSU P37517 BACILLUS SUBTILIS 1423 -11532493 7000688795 yyag transcription regulator laci family homolog yyag (db:pir2.dat) S66011 S66011 Bacillus subtilis 1423 -11532493 7500953026 laci family of transcriptional repressor (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:44782) (re:45717) (di:complement) BAC180K D26185 g467371 Bacillus subtilis 1423 -11532493 214971 yyag (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to transcriptional regulator (laci family)) (le:196714) (re:197649) (di:complement) BSUB0021 Z99124 g2636634 Bacillus subtilis 1423 -11532493 206295 yyag transcriptional regulator laci family homolog yyag (db:pir) S66011 S66011 Bacillus subtilis 1423 -11532493 6500728635 hypothetical protein:hypothetical transcriptional regulator in tetb-exoa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaG yyaG Bacillus subtilis 1423 -11532493

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819149	6916	29072	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819161	6917	29073	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819165	6918	29074	1020	339

Description

GTC ORF with score 102 to: (or:Xenopus laevis) (fn:involved in endocytosis) (sr:african clawed frog) (db:genpept-vrt) (de:xenopus laevis intersectin mrna, complete cds.) (nt:eh domain and sh3 domain containing protein;) (le:193) (re:4005) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819166	6919	29075	660	220

Description

5000689852 hypothetical protein:hypothetical 40.1 kd gtp-binding protein in rpsf-spo0j intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaF yyaF Bacillus subtilis 1423 -11532494 116910 yyaf (de:region) (db:swissprot) YYAF\_BACSU P37518 BACILLUS SUBTILIS 1423 -11532494 7000688794 yyaf probable gtp-binding protein yyaf (cl:yeast probable purine nucleotide-binding protein ybr025c) (db:pir2.dat) S66016 S66016 Bacillus subtilis 1423 -11532494 7500953025 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:47839) (re:48939) (di:complement) BAC180K D26185 g467376 Bacillus subtilis 1423 -11532494 214976 yyaf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins) (le:199771) (re:200871) (di:complement) BSUB0021 Z99124 g2636639 Bacillus subtilis 1423 -11532494 206210 yyaf probable gtp-binding protein yyaf (db:pir) S66016 S66016 Bacillus subtilis 1423 -11532494 6500728636 hypothetical protein:hypothetical 40.1 kd gtp-binding protein in rpsf-spo0j intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaF yyaF Bacillus subtilis 1423 -11532494

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819173	6920	29076	999	333

Description

5000689851 hypothetical protein:hypothetical 73.9 kd protein in rpsf-spo0j intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaE yyaE Bacillus subtilis 1423 -11532495 116909 yyae (de:hypothetical 73.9 kd protein in rpsf-spo0j intergenic region) (db:swissprot) YYAE\_BACSU P37519 BACILLUS SUBTILIS 1423 -11532495 7000688793 yyae formate dehydrogenase homolog yyae:hypothetical protein 6 replication origin region (db:pir2.dat) S66017 S66017 Bacillus subtilis 1423 -11532495 7500953024 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:49066) (re:51069) (di:complement) BAC180K D26185 g467377 Bacillus subtilis 1423 -11532495 214977 yyae (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to formate dehydrogenase) (le:200998) (re:203001) (di:complement) BSUB0021 Z99124 g2636640 Bacillus subtilis 1423 -11532495 206211 yyae formate dehydrogenase homolog yyae:hypothetical protein 6 replication origin region (db:pir) S66017 S66017 Bacillus subtilis 1423 -11532495 6500728637 hypothetical protein:hypothetical 73.9 kd protein in rpsf-spo0j intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaE yyaE Bacillus subtilis 1423 -11532495



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819199	6921	29077	345	114

Description

GTC ORF with score 441 to: (db:genpept-pln1) (ec:3.1.3.2) (de:aspergillus  
ficuum atcc 66876 acid phosphatase (apha) gene,complete cds.)  
(nt:extracellular ph 6.0 optimum; orthophosphoric) (le:320:724:1469:1959)  
(re:675:1419:1909:2310) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819200	6922	29078	483	160

Description

GTC ORF with score 663 to: (db:genpept-pln1) (ec:3.1.3.2) (de:aspergillus  
ficuum atcc 66876 acid phosphatase (apha) gene,complete cds.)  
(nt:extracellular ph 6.0 optimum; orthophosphoric) (le:320:724:1469:1959)  
(re:675:1419:1909:2310) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819204	6923	29079	555	184

Description

GTC ORF with score 650 to: (db:genpept-pln1) (ec:3.1.3.2) (de:aspergillus  
ficuum atcc 66876 acid phosphatase (apha) gene,complete cds.)  
(nt:extracellular ph 6.0 optimum; orthophosphoric) (le:320:724:1469:1959)  
(re:675:1419:1909:2310) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819205	6924	29080	228	75

Description

5000689850 hypothetical protein:hypothetical 37.7 kd protein in rpsf-spo0j intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaD yyaD Bacillus subtilis 1423 -11532496 214978 yyad (de:hypothetical 37.7 kd protein in rpsf-spo0j intergenic region) (db:swissprot) YYAD\_BACSU P37520 BACILLUS SUBTILIS 1423 -11532496 7000688792 yyad conserved hypothetical protein yyad replication origin region (db:pir2.dat) I40448 I40448 Bacillus subtilis 1423 -11532496 7500953023 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:51420) (re:52436) (di:complement) BAC180K D26185 g467378 Bacillus subtilis 1423 -11532496 219470 (db:genpept-bct1) (de:b.subtilis genes rpmh, rnpa, 50kd, gida and gidb.) (nt:unnamed protein product) (le:10964) (re:11980) (di:direct) BSORIGS X62539 g580907 Bacillus subtilis 1423 -11532496 7502851768 yyad (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to hypothetical proteins from b. subtilis) (le:203352) (re:204368) (di:complement) BSUB0021 Z99124 g2636641 Bacillus subtilis 1423 -11532496 116908 yyad (de:hypothetical 37.7 kd protein in rpsf-spo0j intergenic region) (db:swissprot) YYAD\_BACSU P37520 BACILLUS SUBTILIS 1423 -11532496 170222 yyad conserved hypothetical protein yyad replication origin region (db:pir) I40448 I40448 Bacillus subtilis 1423 -11532496 6500728638 hypothetical protein:hypothetical 37.7 kd protein in rpsf-spo0j intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaD yyaD Bacillus subtilis 1423 -11532496

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819208	6925	29081	342	113

Description

GTC ORF with score 414 to: (db:genpept-pln1) (de:aspergillus niger atcc 46951 acid phosphatase (apha) gene, partialcds.) (nt:phosphate-repressible; gene previously called paca) (le:<1:84:829:1323) (re:35:779:1269:1674) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819218	6926	29082	708	235

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819248	6927	29083	1326	441

Description

5000689849 hypothetical protein:hypothetical 22.5 kd protein in rpsf-spo0j intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yyaC yyaC Bacillus subtilis 1423 -11532497  
214979 yyac (de:hypothetical 22.5 kd protein in rpsf-spo0j intergenic region) (db:swissprot) YYAC\_BACSU P37521 BACILLUS SUBTILIS 1423 -11532497  
7000688791 yyac hypothetical protein yyac replication origin region (db:pir2.dat) I40446 I40446 Bacillus subtilis 1423 -11532497 7500953022 unknown (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:52896) (re:53513) (di:direct) BAC180K D26185 g467379 Bacillus subtilis 1423 -11532497 219468 (db:genpept-bct1) (de:b.subtilis genes rpmh, rnpa, 50kd, gida and gidb.) (nt:unnamed protein product) (le:9887) (re:10504) (di:complement) BSORIGS X62539 g40032 Bacillus subtilis 1423 -11532497 7502851769 yyac (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:204828) (re:205445) (di:direct) BSUB0021 Z99124 g2636642 Bacillus subtilis 1423 -11532497 116907 yyac (de:hypothetical 22.5 kd protein in rpsf-spo0j intergenic region) (db:swissprot) YYAC\_BACSU P37521 BACILLUS SUBTILIS 1423 -11532497 170212 yyac hypothetical protein yyac replication origin region (db:pir) I40446 I40446 Bacillus subtilis 1423 -11532497  
6500728639 hypothetical protein:hypothetical 22.5 kd protein in rpsf-spo0j intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1)  
(db:gtc-bacillus subtilis) yyaC yyaC Bacillus subtilis 1423 -11532497

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819252	6928	29084	600	199

Description

GTC ORF with score 100 to: (db:genpept-vrl) (de:murine cytomegalovirus (clone hindiii d) transmembrane proteingene, complete cds; dutpase (dut) gene, complete cds; ul71 genehomologue, complete cds; helicase/primase (hel/pri) gene, completedcds; tegument...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819275	6929	29085	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819280	6930	29086	183	60
<u>Description</u>				
5000689848 hypothetical protein:hypothetical 17.0 kd protein in spo0j-gidb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaB yyaB Bacillus subtilis 1423 -11532498 214982 yyab (de:hypothetical 17.0 kd protein in spo0j-gidb intergenic region) (db:swissprot) YYAB_BACSU P37523 BACILLUS SUBTILIS 1423 -11532498 7000688790 yyab hypothetical protein yyab:hypothetical protein 3 replication origin region (db:pir2.dat) I40443 I40443 Bacillus subtilis 1423 -11532498 7500953021 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:55402) (re:55842) (di:direct) BAC180K D26185 g467382 Bacillus subtilis 1423 -11532498 219465 (db:genpept-bct1) (de:b.subtilis genes rpmh, rnpa, 50kd, gida and gidb.) (nt:unnamed protein product) (le:7558) (re:7998) (di:complement) BSORIGS X62539 g40029 Bacillus subtilis 1423 -11532498 7502851770 yyab (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:207334) (re:207774) (di:direct) BSUB0021 Z99124 g2636645 Bacillus subtilis 1423 -11532498 116906 yyab (de:hypothetical 17.0 kd protein in spo0j-gidb intergenic region) (db:swissprot) YYAB_BACSU P37523 BACILLUS SUBTILIS 1423 -11532498 170207 yyab hypothetical protein yyab:hypothetical protein 3 replication origin region (db:pir) I40443 I40443 Bacillus subtilis 1423 -11532498 6500728640 hypothetical protein:hypothetical 17.0 kd protein in spo0j-gidb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaB yyaB Bacillus subtilis 1423 -11532498				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819282	6931	29087	855	284

Description

5000689847 hypothetical protein:hypothetical 32.8 kd protein in spo0j-gidb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaa yyaa Bacillus subtilis 1423 -11532499  
214983 yyaa (de:hypothetical 32.8 kd protein in spo0j-gidb intergenic region) (db:swissprot) YYAA\_BACSU P37524 BACILLUS SUBTILIS 1423 -11532499  
7000688789 yyaa dna-binding protein spo0j-like homolog yyaa:probable dna binding protein replication origin region (cl:bacillus subtilis transport protein spo0j) (db:pir2.dat) I40442 I40442 Bacillus subtilis 1423 -11532499  
7500953020 dna binding protein probable (sr:bacillus subtilis (sub\_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:55893) (re:56744) (di:complement) BAC180K D26185 g467383 Bacillus subtilis 1423 -11532499  
219464 (db:genpept-bct1) (de:b.subtilis genes rpmh, rnpa, 50kd, gida and gidb.) (nt:unnamed protein product) (le:6656) (re:7507) (di:direct) BSORIGS X62539 g40028 Bacillus subtilis 1423 -11532499 7502851771 yyaa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to dna-binding protein spo0j-like) (le:207825) (re:208676) (di:complement) BSUB0021 Z99124 g2636646 Bacillus subtilis 1423 -11532499 116905 yyaa (de:hypothetical 32.8 kd protein in spo0j-gidb intergenic region) (db:swissprot) YYAA\_BACSU P37524 BACILLUS SUBTILIS 1423 -11532499 170456 yyaa dna-binding protein spo0j-like homolog yyaa:probable dna binding protein replication origin region (db:pir) I40442 I40442 Bacillus subtilis 1423 -11532499 6500728641 hypothetical protein:hypothetical 32.8 kd protein in spo0j-gidb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yyaa yyaa Bacillus subtilis 1423 -11532499

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819283	6932	29088	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819285	6933	29089	1200	400

Description

5000689561 ycxs:rsbs antagonist of rsbt:through dephosphorylation by rsbx and activation:hypothetical 13.3 kd protein in rsbu 5region:orfs (gtcfc:14.3) (keggfc:14.2) (bsorffc:8.3.1) (db:gtc-bacillus subtilis) rsbs rsbs Bacillus subtilis 1423 -11532500 111055 rsbs (de:anti-sigma b factor antagonist) (db:swissprot) RSBS\_BACSU P42410 BACILLUS SUBTILIS 1423 -11532500 7000687505 rsbs negative regulator of sigma-b activity antagonist of rsbt rsbs (db:pir2.dat) F69701 F69701 Bacillus subtilis 1423 -11532500 216651 orfs sigma-b regulator (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (le:53300) (re:53665) (di:direct) AB001488 AB001488 g1881278 Bacillus subtilis 1423 -11532500 302723 (sr:bacillus subtilis (strain 168 marburg) dna) (db:genpept-bct1) (de:bacillus subtilis (clones paw10, paw50) regulator (rsbu) gene,complete cds, positive regulator (rsbv), 5' end.) (nt:orfs; putative) (le:1187) (re:1552) (di:direct) BACRSBU L35574 g642075 Bacillus subtilis 1423 -11532500 7500891133 rsbs antagonist of rsbt through dephosphorylation by (fn:negative regulation of sigma-b activity) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:alternate gene name: ycxs) (le:117044) (re:117409) (di:direct) BSUB0003 Z99106 g2632768 Bacillus subtilis 1423 -11532500 6500728642 ycxs antagonist of rsbt:through dephosphorylation by rsbx and activation:hypothetical 13.3 kd protein in rsbu 5region:orfs (gtcfc:14.3) (keggfc:14.2) (bsorffc:8.3.1) (db:gtc-bacillus subtilis) rsbs rsbs Bacillus subtilis 1423 -11532500

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819290	6934	29090	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819307	6935	29091	411	136

Description

GTC ORF with score 214 to: (sr:homo sapiens male bone marrow myeloblast cell\_line:kg-1 cdna t) (db:genpept-pri2) (de:human mrna for kiaa0212 gene, complete cds.) (nt:containing atp/gtp-binding site motif a(p-loop):) (le:59) (re:2032) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819335	6936	29092	804	267

Description

6500728643 carboxylesterase na (gtcfc:14.3) (ec:3.1.1.1) (keggfc:14.1) (bsorffc:8.3.1) (db:gtc-bacillus subtilis) nap nap Bacillus subtilis 1423 -11532501 7000692325 nap carboxylesterase na nap (db:pir2.dat) C69664 C69664 Bacillus subtilis 1423 -11532501 302796 nap carboxylesterase np (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (le:125521) (re:126423) (di:complement) AB001488 AB001488 g1881351 Bacillus subtilis 1423 -11532501 7500963495 nap carboxylesterase na (db:genpept-bct1) (ec:3.1.1.1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:189267) (re:190169) (di:complement) BSUB0003 Z99106 g2632844 Bacillus subtilis 1423 -11532501

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819340	6937	29093	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819345	6938	29094	279	92

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819346	6939	29095	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819348	6940	29096	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819357	6941	29097	795	264

Description

6500728644 yhae:hit hit-like protein (gtcfc:14.3) (keggfc:14.2) (bsorffc:8.3.1) (db:gtc-bacillus subtilis) hit hit Bacillus subtilis 1423 -11532502 7500883365 hit (de:hit protein) (db:swissprot) HIT\_BACSU O07513 BACILLUS SUBTILIS 1423 -11532502 7000693101 hit cell-cycle regulation histidine triad hit protein (cl:protein kinase c inhibitor:histidine triad homology) (db:pir2.dat) A69642 A69642 Bacillus subtilis 1423 -11532502 7500883367 hit hit-like protein (fn:cell-cycle regulation (inhibition of cell) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: yhae) (le:76488) (re:76925) (di:complement) BSUB0006 Z99109 g2633339 Bacillus subtilis 1423 -11532502 4000714539 yhae hypothetical protein (db:genpept-bct1) (de:bacillus subtilis 10.6 kb chromosomal dna: glyb-prsa region.) (nt:similarity to the hit family of proteins) (le:3988) (re:4425) (di:direct) BSY14077 Y14077 g2226116 Bacillus subtilis 1423 -11532502

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819385	6942	29098	240	80

Description

5000689470 small basic protein (gtcfc:14.3) (keggfc:14.2) (bsorffc:8.3.1) (db:gtc-bacillus subtilis) sbp sbp Bacillus subtilis 1423 -11532503 98001 sbp (de:small basic protein) (db:swissprot) SBP\_BACSU P28265 BACILLUS SUBTILIS 1423 -11532503 7000686566 sbp small basic protein sbp (db:pir2.dat) I39846 I39846 Bacillus subtilis 1423 -11532503 7500891341 sbp (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis ftsza genes, complete cds.) (le:42) (re:407) (di:direct) BACFTSZA M22630 g142939 Bacillus subtilis 1423 -11532503 215631 sbp small basic protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:200541) (re:200906) (di:direct) BSUB0008 Z99111 g2633898 Bacillus subtilis 1423 -11532503 170518 sbp small basic protein sbp (db:pir) I39846 I39846 Bacillus subtilis 1423 -11532503 6500728645 small basic protein (gtcfc:14.3) (keggfc:14.2) (bsorffc:8.3.1) (db:gtc-bacillus subtilis) sbp sbp Bacillus subtilis 1423 -11532503



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819388	6943	29099	261	86

Description

6500728646 ppr:pelb pectate lyase (gtcfc:14.3) (ec:4.2.2.10) (keggfc:14.1) (bsorffc:8.3.1) (db:gtc-bacillus subtilis) pelB pelB Bacillus subtilis 1423 -11532504 7000694352 pelb pectate lyase pelb (db:pir2.dat) E69674 E69674 Bacillus subtilis 1423 -11532504 5500701874 pelb pectin lyase (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to e.carotovora pectin lyase (314 aa)) (le:14737) (re:15774) (di:direct) AF027868 AF027868 g2618998 Bacillus subtilis 1423 -11532504 7500965042 pelb pectate lyase (db:genpept-bct1) (ec:4.2.2.10) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:alternate gene name: ppr) (le:33828) (re:34865) (di:direct) BSUB0011 Z99114 g2634258 Bacillus subtilis 1423 -11532504

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819389	6944	29100	468	155

Description

6500728647 squalene-hopene cyclase (gtcfc:14.3) (ec:5.4.99.-) (keggfc:14.2) (bsorffc:8.3.1) (db:gtc-bacillus subtilis) sqhC sqhC Bacillus subtilis 1423 -11532505 7000694631 sqhc squalene-hopene cyclase sqhc (db:pir2.dat) A69718 A69718 Bacillus subtilis 1423 -11532505 5500701920 sqhc squalene-hopene cyclase (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to b.japonicum squalene-hopene cyclase (658) (le:82163) (re:83833) (di:direct) AF027868 AF027868 g2619017 Bacillus subtilis 1423 -11532505 7500965224 sqhc squalene-hopene cyclase (fn:hopanoid metabolism) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:101254) (re:102924) (di:direct) BSUB0011 Z99114 g2634325 Bacillus subtilis 1423 -11532505

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819391	6945	29101	279	93

Description

6500728648 yzzh:tig prolyl isomerase:trigger factor:tf:vegetative protein 2 (gtcfc:14.3) (keggfc:14.2) (bsorffc:8.3.1) (db:gtc-bacillus subtilis) tig tig Bacillus subtilis 1423 -11532506 7000694829 tig trigger factor prolyl isomerase tig (cl:trigger factor) (db:pir2.dat) F69723 F69723 Bacillus subtilis 1423 -11532506 220350 tig trigger factor prolyl isomerase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: yzzh) (le:90286) (re:91560) (di:complement) BSUB0015 Z99118 g2635288 Bacillus subtilis 1423 -11532506 304223 tig trigger factor (db:genpept-bct1) (de:bacillus subtilis genomic sequence 89009bp.) (nt:homology to trigger factor of haemophilus) (le:78347) (re:79621) (di:direct) BSZ75208 Z75208 g1770074 Bacillus subtilis 1423 -11532506

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819394	6946	29102	537	178

Description

6500728649 hippurate hydrolase isomerase:hippurate hydrolase (gtcfc:14.3) (ec:3.5.1.32) (keggfc:14.1) (bsorffc:8.3.1) (db:gtc-bacillus subtilis) hipo hipo Bacillus subtilis 1423 -11532507 7000693092 hipo hippurate hydrolase hipo (cl:hippurate hydrolase) (db:pir2.dat) E69640 E69640 Bacillus subtilis 1423 -11532507 4000714248 hipo putative hippurate hydrolase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:178157) (re:179407) (di:direct) AF008220 AF008220 g2293256 Bacillus subtilis 1423 -11532507 6000689073 hipo hippurate hydrolase (db:genpept-bct1) (ec:3.5.1.32) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:203660) (re:204910) (di:complement) BSUB0015 Z99118 g2635394 Bacillus subtilis 1423 -11532507 7500964050 hipo hippurate hydrolase (db:genpept-bct1) (ec:3.5.1.32) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:1020) (re:2270) (di:complement) BSUB0016 Z99119 g2635413 Bacillus subtilis 1423 -11532507

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819405	6947	29103	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819408	6948	29104	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819419	6949	29105	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819423	6950	29106	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819425	6951	29107	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819426	6952	29108	789	263

Description

GTC ORF with score 559 to: (sr:human) (db:genpept-pri3) (de:human neuron-specific vesicle coat protein and cerebellar degeneration antigen (beta-nap) mrna, complete cds.) (nt:similar to beta-adaptin and beta-cop proteins;) (le:62) (re:3307) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819446	6953	29109	966	321

Description

6500728650 yuxf:yugv:tgl transglutaminase (gtcfc:14.3) (keggfc:14.2) (bsorffc:8.3.1) (db:gtc-bacillus subtilis) tgl tgl Bacillus subtilis 1423 -11532508 7500892999 tgl (de:tgl protein) (db:swissprot) TGL\_BACSU P40746 BACILLUS SUBTILIS 1423 -11532508 7000694810 tgl transglutaminase tgl (db:pir2.dat) A69722 A69722 Bacillus subtilis 1423 -11532508 6000691380 tgl transglutaminase (fn:cross-links in spore coat proteins (sporulation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: yuxf, yugv) (le:213891) (re:214628) (di:direct) BSUB0016 Z99119 g2635611 Bacillus subtilis 1423 -11532508 7500893001 tgl transglutaminase (fn:cross-links in spore coat proteins (sporulation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate gene name: yuxf, yugv) (le:14661) (re:15398) (di:direct) BSUB0017 Z99120 g2635623 Bacillus subtilis 1423 -11532508 1500693689 yugv unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yugs to mcpb.) (nt:gene was formerly called yuxf) (le:4184) (re:4921) (di:complement) BSZ93935 Z93935 g1934799 Bacillus subtilis 1423 -11532508

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819457	6954	29110	351	117

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501819470	6955	29111	288	96

#### Description

6500728651 estb:pnba intracellular esterase b:para-nitrobenzyl esterase:pnb carboxy-esterase:pnbce (gtcfc:14.3) (keggfc:14.1) (bsorffc:8.3.1) (db:gtc-bacillus subtilis) pnba pnba Bacillus subtilis 1423 -11532509 7000694348 pnba para-nitrobenzyl esterase (cl:cholinesterase homology) (ec:3.1.1.-) (db:pir2.dat) B69680 B69680 Bacillus subtilis 1423 -11532509 220022 estb intracellular esterase b (db:genpept-bct1) (ec:3.1.1.1) (de:bacillus subtilis putative orf1 unknown protein, putativetranscriptional regulator (slr), and intracellular esterase b(estb) genes, complete cds.) (nt:estb; esterase of the serine-hydrolase family) (le:1035) (re:2504)... BSU46134 U46134 g1762126 Bacillus subtilis 1423 -11532509 220250 pnba para-nitrobenzyl esterase intracellular (db:genpept-bct1) (ec:3.1.1.1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: estb) (le:130145) (re:131614) (di:direct) BSUB0018 Z99121 g2635952 Bacillus subtilis 1423 -11532509 1500689779 pnba para-nitrobenzyl esterase (db:genpept-bct1) (de:b.subtilis pnba, sigl, yve(j,k,l,m,n,o,p,q,r,s,t) andyvf(a,b,c,d,e,f,g,h) genes.) (le:132) (re:1601) (di:complement) BSYVEFGNS Z71928 g1495277 Bacillus subtilis 1423 -11532509 7500965038 pnba para-nitrobenzyl esterase (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (le:50057) (re:51526) (di:complement) BSZ94043 Z94043 g1945688 Bacillus subtilis 1423 -11532509

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501819473	6956	29112	411	136

#### Description

6500728652 yveh:padc ferulate decarboxylase (gtcfc:14.3) (keggfc:14.2) (bsorffc:8.3.1) (db:gtc-bacillus subtilis) padC padC Bacillus subtilis 1423 -11532510 7000692987 padc ferulate decarboxylase padc (db:pir2.dat) D69671 D69671 Bacillus subtilis 1423 -11532510 1500694052 padc ferulate decarboxylase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: yveh) (le:131835) (re:132320) (di:complement) BSUB0018 Z99121 g2635953 Bacillus subtilis 1423 -11532510 5500687473 yveh hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to trembl:bpfdcgene\_1 b.pumilus fdc gene) (le:49351) (re:49836) (di:direct) BSZ94043 Z94043 g1945687 Bacillus subtilis 1423 -11532510 7500963981 padc phenolic acid decarboxylase (fn:caffeate decarboxylase) (db:genpept-bct2) (de:bacillus subtilis phenolic acid decarboxylase (padc) gene, completecds.) (le:250) (re:735) (di:direct) AF017117 AF017117 g2394282 Bacillus subtilis 1423 -11532510

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819474	6957	29113	363	120
<u>Description</u>				
6500728653 yvcm:crh catabolite repression hpr-like protein (gtcfc:14.3) (keggfc:14.2) (bsorffc:8.3.1) (db:gtc-bacillus subtilis) crh crh Bacillus subtilis 1423 -11532511 7000692328 crh catabolite repression hpr-like protein crh (cl:phosphotransferase system phosphohistidine-containing protein:phosphotransferase system phosphohistidine-containing protein homology) (db:pir2.dat) D69607 D69607 Bacillus subtilis 1423 -11532511 1500694019 crh catabolite repression hpr-like protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: yvcm) (le:168802) (re:169059) (di:complement) BSUB0018 Z99121 g2635987 Bacillus subtilis 1423 -11532511 7500963496 crh hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:catabolic repression (hpr family)) (le:12612) (re:12869) (di:direct) BSZ94043 Z94043 g1945653 Bacillus subtilis 1423 -11532511				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819475	6958	29114	300	99
<u>Description</u>				
6500728654 hisf cyclase-like protein (gtcfc:14.3) (ec:2.4.2.-) (keggfc:14.1) (bsorffc:8.3.1) (db:gtc-bacillus subtilis) hisF hisF Bacillus subtilis 1423 -11532512 7502851772 hisf (de:hisf protein (cyclase)) (db:swissprot) HIS6_BACSU 034727 BACILLUS SUBTILIS 1423 -11532512 7000693094 hisf hisf cyclase-like protein hisf (cl:cyclase hisf) (db:pir2.dat) B69641 B69641 Bacillus subtilis 1423 -11532512 5500701776 hisf hisf cyclase-like protein (fn:synthesis of d-erythro-imidazole glycerol) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:183072) (re:183830) (di:complement) BSUB0018 Z99121 g2636000 Bacillus subtilis 1423 -11532512 7500954437 hisf cyclase (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (nt:hisf protein) (le:44003) (re:44761) (di:direct) AF017113 AF017113 g2618870 Bacillus subtilis 1423 -11532512				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819482	6959	29115	342	113
<u>Description</u>				
6500728655 yxli:katx catalase:catalase x (gtcfc:14.3) (ec:1.11.1.6) (keggfc:14.1) (bsorffc:8.3.1) (db:gtc-bacillus subtilis) katX katX Bacillus subtilis 1423 -11532513 5500684972 katx (ec:1.11.1.6) (de:catalase x,) (db:swissprot) CATX_BACSU P94377 BACILLUS SUBTILIS 1423 -11532513 7000684759 katx catalase katx (cl:catalase) (db:pir2.dat) E69647 E69647 Bacillus subtilis 1423 -11532513 222889 katx catalase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: yxli) (le:165390) (re:167033) (di:direct) BSUB0020 Z99123 g2636398 Bacillus subtilis 1423 -11532513 301556 katx catalase (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:putative) (le:57432) (re:59075) (di:complement) D83026 D83026 g1783263 Bacillus subtilis 1423 -11532513				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819486	6960	29116	414	137
<u>Description</u>				
6500728656 acca:b0185 acetyl-coenzyme a carboxylase carboxyl transferase subunit alpha (gtcfc:1.10:1.8:3.1) (ec:6.4.1.2) (keggfc:1.8:1.10:3.1) (rileyfc:1.8.0) (db:gtc-escherichia coli) b0185 b0185 Escherichia coli 562 -11532514 126064 acca acetyl-coa carboxylase::carboxyltransferase alpha chain (cl:acetyl-coa carboxylase, carboxyltransferase alpha chain) (ec:6.4.1.2) (db:pir1.dat) (mp:4.3 min) A43452 A43452 Escherichia coli 562 -11532514 222543 acca acca:alpha subunit of acetyl-coa carboxylase (sr:escherichia coli (strain:k-12, isolate:w3110) dna) (db:genpept-bct1) (de:escherichia coli genes for dnae, acca, ldcc, yaer, yaen, yaeo,yaep, yaeq, yaej, nlpe, yaef complete cds and partial cds.) (le:88) (re:1047) (di:direct) D49445 D49445 g1785841 Escherichia coli 562 -11532514 239813 acca acetyl-coa carboxylase (sr:escherichia coli (sub_strain w3110, strain k-12) female lambd) (db:genpept-bct1) (de:escherichia coli dna polymerase iii catalytic subunit (polc ordnae) gene, 3' end; acetyl-coa carboxylase (acca) gene, completeds.) (le:349) (re:1308) (di:direct) ECOPOLCACC M96394 g147322 Escherichia coli 562 -11532514 7500953390 acca acetyl-coa carboxylase alpha subunit (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:39696) (re:40655) (di:direct) ECU70214 U70214 g1552762 Escherichia coli 562 -11532514 235520 acca acetylcoa carboxylase:carboxytransferase (fn:enzyme; fatty acid and phosphatidic acid) (db:genpept-bct2) (ec:6.4.1.2) (de:escherichia coli k-12 mg1655 section 17 of 400 of the completengenome.) (nt:o319; 99 pct identical to acca_ecoli sw: p30867) (le:13841) (re:14800) (di:direct) AE000127 AE000127 g1786382 Escherichia coli 562 -11532514 5000689988 (de:(ecoli_185) (pn:acetylcoa carboxylase, carboxytransferase component, alpha subunit) (gn:acca) (gtcfc:1.10:1.8:3.1) (ec:6.4.1.2) (acca_ecoli) (keggfc:1.8:1.10:3.1) (rileyfc:1.8.0) (db:gtc-escherichia coli)) ECOLI_185 ECOLI_185 Escherichia coli 562 10066531				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501819495	6961	29117	789	263

Description

6500728657 succ:b0728 succinyl-coa synthetase beta chain:scs-beta  
(gtcfc:1.10:1.12:1.2:2.5) (ec:6.2.1.5) (keggfc:1.2:1.10:1.12:2.4)  
(rileyfc:1.2.3) (db:gtc-escherichia coli) (gtcfc:carbohydrate  
metabolism-propanoate metabolism:carbohydrate metabolism-c5-branched dibasic  
acid metabolism:carbohydrate metabolism-citrate... b0728 b0728 Escherichia  
coli 562 -11532515 99800 succ (ec:6.2.1.5) (de:succinyl-coa synthetase beta  
chain, (scs-beta)) (db:swissprot) SUCC\_ECOLI P07460 ESCHERICHIA COLI 562  
-11532515 125957 succ succinate--coa ligase adp-forming:beta  
chain:succinyl-coa synthetase adp-forming beta chain (cl:succinate--coa  
ligase (adp-forming) beta chain) (ec:6.2.1.5) (db:pir1.dat) (mp:17 min)  
SYECSB A24090 Escherichia coli 562 -11532515 223175 succ succinate-coa  
ligase adp-forming:beta chain (sr:escherichia coli(strain:k12) dna,  
clone:kohara clone #176) (db:genpept-bct1) (de:escherichia coli genomic dna.  
(16.1 - 16.4 min).) (le:12238) (re:13404) (di:direct) D90711 D90711 g1651323  
Escherichia coli 562 -11532515 7500892229 succ succinyl-coa synthetase  
beta-subunit (sr:escherichia coli k12 dna) (db:genpept-bct1) (ec:6.2.1.5)  
(de:e.coli glta gene, sdhcdab operon and sucabcd operon encoding  
ninecomplete proteins.) (le:10916) (re:12082) (di:direct) ECOGLTA J01619  
g146203 Escherichia coli 562 -11532515 234535 succ succinyl-coa  
synthetase:beta subunit (fn:enzyme; energy metabolism, carbon: tca cycle)  
(db:genpept-bct2) (ec:6.2.1.5) (de:escherichia coli k-12 mg1655 section 66  
of 400 of the completegenome.) (nt:o388; 100 pct identical to succ\_ecoli sw:  
p07460) (le:168) (re:1334) (di:direct) AE000176 AE000176 g1786948  
Escherichia coli 562 -11532515 5000689989 succ succinate-coa ligase  
adp-forming ec 6.2.1.5 (sr:escherichia coli(strain:k12) dna, clone:kohara  
clone #176) (db:genpept) (de:escherichia coli genomic dna. (16.2 - 16.5  
min).) (nt:orf\_id:o177#2; similar to pir accession number) (le:12238)  
(re:13404) (di:direct) D90711 D90711 g1651323 Escherichia coli 562 -11532515

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501819498	6962	29118	228	75

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501819517	6963	29119	525	174
<u>Description</u>				
6500728658 succd:b0729 succinyl-coa synthetase alpha chain:scs-alpha (gtcfc:1.10:1.12:1.2:2.5) (ec:6.2.1.5) (keggfc:1.2:1.10:1.12:2.4) (rileyfc:1.2.3) (db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-propanoate metabolism:carbohydrate metabolism-c5-branched dibasic acid metabolism:carbohydrate metabolism-citrate... b0729 b0729 Escherichia coli 562 -11532516 125954 succd succinate--coa ligase adp-forming:alpha chain:succinyl-coa synthetase adp-forming alpha chain (cl:succinate--coa ligase (adp-forming) alpha chain) (ec:6.2.1.5) (db:pir1.dat) (mp:17 min) SYECSA A90499 Escherichia coli 562 -11532516 223176 succd succinate-coa ligase adp-forming:alpha chain (sr:escherichia coli(strain:k12) dna, clone:kohara clone #176) (db:genpept-bct1) (de:escherichia coli genomic dna. (16.1 - 16.4 min).) (le:13404) (re:14273) (di:direct) D90711 D90711 g1651324 Escherichia coli 562 -11532516 7500953378 succd succinyl-coa synthetase alpha-subunit (sr:escherichia coli k12 dna) (db:genpept-bct1) (de:e.coli glta gene, sdhcdab operon and sucabcd operon encoding ninecomplete proteins.) (le:12082) (re:12951) (di:direct) ECOGLTA J01619 g146204 Escherichia coli 562 -11532516 234536 succd succinyl-coa synthetase:alpha subunit (fn:enzyme; energy metabolism, carbon: tca cycle) (db:genpept-bct2) (ec:6.2.1.5) (de:escherichia coli k-12 mg1655 section 66 of 400 of the completegenome.) (nt:o289; 100 pct identical to succd_ecoli sw: p07459) (le:1334) (re:2203) (di:direct) AE000176 AE000176 g1786949 Escherichia coli 562 -11532516 5000689990 succd succinate-coa ligase adp-forming ec 6.2.1.5 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #176) (db:genpept) (de:escherichia coli genomic dna. (16.2 - 16.5 min).) (nt:orf_id:o177#3; similar to pir accession number) (le:13404) (re:14273) (di:direct) D90711 D90711 g1651324 Escherichia coli 562 -11532516				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819518	6964	29120	870	289
<u>Description</u>				
6500728659 aldh:b1300 putative aldehyde dehydrogenase (gtcfc:1.4:1.8:3.2:3.5:8.1) (ec:1.2.1.3) (keggfc:1.7:1.8:1.10:1.11:3.2:3.5:5.6:5.9:5.10:5.11:5.12:5.14:6.1:8.1) (rileyfc:1.2.7) (db:gtc-escherichia coli) b1300 b1300 Escherichia coli 562 -11532517 68396 aldh (ec:1.2.1.3) (de:putative aldehyde dehydrogenase,) (db:swissprot) DHAL_ECOLI P23883 ESCHERICHIA COLI 562 -11532517 7000685031 aldh aldehyde dehydrogenase nad+ (cl:aldehyde dehydrogenase (nad+):aldehyde dehydrogenase homology) (ec:1.2.1.3) (db:pir2.dat) G64878 G64878 Escherichia coli 562 -11532517 223542 aldh aldehyde dehydrogenase homolog (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #257(29.1-29.6 min.)) (nt:orf_id:o257#9; similar to (pir accession number) (le:10113) (re:11600) (di:direct) D90768 D90768 g1742130 Escherichia coli 562 -11532517 300332 aldh aldehyde dehydrogenase:prefers nadp over nad (fn:enzyme; energy metabolism, carbon:) (db:genpept-bct2) (ec:1.2.1.3) (de:escherichia coli k-12 mg1655 section 118 of 400 of the completegenome.) (nt:o495; 99 pct identical to dhal_ecoli sw: p23883) (le:3408) (re:4895) (di:direct) AE000228 AE000228 g1787558 Escherichia coli 562 -11532517 5000689991 (de:(ecoli_1260) (pn:aldehyde dehydrogenase, prefers nadp over nad) (gn:aldh) (gtcfc:1.10:1.11:1.7:1.8:3.2:3.5:5.10:5.11:5.14:5.6:6.1:8.1) (ec:1.2.1.3) (dhal_ecoli) (keggfc:1.7:1.8:1.10:1.11:3.2:3.5:5.6:5.10:5.11:5.14:6.1:8.1) () ECOLI_1260 ECOLI_1260 Escherichia coli 562 10119512				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501819520	6965	29121	234	77

Description

6500728660 goag:b1302 gaba-aminotransferase:4-aminobutyrate  
aminotransferase:gamma-amino-n-butyrate transaminase:gaba  
transaminase:glutamate:succinic semialdehyde transaminase:gaba  
aminotransferase (gtcfc:1.10:1.11:5.1:5.2:6.1) (ec:2.6.1.19)  
(keggfc:1.10:1.11:5.1:5.2:6.1) (rileyfc:5.8.0) (db:gtc-escherichia coli)  
b1302 b1302 Escherichia coli 562 -11532518 74260 goag (ec:2.6.1.19)  
(de:transaminase) (gaba aminotransferase)) (db:swissprot) GOAG\_ECOLI P50457  
ESCHERICHIA COLI 562 -11532518 7000685438 goag 4-aminobutyrate  
transaminase:goag:gaba aminotransferase (ec:2.6.1.19) (db:pir2.dat) A64879  
A64879 Escherichia coli 562 -11532518 223544 goag 4-aminobutyrate  
aminotransferase ec 2.6.1.19 (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #257(29.1-29.6 min.)) (nt:orf\_id:o257#11; similar to  
(swissprot accession) (le:12920) (re:14185) (di:direct) D90768 D90768  
g1742132 Escherichia coli 562 -11532518 239556 goag 4-aminobutyrate  
aminotransferase (fn:enzyme; central intermediary metabolism: pool,)  
(db:genpept-bct2) (ec:2.6.1.19) (de:escherichia coli k-12 mg1655 section 118  
of 400 of the completegenome.) (nt:o421; 100 pct identical to goag\_ecoli sw:  
p50457) (le:6215) (re:7480) (di:direct) AE000228 AE000228 g1787560  
Escherichia coli 562 -11532518 300334 goag gaba-aminotransferase  
(sr:escherichia coli strain=k-12) (db:genpept-bct2) (de:escherichia coli  
oxidoreductase (ordl) and gaba-aminotransferase(goag) genes, complete cds.)  
(nt:hypothetical 44.7kda protein; goag; orfx) (le:1319) (re:2584)  
(di:direct) ECU38543 U38543 g1054922 Escherichia coli 562 -11532518  
5000689992 (de:(ecoli\_1262) (pn:glutamate:succinic semialdehyde  
transaminase:4-aminobutyrate aminotransferase:gamma-amino-n-butyrate  
transaminase:gaba transaminase:glutamate, succinic semialdehyde  
transaminase:gaba aminotransferase) (gn:goag) (gtc) ECOLI\_1262 ECOLI\_1262  
Escherichia coli 562 10016782

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501819530	6966	29122	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501819531	6967	29123	762	253

#### Description

6500728661 ydbs:b1393 hypothetical protein:probable enoyl-coa hydratase (gtcfc:14.3) (ec:4.2.1.17) (keggfc:1.10:1.11:3.1:3.2:5.6:5.9:5.14:6.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1393 b1393 Escherichia coli 562 -11532519 4000707890 paaf (ec:4.2.1.17) (de:probable enoyl-coa hydratase paaf,) (db:swissprot) PAAF\_ECOLI P76082 ESCHERICHIA COLI 562 -11532519 7000685134 ydbs probable enoyl-coa hydratase:ydbs (cl:naphthoate synthase:enoyl-coa hydratase homology) (ec:4.2.1.17) (db:pir2.dat) D64890 D64890 Escherichia coli 562 -11532519 7500887575 ydbs putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 126 of 400 of the completegenome.) (nt:o255; this 255 aa orf is 47 pct identical (0 gaps)) (le:6054) (re:6821) (di:direct) AE000236 AE000236 g1787659 Escherichia coli 562 -11532519 5000692197 (de:(ecoli\_1353) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_1353 ECOLI\_1353 Escherichia coli 562 10123300

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501819538	6968	29124	459	152

#### Description

6500728662 atod:b2221 acetate coa-transferase alpha subunit:acetyl-coa:acetoacetate coa transferase (gtcfc:1.10:1.11) (ec:2.8.3.8) (keggfc:1.10:1.11) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2221 b2221 Escherichia coli 562 -11532520 1500685872 atod (ec:2.8.3.8) (de:coa:acetoacetate coa transferase) (db:swissprot) ATOD\_ECOLI P76458 ESCHERICHIA COLI 562 -11532520 7000684660 atod atod protein (cl:3-oxoadipate coa-transferase alpha chain:3-oxoadipate coa-transferase alpha chain homology) (db:pir2.dat) C64992 C64992 Escherichia coli 562 -11532520 224701 acetyl-coa:acetoacetyl-coa transferase a subunit (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #374(49.8-50.1 min.)) (nt:orf\_id:o374#4; similar to (swissprot accession) (le:9355) (re:10017) (di:direct) D90851 D90851 g1736876 Escherichia coli 562 -11532520 301341 atod acetyl-coa:acetoacetyl-coa transferase alpha (fn:enzyme; degradation of small molecules: fatty) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 201 of 400 of the completegenome.) (nt:o220; this 220 aa orf is 63 pct identical (0 gaps)) (le:6550) (re:7212) (di:direct) AE000311 AE000311 g1788551 Escherichia coli 562 -11532520 5000692785 (de:(ecoli\_2170) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2170 ECOLI\_2170 Escherichia coli 562 10059352

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501819542	6969	29125	267	88

Description

6500728663 atoa:b2222 acetate coa-transferase beta  
subunit:acetyl-coa:acetoacetate coa transferase (gtcfc:1.10:1.11)  
(ec:2.8.3.8) (keggfc:1.10:1.11) (rileyfc:5.9.0) (db:gtc-escherichia coli)  
b2222 b2222 Escherichia coli 562 -11532521 1500685873 atoa (ec:2.8.3.8)  
(de:coa:acetoacetate coa transferase)) (db:swissprot) ATOA\_ECOLI P76459  
ESCHERICHIA COLI 562 -11532521 7000684657 atoa atoa protein  
(cl:3-oxoadipate coa-transferase beta chain:3-oxoadipate coa-transferase  
beta chain homology) (db:pir2.dat) D64992 D64992 Escherichia coli 562  
-11532521 224702 acetyl-coa:acetoacetyl-coa transferase b subunit  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #374(49.8-50.1  
min.)) (nt:orf\_id:o374#5; similar to (swissprot accession) (le:10017)  
(re:10667) (di:direct) D90851 D90851 g1736877 Escherichia coli 562 -11532521  
301342 atoa acetyl-coa:acetoacetyl-coa transferase beta (fn:enzyme;  
degradation of small molecules: fatty) (db:genpept-bct2) (de:escherichia  
coli k-12 mg1655 section 201 of 400 of the completegenome.) (nt:o216;  
residues 62-206 are 73 pct identical to) (le:7212) (re:7862) (di:direct)  
AE000311 AE000311 g1788552 Escherichia coli 562 -11532521 5000692786  
(de:(ecoli\_2171) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)  
(keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2171  
ECOLI\_2171 Escherichia coli 562 10059353

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501819547	6970	29126	528	175

Description

6500728664 atob:b2224 hypothetical protein:acetyl-coa  
acetyltransferase:acetoacetyl-coa thiolase (gtcfc:1.10:1.11:1.8:3.1:3.2:3.3)  
(ec:2.3.1.9) (keggfc:1.8:1.10:1.11:3.1:3.2:3.3:5.9:5.14) (rileyfc:5.7.0)  
(db:gtc-escherichia coli) b2224 b2224 Escherichia coli 562 -11532522  
1500687424 atob (ec:2.3.1.9) (de:acetyl-coa acetyltransferase,  
(acetoacetyl-coa thiolase)) (db:swissprot) ATOB\_ECOLI P76461 ESCHERICHIA  
COLI 562 -11532522 7000684658 hypothetical protein b2224 (cl:acetyl-coa  
acetyltransferase) (db:pir2.dat) F64992 F64992 Escherichia coli 562  
-11532522 224704 acetyl-coa:acetyltransferase ec 2.3.1.9 (sr:escherichia  
coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #374(49.8-50.1 min.)).)  
(nt:orf\_id:o374#7; similar to (swissprot accession) (le:12017) (re:13201)  
(di:direct) D90851 D90851 g1736879 Escherichia coli 562 -11532522 301344  
atob acetyl-coa acetyltransferase (fn:enzyme; degradation of small  
molecules: fatty) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section  
201 of 400 of the completegenome.) (nt:o394; this 394 aa orf is 66 pct  
identical (0 gaps)) (le:9212) (re:10396) (di:direct) AE000311 AE000311  
g1788554 Escherichia coli 562 -11532522 5000692788 (de:(ecoli\_2173)  
(pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2)  
(rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2173 ECOLI\_2173 Escherichia  
coli 562 10064998

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501819559	6971	29127	540	179

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819560	6972	29128	426	141

Description

6500728665 acka:b2296 acetate kinase:acetokinase (gtcfc:1.10:1.8:2.8)  
(ec:2.7.2.1) (keggfc:1.8:1.10) (rileyfc:1.2.6) (db:gtc-escherichia coli)  
b2296 b2296 Escherichia coli 562 -11532523 58185 acka (ec:2.7.2.1)  
(de:acetate kinase, (acetokinase)) (db:swissprot) ACKA\_ECOLI P15046  
ESCHERICHIA COLI 562 -11532523 123839 acka acetate kinase::acetokinase  
(cl:acetate kinase) (ec:2.7.2.1) (db:pir1.dat) KIECAA JT0498 Escherichia  
coli 562 -11532523 224822 acka acetate kinase ec 2.7.2.1 (sr:escherichia  
coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #405(52.0-52.3 min.)) (nt:similar to  
(pir accession number jt0498)) (le:3459) (re:4661) (di:direct) D90861 D90861  
g1799669 Escherichia coli 562 -11532523 7500876317 (sr:e.coli (strain k-12)  
dna, clones pak12(4,5)) (db:genpept-bct1) (de:e.coli acka gene encoding  
acetate kinase, complete cds.) (nt:acetate kinase (ec 2.7.2.1)) (le:472)  
(re:1674) (di:direct) ECOACKA M22956 g145171 Escherichia coli 562 -11532523  
233709 acka acetate kinase (fn:enzyme; energy metabolism, carbon: electron)  
(db:genpept-bct2) (ec:2.7.2.1) (de:escherichia coli k-12 mg1655 section 208  
of 400 of the completegenome.) (nt:o400; 100 pct identical to acka\_ecoli sw:  
p15046) (le:9596) (re:10798) (di:direct) AE000318 AE000318 g1788633  
Escherichia coli 562 -11532523 5000689993 (de:(ecoli\_2245) (pn:acetate  
kinase) (gn:acka) (gtcfc:1.10:1.8) (ec:2.7.2.1) (acka\_ecoli)  
(keggfc:1.8:1.10) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI\_2245  
ECOLI\_2245 Escherichia coli 562 10000965

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819561	6973	29129	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819567	6974	29130	264	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819587	6975	29131	2256	752

Description

6500728666 accd:dedb:usg:b2316 acetyl-coa carboxylase beta subunit:acetyl-coenzyme a carboxylase carboxyl transferase subunit beta (gtcfc:1.10:1.8:3.1) (ec:6.4.1.2) (keggfc:1.8:1.10:3.1) (rileyfc:1.8.0) (db:gtc-escherichia coli) b2316 b2316 Escherichia coli 562 -11532524 58004 accd:dedb:usg (ec:6.4.1.2) (de:(ec 6.4.1.2)) (db:swissprot) ACCD\_ECOLI P08193 ESCHERICHIA COLI 562 -11532524 7000684490 accd:dedb:usg acetyl-coa carboxylase::carboxyltransferase beta chain (cl:acetyl-coa carboxylase, carboxyltransferase beta chain) (ec:6.4.1.2) (db:pir1.dat) (mp:50 min) XMECBD B65004 Escherichia coli 562 -11532524 224860 accd acetyl-coa carboxylase ec 6.4.1.2 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #407(52.4-52.8 min.)) (nt:similar to (pir accession number c29803)) (le:3654) (re:4568) (di:complement) D90863 D90863 g1799709 Escherichia coli 562 -11532524 7500876294 accd acetylcoa carboxylase:carboxytransferase (fn:enzyme; fatty acid and phosphatidic acid) (db:genpept-bct2) (ec:6.4.1.2) (de:escherichia coli k-12 mg1655 section 210 of 400 of the completegenome.) (nt:f304; 95 pct identical accd\_ecoli sw: p08193;) (le:7081) (re:7995) (di:complement) AE000320 AE000320 g1788655 Escherichia coli 562 -11532524 5000689994 (de:(ecoli\_2265) (pn:acetylcoa carboxylase, carboxytransferase component, beta subunit) (gn:accd) (gtcfc:1.10:1.8:3.1) (ec:6.4.1.2) (accd\_ecoli) (keggfc:1.8:1.10:3.1) (rileyfc:1.8.0) (db:gtc-escherichia coli)) ECOLI\_2265 ECOLI\_2265 Escherichia coli 562 10120116

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501819588	6976	29132	570	189

#### Description

6500728667 gabt:b2662 4-aminobutyrate  
aminotransferase:gamma-amino-n-butyrate transaminase:gaba  
transaminase:glutamate:succinic semialdehyde transaminase:gaba  
aminotransferase (gtcfc:1.10:1.11:2.3:5.1:5.2:6.1) (ec:2.6.1.19)  
(keggfc:1.10:1.11:5.1:5.2:6.1) (rileyfc:1.3.1) (db:gtc-escherichia coli)  
b2662 b2662 Escherichia coli 562 -11532525 72879 gabt (ec:2.6.1.19)  
(de:transaminase) (gaba aminotransferase)) (db:swissprot) GABT\_ECOLI P22256  
ESCHERICHIA COLI 562 -11532525 162623 gabt 4-aminobutyrate  
transaminase::4-aminobutyrate aminotransferase (ec:2.6.1.19) (db:pir2.dat)  
A37846 A37846 Escherichia coli 562 -11532525 225216 4-aminobutyrate  
transaminase ec 2.6.1.19 (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #443(59.8-60.2 min.)) (nt:similar to (pir accession number  
a37846)) (le:12904) (re:14184) (di:direct) D90890 D90890 g1800048  
Escherichia coli 562 -11532525 236055 gabt 4-aminobutyrate aminotransferase  
activity (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2)  
(ec:2.6.1.19) (de:escherichia coli k-12 mg1655 section 241 of 400 of the  
completegenome.) (nt:o426; 100 pct identical to gabt\_ecoli sw: p22256)  
(le:4458) (re:5738) (di:direct) AE000351 AE000351 g1789016  
Escherichia coli 562 -11532525 324885 gabt gaba transaminase (sr:escherichia  
coli (strain k-12) dna) (db:genpept-bct2) (ec:2.6.1.19) (de:e.coli succinic  
semialdehyde dehydrogenase (gabd) gene, completecds; gaba transaminase  
(gabt) gene, complete cds; gaba permease(gabp) gene, complete cds.)  
(le:2100) (re:3380) (... ECOSUSEDEH M88334 g147902  
Escherichia coli 562 -11532525 7502851773 1-2-amino-4-methylphosphinobutyric  
acid-specific (db:genpept-pat) (de:synthetic gene for 1-2-amino-4-methylphosphinobutyric  
acid-specifictransaminase.) (le:1) (re:1281) (di:direct) A07633 A07633  
g413130 unidentified 32644 -11532525 5000689995 (de:(ecoli\_2595)  
(pn:4-aminobutyrate aminotransferase activity) (gn:gabt) (gtcfc:1.10:1.11:5.1:5.2:6.1)  
(ec:2.6.1.19) (gabt\_ecoli) (keggfc:1.10:1.11:5.1:5.2:6.1) (rileyfc:1.3.1)  
(db:gtc-escherichia coli)) ECOLI\_2595 ECOLI\_2595 Escherichia coli 562 10015425

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501819601	6977	29133	189	62

#### Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501819618	6978	29134	189	62

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819619	6979	29135	1053	350

Description

GTC ORF with score 314 to: (fn:activities of formation of isobutene and)  
(sr:rhodotorula minuta (strain:ifo1102) dna) (db:genpept-pln1)  
(de:rhodotorula minuta dna for isobutene-forming enzyme and  
benzoate4-hydroxylase, complete cds.) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819620	6980	29136	627	209

Description

6500728668 sbm:b2917 sbm protein (gtcfc:1.10:3.2:5.6) (ec:5.4.99.2)  
(keggfc:1.10:5.6) (rileyfc:1.1.3) (db:gtc-escherichia coli) b2917 b2917  
Escherichia coli 562 -11532526 7000691912 sbm sbm protein (db:pir2.dat)  
D65076 D65076 Escherichia coli 562 -11532526 7500960455 sbm  
(db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68  
minutes.) (le:15241) (re:17385) (di:direct) ECU28377 U28377 g882446  
Escherichia coli 562 -11532526 239130 sbm methylmalonyl-coa mutase mcm  
(fn:enzyme; degradation of small molecules: fatty) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 265 of 400 of the completegenome.)  
(nt:o714; 99 pct identical to sbm\_ecoli sw: p27253) (le:1198) (re:3342)  
(di:direct) AE000375 AE000375 g1789284 Escherichia coli 562 -11532526  
5000689996 (de:(ecoli\_2839) (pn:methylmalonyl-coa mutase:mcm) (gn:sbm)  
(gtcfc:1.10:5.6) (ec:5.4.99.2) (sbm\_ecoli) (keggfc:1.10:5.6) (rileyfc:1.1.3)  
(db:gtc-escherichia coli)) ECOLI\_2839 ECOLI\_2839 Escherichia coli 562  
10123906

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819629	6981	29137	300	99

Description

GTC ORF with score 117 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna  
to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds,  
clone: sy 0539.) (nt:similar to xenopus laevis developing gtp-binding)  
(le:41) (re:1141) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819630	6982	29138	204	67

Description

GTC ORF with score 123 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna  
to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds,  
clone: sy 0539.) (nt:similar to xenopus laevis developing gtp-binding)  
(le:41) (re:1141) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819635	6983	29139	378	125

Description

GTC ORF with score 367 to: (sr:xenopus laevis (library: lambda unizap) mixed embryonic stages 10) (db:genpept-vrt) (de:x.laevis mrna for gtp-binding protein drg, complete cds.) (nt:drg is evolutionarily conserved protein. for mouse) (le:39) (re:1142) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819638	6984	29140	273	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819642	6985	29141	270	89

Description

6500728669 accb:fabe:b3255 biotin carboxyl carrier protein:biotin carboxyl carrier protein of acetyl-coa carboxylase:bccp (gtcfc:9.6:1.8:3.1) (ec:6.4.1.2) (keggfc:1.8:1.10:3.1) (rileyfc:1.8.0) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:carbohydrate metabolism-pyruvate and acetyl-coa metabolism:lipid... b3255 b3255 Escherichia coli 562 -11532527 233713 accb:fabe (ec:6.4.1.2) (de:(ec 6.4.1.2) (bccp)) (db:swissprot) BCCP\_ECOLI P02905 ESCHERICHIA COLI 562 -11532527 130677 accb:fabe acetyl-coa carboxylase::biotin carboxyl carrier protein (cl:biotin carboxyl carrier protein:lipoyl/biotin-binding homology) (ec:6.4.1.2) (db:pir1.dat) (mp:72 min) BKEC9 A93687 Escherichia coli 562 -11532527 5000689997 (db:genpept-bct1) (de:e. coli fabe gene for acetyl-coa carboxylase (ec 6.4.1.2).) (nt:acetyl-coa carboxylase (aa 1 - 156)) (le:268) (re:738) (di:direct) ECFABE X14825 g41362 Escherichia coli 562 -11532527 234292 fabe biotin carboxyl carrier protein (fn:subunit of acetyl-coa carboxylase) (sr:escherichia coli (strain k-12) f- dna) (db:genpept-bct1) (de:e.coli biotin carboxylase and biotin carboxyl carrier protein(fabe) and orf1 35 kda protein genes, complete cds.) (le:2443) (re:2913) (di:direct) ECOACOAC M80458 g145174 Escherichia coli 562 -11532527 234293 (sr:e.coli dna) (db:genpept-bct1) (de:e.coli biotin carboxyl carrier protein (fabe) gene, complete cds.) (nt:biotin carboxyl carrier protein (fabe)) (le:269) (re:739) (di:direct) ECOFABEA M32214 g145890 Escherichia coli 562 -11532527 236494 fabe biotin carboxyl carrier protein (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (ec:6.4.1.2) (de:escherichia coli biotin carboxyl carrier biotin carboxylase (fabg),complete cds, and pantothenate permease (panf) genes, 5' end.) (le:801) (re:1271) (di:direct) ECOFABEGF M83198 g145892 Escherichia coli 562 -11532527 7500877706 accb biotin carboxyl carrier protein (fn:subunit of acetyl-coa carboxylase) (db:genpept-bct1) (ec:6.4.1.2) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 796; alternate name fabe) (le:186181) (re:186651) (di:direct) ECOUW67 U18997 g606195 Escherichia coli 562 -11532527 232787 accb acetylcoa carboxylase:bccp subunit:carrier of (fn:carrier; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:6.4.1.2) (de:escherichia coli k-12 mg1655 section 294 of 400 of the completegenome.) (nt:ol56; cg site no. 796; alternate name fabe; 100 pct) (le:9174) (re:9644) (di:direct) AE000404 AE000404 g1789653 Escherichia coli 562 -11532527 61448 accb:fabe (ec:6.4.1.2) (de:(ec 6.4.1.2) (bccp)) (db:swissprot) BCCP\_ECOLI P02905 ESCHERICHIA COLI 562 -11532527

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819646	6986	29142	315	104

Description

6500728670 fadb:olddb:b3846 large:alpha subunit of the fatty acid-oxidizing multienzyme complex:fatty oxidation complex alpha subunit:contain:enoyl-coa hydratase:delta:3-cis-delta:2-trans-enoyl-coa isomerase:3-hydroxyacyl-coa dehydrogenase:and 3-hydroxybutyryl-coa epimerase  
(gtcfc:1.10:1.11:3.1:3.2:5.14:5.6:5.9:6.1)  
(keggfc:1.10:1.11:3.1:3.2:5.6:5.9:5.14:6.1) (rileyfc:1.1.3)  
(db:gtc-escherichia coli) b3846 b3846 Escherichia coli 562 -11532528 71036 fadb:olddb (ec:4.2.1.17:5.3.3.8:1.1.1.35:5.1.2.3) (de:hydroxybutyryl-coa epimerase,)) (db:swissprot) FADB\_ECOLI P21177 ESCHERICHIA COLI 562 -11532528 163021 fadb fatty acid beta oxidation complex alpha chain (cl:enoyl-coa hydratase/3-hydroxyacyl-coa dehydrogenase:3-hydroxyacyl-coa dehydrogenase homology:enoyl-coa hydratase homology) (db:pir2.dat) (mp:87 min) A39592 A39592 Escherichia coli 562 -11532528 237071 fadb 79-kda multifunctional protein (sr:escherichia coli (clone pk52, strain k-12) dna)  
(db:genpept-bct1) (de:e. coli fadb and fada genes (fadba operon), complete cds.) (nt:enoyl-coa hydratase (ec 4.2.1.17); 1-3) (le:382) (re:2571)  
(di:direct) ECOFADBA M74164 g145903 Escherichia coli 562 -11532528 7500881317 fadb::cgsc no. 793 large alpha subunit of the fatty  
(db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (le:81846) (re:84035) (di:complement) ECOUW85 M87049 g148246 Escherichia coli 562 -11532528 234300 fadb 4-enzyme  
protein:3-hydroxyacyl-coa (fn:enzyme; degradation of small molecules: fatty)  
(db:genpept-bct2) (ec:1.1.1.35:4.2.1.17:5.1.2.3:5.3.3.8) (de:escherichia coli k-12 mg1655 section 350 of 400 of the completegenome.) (nt:f729; 100 pct identical amino acid sequence and) (le:1523) (re:3... AE000460 AE000460 g1790281 Escherichia coli 562 -11532528 5000689999 (de:(ecoli\_3751)  
(pn:3-hydroxyacyl-coa dehydrogenase; 3-hydroxyacyl-epimerase;  
delta:3-cis-delta:2-trans-enoyl-coa-hydratase; enoyl-coa-hyd) (gn:fadb)  
(gtcfc:1.10:1.11:3.1:3.2:5.14:5.6:5.9:6.1) (ec:5.3.3.8) (fadb\_ecoli)  
(keggfc:1) ECOLI\_3751 ECOLI\_3751 Escherichia coli 562 10013611

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819647	6987	29143	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819652	6988	29144	747	248

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819658	6989	29145	234	78

Description

6500728671 acs:b4069 acetyl-coa sythetase:acetyl-coenzyme a  
synthetase:acetate--coa ligase:acyl-activating enzyme  
(gtcfc:1.10:1.8:2.5:3.1) (ec:6.2.1.1) (keggfc:1.8:1.10:2.4) (rileyfc:1.8.0)  
(db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-propanoate  
metabolism:carbohydrate metabolism-pyruvate and acetyl-coa metabolism:energy  
metabolism-reductive carboxylat... b4069 b4069 Escherichia coli 562  
-11532529 58308 acs (ec:6.2.1.1) (de:activating enzyme)) (db:swissprot)  
ACSA\_ECOLI P27550 ESCHERICHIA COLI 562 -11532529 7000684510 acs  
acetate--coa ligase::acetyl-coa synthetase (cl:acetate--coa  
ligase:acetate--coa ligase homology) (ec:6.2.1.1) (db:pir2.dat) D65215  
D65215 Escherichia coli 562 -11532529 237275 acs acetyl-coa synthetase  
(fn:enzyme; fatty acid and phosphatidic acid) (db:genpept-bct2) (ec:6.2.1.1)  
(de:escherichia coli k-12 mg1655 section 370 of 400 of the completegenome.)  
(nt:f652; 100 pct identical to acsa\_ecoli sw:) (le:5516) (re:7474)  
(di:complement) AE000480 AE000480 g1790505 Escherichia coli 562 -11532529  
7500876381 acs acetyl-coa sythetase (sr:escherichia coli (sub\_strain  
mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli  
chromosomal region from 89.2 to 92.8 minutes.) (nt:matches ps00018: ef-hand  
calcium-binding domain,) (le:150653) (re:152611) (di:complement) ECOUW89  
U00006 g396404 Escherichia coli 562 -11532529 5000690000 (de:(ecoli\_3955)  
(pn:acetyl-coa synthetase) (gn:acs) (gtcfc:1.10:1.8:2.5) (ec:6.2.1.1)  
(acsa\_ecoli) (keggfc:1.8:1.10:2.4) (rileyfc:1.8.0) (db:gtc-escherichia  
coli)) ECOLI\_3955 ECOLI\_3955 Escherichia coli 562 10001088

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819661	6990	29146	750	249

Description

6500728672 acee:b0114 pyruvate dehydrogenase e1 component  
(gtcfc:1.1:1.11:1.8:5.7) (ec:1.2.4.1) (keggfc:1.1:1.8:1.11:5.7)  
(rileyfc:1.2.2) (db:gtc-escherichia coli) b0114 b0114 Escherichia coli 562  
-11532530 7000688844 acee pyruvate dehydrogenase lipoamide::pyruvate  
dehydrogenase complex component e1 (cl:pyruvate dehydrogenase  
(lipoamide):thiamine pyrophosphate-binding domain homology) (ec:1.2.4.1)  
(db:pir1.dat) (mp:3 min) DEECPV B64734 Escherichia coli 562 -11532530  
7500953192 acee pyruvate dehydrogenase decarboxylase (fn:enzyme; energy  
metabolism, carbon: pyruvate) (db:genpept-bct2) (ec:1.2.4.1) (de:escherichia  
coli k-12 mg1655 section 10 of 400 of the completegenome.) (nt:o887; 99 pct  
identical (1 gap) to odp1\_ecoli) (le:5397) (re:8060) (di:direct) AE000120  
AE000120 g1786304 Escherichia coli 562 -11532530 5000689931 (de:(ecoli\_114)  
(pn:pyruvate dehydrogenase:decarboxylase component) (gn:acee)  
(gtcfc:1.1:5.7) (ec:1.2.4.1) (odp1\_ecoli) (keggfc:1.1:5.7) (rileyfc:1.2.2)  
(db:gtc-escherichia coli)) ECOLI\_114 ECOLI\_114 Escherichia coli 562 10122665

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501819667	6991	29147	264	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501819672	6992	29148	423	140

Description

6500728673 acef:b0115 e2 of pyruvate dehydrogenase:dihydrolipoamide acetyltransferase component:e2 of pyruvate dehydrogenase complex (gtcfc:1.1:1.8) (ec:2.3.1.12) (keggfc:1.1:1.8) (rileyfc:1.2.2) (db:gtc-escherichia coli) b0115 b0115 Escherichia coli 562 -11532531 123345 acef dihydrolipoamide s-acetyltransferase::dihydrolipoyl transacetylase component:lipoate acetyltransferase:pyruvate dehydrogenase complex component e2 (cl:dihydrolipoamide acetyltransferase:lipoyl/biotin-binding homology) (ec:2.3.1.12) (db:pir1.dat) (mp:3 min) XXECDP A30278 Escherichia coli 562 -11532531 228040 (db:genpept-bct1) (de:e. coli genes acee, a, acef and lpd. gene acee encodes the e1 component of pyruvate dehydrogenase. gene a is an unidentified reading frame. gene acef encodes dihydrolipoamide acetyltransferase component (e2) of the pyruvate dehydroge... ECACEX V01498 g434011 Escherichia coli 562 -11532531 301595 acef dihydrolipoamide acetyltransferase e2 (sr:escherichia coli (sub\_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (ec:2.3.1.12) (de:escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bp from 0 min).) (le:14410) (re:16302) (di:direct) ECO82K D26562 g473784 Escherichia coli 562 -11532531 233657 acef pyruvate dehydrogenase (fn:enzyme; energy metabolism, carbon: pyruvate) (db:genpept-bct2) (ec:2.3.1.12) (de:escherichia coli k-12 mg1655 section 10 of 400 of the complete genome.) (nt:o630; 100 pct identical to odp2\_ecoli sw: p06959) (le:8075) (re:9967) (di:direct) AE000120 AE000120 g1786305 Escherichia coli 562 -11532531 5000689932 (de:(ecoli\_115) (pn:pyruvate dehydrogenase:dihydrolipoyltransacetylase component) (gn:acef) (gtcfc:1.1) (ec:2.3.1.12) (odp2\_ecoli) (keggfc:1.1) (rileyfc:1.2.2) (db:gtc-escherichia coli)) ECOLI\_115 ECOLI\_115 Escherichia coli 562 10065795

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819673	6993	29149	1017	338

Description

6500728674 lpda:lpd:b0116 dihydrolipoamide dehydrogenase:e3 component of pyruvate and 2-oxoglutarate dehydrogenases complexes:glycine cleavage system l protein (gtcfc:1.1:1.2:1.8:5.3) (ec:1.8.1.4) (keggfc:1.1:1.2:1.8:5.3) (rileyfc:1.2.2) (db:gtc-escherichia coli) b0116 b0116 Escherichia coli 562 -11532532 122785 lpda:lpd dihydrolipoamide dehydrogenase::2-oxoglutarate dehydrogenase complex e3 component:alpha-ketoacid dehydrogenase complex e3 component:diaphorase:glycine cleavage system l protein:lipoamide reductase (cl:dihydrolipoamide dehydrogenase:dihydrolipoamide dehydrogenase homology) (ec:1.8.1.4) (db:pir1.dat) (mp:3 min) DEECLP S45195 Escherichia coli 562 -11532532 301596 lpd dihydrolipoamide dehydrogenase e3 component of (sr:escherichia coli (sub\_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (ec:1.8.1.4) (de:escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0 min).) (le:16627) (re:18051) (di:direct) ECO82K D26562 g473785 Escherichia coli 562 -11532532 233658 lpda lipoamide dehydrogenase nadh:component of (fn:enzyme; energy metabolism, carbon: pyruvate) (db:genpept-bct2) (ec:1.8.1.4) (de:escherichia coli k-12 mg1655 section 11 of 400 of the completegenome.) (nt:o474; 100 pct identical to dldh\_ecoli sw: p00391) (le:193) (re:1617) (di:direct) AE000121 AE000121 g1786307 Escherichia coli 562 -11532532 5000689933 (de:(ecoli\_116) (pn:lipoamide dehydrogenase:nadh ; component of 2- oxodehydrogenase and pyruvate complexes; l-protein of glycine cleavage c) (gn:lpda) (gtcfc:1.1:1.2:5.3) (ec:1.8.1.4) (dldh\_ecoli) (keggfc:1.1:1.2:5.3) (rileyfc:1) ECOLI\_116 ECOLI\_116 Escherichia coli 562 10065626

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819695	6994	29150	228	75

Description

6500728675 yadi:b0129 hypothetical protein in hpt-pand intergenic region:hypothetical phosphotransferase enzyme ii:a component in hpt-pand intergenic region (gtcfc:12.6:14.3) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0129 b0129 Escherichia coli 562 -11532533 109650 yadi (ec:2.7.1.69) (de:intergenic region,) (db:swissprot) YADI\_ECOLI P36881 ESCHERICHIA COLI 562 -11532533 7000687171 yadi yadi protein (db:pir2.dat) A64736 A64736 Escherichia coli 562 -11532533 7500896070 yadi putative pts enzyme ii b component (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 12 of 400 of the completegenome.) (nt:o146; 100 pct identical to yadi\_ecoli sw:) (le:5873) (re:6313) (di:direct) AE000122 AE000122 g1786321 Escherichia coli 562 -11532533 5000691388 (de:(ecoli\_129) (pn:hypothetical 11) (gn:yadi) (gtcfc:13.7:14.1) (ec:) (yadi\_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_129 ECOLI\_129 Escherichia coli 562 10122674



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501819696	6995	29151	261	86

Description

6500728676 adhc:b0356 alcohol--acetaldehyde dehydrogenase:alcohol  
dehydrogenase class iii:glutathione-dependent formaldehyde  
dehydrogenase:fdh:faldh (gtcfc:1.4:1.8:2.2:3.2:8.1)  
(keggfc:1.4:1.8:2.2:3.2:3.5:8.1) (rileyfc:1.2.7) (db:gtc-escherichia coli)  
b0356 b0356 Escherichia coli 562 -11532534 58685 adhc (ec:1.1.1.1:1.2.1.1)  
(de:formaldehyde dehydrogenase), (fdh) (faldh) (db:swissprot) ADH3\_ECOLI  
P25437 ESCHERICHIA COLI 562 -11532534 7000684528 adhc alcohol  
dehydrogenase:c:class iii alcohol dehydrogenase (cl:alcohol  
dehydrogenase:long-chain alcohol dehydrogenase homology) (ec:1.1.1.1)  
(db:pirl.dat) D64763 D64763 Escherichia coli 562 -11532534 5500687872  
formaldehyde dehydrogenase (sr:escherichia coli dna, clone\_lib:miniset  
library of kohara et al.) (db:genpept-bct1) (ec:1.2.1.1) (de:escherichia  
coli dna for formaldehyde dehydrogenase, complete cds.)  
(nt:glutathione-dependent) (le:274) (re:1383) (di:direct) D38504 D38504  
g2443392 Escherichia coli 562 -11532534 7500876573 adhc alcohol  
dehydrogenase class iii:formaldehyde (fn:enzyme; energy metabolism, carbon:)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 32 of 400 of the  
completegenome.) (nt:f369; 95 pct identical to 45aa fragment) (le:9920)  
(re:11029) (di:complement) AE000142 AE000142 g1786552 Escherichia coli 562  
-11532534 5000689934 (de:(ecoli\_340) (pn:alcohol dehydrogenase class iii;  
formaldehyde dehydrogenase, glutathione-dependent) (gn:adhc)  
(gtcfc:1.1:1.8:2.2:3.2:3.5:5.12) (ec:1.1.1.1) (adh3\_ecoli)  
(keggfc:1.1:1.8:2.2:3.2:3.5:5.12) (rileyfc:1.2.7) (db:g) ECOLI\_340 ECOLI\_340  
Escherichia coli 562 10122789

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501819715	6996	29152	438	145

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501819738	6997	29153	216	72

#### Description

6500728677 nage:psn:b0679 pts system:n-acetylglucosamine-specific iiabc component:eiiabc-nag:n-acetylglucosamine-permease iiabc component:phosphotransferase enzyme ii:abc component:eii-nag (gtcfc:1.1:1.5:1.6:7.1:7.2:12.1) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b0679 b0679 Escherichia coli 562 -11532535 92118 nage:psn (ec:2.7.1.69) (de:enzyme ii, abc component), (eii-nag)) (db:swissprot) PTAA\_ECOLI P09323 ESCHERICHIA COLI 562 -11532535 123814 nage:psn phosphotransferase system enzyme ii::n-acetylglucosamine-specific:protein-n pi -phosphohistidine-n-acetylglucosamine phosphotransferase (cl:phosphotransferase system n-acetylglucosamine-specific enzyme ii:phosphotransferase system glucose-specific enzyme ii, factor ii homology:phosphotransferase system glucose-specific enzyme ii, factor iii homology) (ec:2.7.1.69) (db:pir1.dat) (mp:16 ... WQEC2N B29895 Escherichia coli 562 -11532535 223144 nage phosphotransferase enzyme ii:abc component (sr:escherichia coli(strain:k12) dna, clone:kohara clone #172) (db:genpept-bct1) (de:escherichia coli genomic dna. (15.0 - 15.4 min).) (le:3772) (re:5718) (di:direct) D90707 D90707 g1651288 Escherichia coli 562 -11532535 7500888922 nage (sr:e.coli dna, (library of l.clarke and j.carbon) (1), clone ppy10) (db:genpept-bct1) (de:e.coli n-acetylglucosamine transport protein (nage), andglucosamine-6-phosphate deaminase (nagb) genes, complete cds.) (nt:n-acetylglucosamine transport protein)... ECONAGBE M19284 g146913 Escherichia coli 562 -11532535 235212 nage pts system:n-acetylglucosamine-specific enzyme (fn:enzyme; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 61 of 400 of the completegenome.) (nt:o648; 100 pct identical to ptaa\_ecoli sw: p09323;) (le:6651) (re:8597) (di:direct) AE000171 AE000171 g1786894 Escherichia coli 562 -11532535 5000689935 nage pts system:n-acetylglucosamine-specific iiabc (sr:escherichia coli(strain:k12) dna, clone:kohara clone #172) (db:genpept) (de:escherichia coli genomic dna. (15.1 - 15.5 min).) (nt:orf\_id:o172#4; similar to swissprot accession) (le:3772) (re:5718) (di:direct) D90707 D90707 g1651288 Escherichia coli 562 -11532535

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501819740	6998	29154	318	105

#### Description

GTC ORF with score 156 to: (sr:homo sapiens b-lymphoblastoid cell\_line:gml30b dna) (db:genpept-pri2) (de:homo sapiens dna for tmem1 protein, pwp2 protein, knp-i alphaprotein and knp-i beta protein, partial and complete cds.) (le:6462:8029:12798:13224) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819741	6999	29155	600	199

Description

6500728678 pgm:b0688 phosphoglucomutase:glucose phosphomutase:pgm  
(gtcf:1.1:1.4:1.6:7.2) (ec:5.4.2.2) (keggfc:1.1:1.6:7.1) (rileyfc:1.1.1)  
(db:gtc-escherichia coli) b0688 b0688 Escherichia coli 562 -11532536 89347  
pgm (ec:5.4.2.2) (de:phosphoglucomutase, (glucose phosphomutase) (pgm))  
(db:swissprot) PGMU\_ECOLI P36938 ESCHERICHIA COLI 562 -11532536 7000686128  
pgm phosphoglucomutase (ec:5.4.2.2) (db:pir2.dat) G64803 G64803 Escherichia  
coli 562 -11532536 223149 pgm phosphoglucomutase (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #172) (db:genpept-bct1)  
(de:escherichia coli genomic dna. (15.0 - 15.4 min).) (le:13385) (re:15025)  
(di:direct) D90707 D90707 g1651293 Escherichia coli 562 -11532536 223153  
pgm phosphoglucomutase (sr:escherichia coli(strain:k12) dna, clone:kohara  
clone #173) (db:genpept-bct1) (de:escherichia coli genomic dna. (15.3 - 15.6  
min).) (le:3180) (re:4820) (di:direct) D90708 D90708 g1651298 Escherichia  
coli 562 -11532536 7500887975 pgm phosphoglucomutase (db:genpept-bct1)  
(de:escherichia coli phosphoglucomutase (pgm) gene, complete cds.) (le:121)  
(re:1761) (di:direct) ECU08369 U08369 g473888 Escherichia coli 562 -11532536  
238543 pgm phosphoglucomutase (fn:enzyme; degradation of small molecules:  
carbon) (db:genpept-bct2) (ec:5.4.2.2) (de:escherichia coli k-12 mg1655  
section 62 of 400 of the completegenome.) (nt:o546; 99 pct identical to  
pgmu\_ecoli sw: p36938) (le:5543) (re:7183) (di:direct) AE000172 AE000172  
g1786904 Escherichia coli 562 -11532536 5000689936 pgm phosphoglucomutase  
ec 5.4.2.2 glucose (sr:escherichia coli(strain:k12) dna, clone:kohara clone  
#172) (db:genpept) (de:escherichia coli genomic dna. (15.1 - 15.5 min).)  
(nt:orf\_id:o173#6; similar to swissprot accession) (le:13385) (re:15025)  
(di:direct) D90707 D90707 g1651293 Escherichia coli 562 -11532536  
7502851774 pgm phosphoglucomutase ec 5.4.2.2 glucose (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #173) (db:genpept) (de:escherichia  
coli genomic dna. (15.3 - 15.7 min).) (nt:orf\_id:o173#6; similar to  
swissprot accession) (le:3180) (re:4820) (di:direct) D90708 D90708 g1651298  
Escherichia coli 562 -11532536

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501819745	7000	29156	336	111

Description

6500728679 hrse:b0731 heat-responsive regulatory protein:hrsa protein  
(gtcfc:12.13:13.4) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1)  
(rileyfc:5.8.0) (db:gtc-escherichia coli) b0731 b0731 Escherichia coli 562  
-11532537 77643 hrse (ec:2.7.1.69) (de:hrsa protein,) (db:swissprot)  
HRSA\_ECOLI P54745 ESCHERICHIA COLI 562 -11532537 163175 hrse  
phosphotransferase system enzyme ii:hrsa:heat-responsive regulatory  
protein:protein-npi-phosphohistidine--sugar phosphotransferase hrse  
(cl:phosphotransferase system mannitol-specific enzyme ii factor iii  
homology) (ec:2.7.1.69) (db:pir2.dat) (mp:17 min) JC4598 JC4598 Escherichia  
coli 562 -11532537 301431 hrse hrse (fn:hrse is involved in thermoinduction  
of ompc and) (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia  
coli heat-responsive gene for hrse, complete cds.) (le:229) (re:2205)  
(di:direct) ECOTRSAA D64014 g976025 Escherichia coli 562 -11532537 236152  
hrse protein modification enzyme:induction of ompc (fn:enzyme; proteins -  
translation and) (db:genpept-bct2) (ec:2.7.1.69) (de:escherichia coli k-12  
mg1655 section 66 of 400 of the completegenome.) (nt:o658; 100 pct identical  
to hrse\_ecoli sw: p54745) (le:3138) (re:5114) (di:direct) AE000176 AE000176  
g1786951 Escherichia coli 562 -11532537 5000689937 (de:(ecoli\_705) (pn:hrse  
protein) (gn:hrse) (gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69) (hrse\_ecoli)  
(keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:5.7.0) (db:gtc-escherichia coli))  
ECOLI\_705 ECOLI\_705 Escherichia coli 562 10020003

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501819758	7001	29157	675	225

Description

6500728680 gpma:gpm:b0755 phosphoglycerate mutase 1:phosphoglyceromutase  
1:pgam 1:bpg-dependent pgam 1 (gtcfc:1.1) (ec:5.4.2.1) (keggfc:1.1)  
(rileyfc:1.2.1) (db:gtc-escherichia coli) b0755 b0755 Escherichia coli 562  
-11532538 7000691883 gpma phosphoglycerate mutase:1 (cl:phosphoglycerate  
mutase:phosphoglycerate mutase homology) (ec:5.4.2.1) (db:pir2.dat) C64811  
C64811 Escherichia coli 562 -11532538 7500954456 gpma phosphoglyceromutase  
1 (fn:enzyme; energy metabolism, carbon: glycolysis) (db:genpept-bct2)  
(ec:5.4.2.1) (de:escherichia coli k-12 mg1655 section 68 of 400 of the  
completegenome.) (nt:f250; 100 pct identical to pmg1\_ecoli sw: p31217;)  
(le:1993) (re:2745) (di:complement) AE000178 AE000178 g1786970 Escherichia  
coli 562 -11532538 5000689938 gpm phosphoglycerate mutase 1 ec 5.4.2.1  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #179) (db:genpept)  
(de:escherichia coli genomic dna. (16.8 - 17.1 min).) (nt:orf\_id:ol79#6;  
similar to swissprot accession) (le:6907) (re:7659) (di:complement) D90714  
D90714 g4062326 Escherichia coli 562 -11532538

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819764	7002	29158	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819768	7003	29159	981	326

Description

6500728681 galm:b0756 aldose 1-epimerase:mutarotase (gtcfc:1.1:2.3) (ec:5.1.3.3) (keggfc:1.1) (rileyfc:1.3.1) (db:gtc-escherichia coli) b0756 b0756 Escherichia coli 562 -11532539 73083 galm (ec:5.1.3.3) (de:aldose 1-epimerase, (mutarotase)) (db:swissprot) GALM\_ECOLI P40681 ESCHERICHIA COLI 562 -11532539 7000685363 galm aldose 1-epimerase::mutarotase (cl:aldose 1-epimerase) (ec:5.1.3.3) (db:pir2.dat) D64811 D64811 Escherichia coli 562 -11532539 223191 galm aldose 1-epimerase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #179) (db:genpept-bct1) (de:escherichia coli genomic dna. (16.8 - 17.1 min).) (le:7861) (re:8901) (di:complement) D90714 D90714 g1651341 Escherichia coli 562 -11532539 7500882090 galm aldose-1-epimerase (db:genpept-bct1) (ec:5.1.3.3) (de:escherichia coli galactose kinase (galk) gene, partial cds andaldose-1-epimerase (galm) gene, complete cds.) (nt:gtg start) (le:34) (re:1074) (di:direct) ECOGALM U13636 g725494 Escherichia coli 562 -11532539 234434 galm galactose-1-epimerase mutarotase (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (ec:5.1.3.3) (de:escherichia coli k-12 mg1655 section 68 of 400 of the completegenome.) (nt:f346; 100 pct identical to galm\_ecoli sw: p40681) (le:2947) (re:3987) (di:complement) AE000178 AE000178 g1786971 Escherichia coli 562 -11532539 5000689939 galm aldose 1-epimerase ec 5.1.3.3 mutarotase . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #179) (db:genpept) (de:escherichia coli genomic dna. (16.8 - 17.1 min).) (nt:orf\_id:o179#7; similar to swissprot accession) (le:7861) (re:8901) (di:complement) D90714 D90714 g1651341 Escherichia coli 562 -11532539

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819771	7004	29160	531	177

Description

6500728682 agp:b1002 glucose-1-phosphatase precursor:glpase (gtcfc:1.1:2.3) (ec:3.1.3.10) (keggfc:1.1) (rileyfc:1.3.1) (db:gtc-escherichia coli) b1002 b1002 Escherichia coli 562 -11532540 58971 agp (ec:3.1.3.10) (de:glucose-1-phosphatase precursor, (glpase)) (db:swissprot) AGP\_ECOLI P19926 ESCHERICHIA COLI 562 -11532540 163113 agp glucose-1-phosphatase:precursor (ec:3.1.3.10) (db:pir2.dat) (mp:23 min) JV0087 JV0087 Escherichia coli 562 -11532540 223327 agp glucose-1-phosphatase precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #227) (db:genpept-bct1) (de:escherichia coli genomic dna. (22.7 - 23.0 min).) (le:11082) (re:12323) (di:direct) D90737 D90737 g1651498 Escherichia coli 562 -11532540 7500876686 (sr:e.coli dna, clone pep1376) (db:genpept-bct1) (de:e.coli periplasmic acid glucose-1-phosphatase (agp) gene, completecds.) (nt:glucose-1-phosphatase precursor (agp)) (le:167) (re:1408) (di:direct) ECOAGPA M33807 g145218 Escherichia coli 562 -11532540 233750 agp periplasmic glucose-1-phosphatase (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (ec:3.1.3.10) (de:escherichia coli k-12 mg1655 section 92 of 400 of the completegenome.) (nt:o413; 100 pct identical to agp\_ecoli sw: p19926) (le:3141) (re:4382) (di:direct) AE000202 AE000202 g1787237 Escherichia coli 562 -11532540 5000689940 agp glucose-1-phosphatase precursor ec 3.1.3.10 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #227) (db:genpept) (de:escherichia coli genomic dna. (22.8 - 23.1 min).) (nt:orf\_id:o227#9; similar to swissprot accession) (le:11082) (re:12323) (di:direct) D90737 D90737 g1651498 Escherichia coli 562 -11532540

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819774	7005	29161	504	168

Description

GTC ORF with score 135 to: (sr:bodo saltans) (db:genpept-inv) (de:bodo saltans nadh dehydrogenase subunit 5 (nd5) mrna, kinetoplastgene encoding kinetoplast protein, partial cds.) (nt:partially edited mrna) (le:<1) (re:639) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501819777	7006	29162	540	180

Description

6500728683 ptsg:glca:umg:b1101 pts system:glucose-specific iibc component:eiibc-glc:glucose-permease iibc component:phosphotransferase enzyme ii:bc component:eii-glc (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b1101 b1101 Escherichia coli 562 -11532541 92168 ptsg:glca:umg (ec:2.7.1.69) (de:(ec 2.7.1.69) (eii-glc)) (db:swissprot) PTGB\_ECOLI P05053 ESCHERICHIA COLI 562 -11532541 123813 ptsg:glca:umg phosphotransferase system enzyme ii::glucose-specific:factor ii:glucose-permease:factor ii:phosphotransferase system enzyme ii-glc:protein-n pi -phosphohistidine-glucose phosphotransferase:factor ii (cl:phosphotransferase system glucose-specific enzyme ii, factor ii:phosphotransferase system glucose-specific enzyme ii, factor ii homology) (ec:2.7.1.69) (db:pir1.dat) (mp:24 min) WQEC2G A25336 Escherichia coli 562 -11532541 223362 ptsg pts system:glucose permease iibc component (sr:escherichia coli(strain:k12) dna, clone:kohara clone #236) (db:genpept-bct1) (de:escherichia coli genomic dna.(24.7 - 25.1 min).) (le:8511) (re:9944) (di:direct) D90745 D90745 g1651541 Escherichia coli 562 -11532541 7500888952 ptsg (sr:e.coli dna strain ptsg4) (db:genpept-bct1) (de:e. coli ptsg gene encoding glucose-specific enzyme ii ofphosphotransferase system.) (nt:glucose-specific enzyme ii of phosphotransferase) (le:39) (re:1472) (di:direct) ECOPTSG J02618 g147393 Escherichia coli 562 -11532541 235590 ptsg pts system:glucose-specific iibc component (fn:transport; transport of small molecules:) (db:genpept-bct2) (ec:2.7.1.69) (de:escherichia coli k-12 mg1655 section 100 of 400 of the completegenome.) (nt:o477; 100 pct identical to ptgb\_ecoli sw: p05053) (le:9174) (re:10607) (di:direct) AE000210 AE000210 g1787343 Escherichia coli 562 -11532541 5000689941 glca pts system:glucose-specific iibc component (sr:escherichia coli(strain:k12) dna, clone:kohara clone #236) (db:genpept) (de:escherichia coli genomic dna. (24.8 - 25.2 min).) (nt:orf\_id:o236#10; similar to swissprot accession) (le:8511) (re:9944) (di:direct) D90745 D90745 g1651541 Escherichia coli 562 -11532541

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501819780	7007	29163	444	147

Description

6500728684 adhe:ana:b1241 alcohol/acetaldehyde dehydrogenase:alcohol dehydrogenase:adh / acetaldehyde dehydrogenase:acetylating:acdh / pyruvate-formate-lyase deactivase:pfl deactivase (gtcfc:1.4:1.8:2.2:3.2:8.1) (keggfc:1.4:1.8:3.2:3.5:5.12:8.1) (rileyfc:1.2.7) (db:gtc-escherichia coli) b1241 b1241 Escherichia coli 562 -11532542 122561 adhe acetaldehyde dehydrogenase acetylating:alcohol dehydrogenase::acetaldehyde/alcohol dehydrogenase:adhe:aldehyde reductase (cl:acetaldehyde/alcohol dehydrogenase:aldehyde dehydrogenase homology:lactaldehyde reductase homology) (ec:1.2.1.10:1.1.1.1) (db:pir1.dat) DEEC JS0406 Escherichia coli 562 -11532542 223448 adhe alcohol dehydrogenase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #250) (db:genpept-bct1) (de:escherichia coli genomic dna (27.6-28.0 min).) (le:12442) (re:15117) (di:complement) D90759 D90759 g1651639 Escherichia coli 562 -11532542 224718 adhe alcohol dehydrogenase ec 1.1.1.1 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #251(27.7-28.2 min).) (nt:orf\_id:o250#6; similar to (pir accession number) (le:12442) (re:15117) (di:complement) D90852 D90852 g1805517 Escherichia coli 562 -11532542 228045 adhe alcohol dehydrogenase (db:genpept-bct1) (ec:1.1.1.1) (de:e.coli adhe gene for alcohol dehydrogenase.) (le:2021) (re:4696) (di:direct) ECADHEG X59263 g40900 Escherichia coli 562 -11532542 301358 (sr:e.coli dna) (db:genpept-bct1) (de:e.coli alcohol-dehydrogenase (adhe) gene, complete cds.) (nt:alcohol dehydrogenase (adhe)) (le:84) (re:2759) (di:direct) ECOADHEX M33504 g145206 Escherichia coli 562 -11532542 233732 adhe coa-linked acetaldehyde dehydrogenase and (fn:enzyme; energy metabolism, carbon:) (db:genpept-bct2) (ec:1.1.1.1) (de:escherichia coli k-12 mg1655 section 112 of 400 of the completegenome.) (nt:f891; 99 pct identical to adhe\_ecoli sw: p17547) (le:5280) (re:7955) (di:complement) AE000222 AE000222 g1787493 Escherichia coli 562 -11532542 5000689942 adhe alcohol dehydrogenase ec 1.1.1.1 . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #250) (db:genpept) (de:escherichia coli genomic dna. (27.7 - 28.1 min).) (nt:orf\_id:o251#7; similar to pir accession number) (le:12442) (re:15117) (di:complement) D90759 D90759 g1651639 Escherichia coli 562 -11532542



ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501819784	7008	29164	351	116

Description

6500728685 gapc\_2:b1416 (gtcfc:14.3) (ec:1.2.1.12) (keggfc:1.1:6.7) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1416 b1416 Escherichia coli 562 -11532543 7000690886 gapc\_2 gapc-2 protein:truncated (cl:glyceraldehyde-3-phosphate dehydrogenase) (db:pir2.dat) C64893 C64893 Escherichia coli 562 -11532543 7500959743 gapc\_2 glyceraldehyde-3-phosphate dehydrogenase second (fn:enzyme; energy metabolism, carbon: glycolysis) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 129 of 400 of the completegenome.) (nt:f83; this 83 aa orf is 98 pct identical to) (le:2644) (re:2895) (di:complement) AE000239 AE000239 g1787685 Escherichia coli 562 -11532543 5000689943 (de:(ecoli\_1376) (pn:glyceraldehyde 3-phosphate dehydrogenase c:gapdh-c) (gn:gapc) (gtcfc:1.1:6.14:6.8) (ec:1.2.1.12) (g3p3\_ecoli) (keggfc:1.1:6.7) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_1376 ECOLI\_1376 Escherichia coli 562 10123312

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501819785	7009	29165	672	224

Description

6500728686 gapc\_1:b1417 glyceraldehyde 3-phosphate dehydrogenase c (gtcfc:1.1:6.14:6.8) (ec:1.2.1.12) (keggfc:1.1:6.7) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1417 b1417 Escherichia coli 562 -11532544 7000690894 gapc\_1 gapc-1 protein:truncated (cl:glyceraldehyde-3-phosphate dehydrogenase) (db:pir2.dat) D64893 D64893 Escherichia coli 562 -11532544 7500953834 gapc\_1 glyceraldehyde 3-phosphate dehydrogenase c (fn:enzyme; energy metabolism, carbon: glycolysis) (db:genpept-bct2) (ec:1.2.1.12) (de:escherichia coli k-12 mg1655 section 129 of 400 of the completegenome.) (nt:f134; this 134 aa orf is 99 pct identical (0 gaps)) (le:2892) (re:3296) (di:complement) AE000239 AE000239 g1787686 Escherichia coli 562 -11532544 5000689944 (de:(ecoli\_1377) (pn:glyceraldehyde 3-phosphate dehydrogenase c:gapdh-c) (gn:gapc) (gtcfc:1.1:6.14:6.8) (ec:1.2.1.12) (g3p3\_ecoli) (keggfc:1.1:6.7) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_1377 ECOLI\_1377 Escherichia coli 562 10123313

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501819795	7010	29166	1608	535

# Description

6500728687 malx:b1621 pts system:maltose and glucose-specific ii abc component:pts system:maltose and glucose-specific iiabc component:maltose and glucose-permease iiabc component:phosphotransferase enzyme ii:abc component (gtcfc:12.2:1.1) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b1621 b1621 Escherichia coli 562 -11532545 92260 malx (ec:2.7.1.69) (de:component),) (db:swissprot) PTOA\_ECOLI P19642 ESCHERICHIA COLI 562 -11532545 7000686224 malx phosphotransferase system enzyme ii:factor ii:maltose-and glucose-specific (cl:phosphotransferase system glucose-specific enzyme ii, factor ii:phosphotransferase system glucose-specific enzyme ii, factor ii homology) (ec:2.7.1.69) (db:pir2.dat) (mp:36 min) G64918 G64918 Escherichia coli 562 -11532545 224050 malx phosphotransferase system enzyme ii ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #314(36.3-36.7 min.)) (nt:orf\_id:o314#7; similar to (pir accession number) (le:14039) (re:15631) (di:direct) D90805 D90805 g1742675 Escherichia coli 562 -11532545 224057 malx phosphotransferase system enzyme ii ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #315(36.6-36.9 min.)) (nt:orf\_id:o314#7; similar to (pir accession number) (le:2351) (re:3943) (di:direct) D90806 D90806 g1742683 Escherichia coli 562 -11532545 300770 malx phosphotransferase system enzyme ii ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #317(36.6-36.9 min.)) (nt:orf\_id:o314#7; similar to (pir accession number) (le:2452) (re:4044) (di:direct) D90808 D90808 g1742715 Escherichia coli 562 -11532545 300745 malx pts system:maltose and glucose-specific ii abc (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 148 of 400 of the completegenome.) (nt:o530; 99 pct identical to ptoa\_ecoli sw: p19642; cg) (le:76) (re:1668) (di:direct) AE000258 AE000258 g1787908 Escherichia coli 562 -11532545 224087 malx phosphotransferase system enzyme ii ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #317(36.6-36.9 min.)) (nt:orf\_id:o314#7; similar to (pir accession number) (le:2452) (re:4044) (di:direct) D90808 D90808 g1742715 Escherichia coli 562 -11532545 5000689945 (de:(ecoli\_1580) (pn:pts system, maltose and glucose-specific iiabc component:maltose and glucose-permease iiabc component:phosphotransferase enzyme ii, abc component) (gn:malx) (gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69) (ptoa\_ecol) ECOLI\_1580 ECOLI\_1580 Escherichia coli 562 10119736

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819801	7011	29167	306	101

Description

6500728688 pykf:b1676 pyruvate kinase:pyruvate kinase i:pk-1  
 (gtcfc:1.1:1.8:2.4) (ec:2.7.1.40) (keggfc:1.1:1.8:2.3) (rileyfc:1.2.1)  
 (db:gtc-escherichia coli) b1676 b1676 Escherichia coli 562 -11532546 81026  
 pykf (ec:2.7.1.40) (de:pyruvate kinase i, (pk-1)) (db:swissprot) KPY1\_ECOLI  
 P14178 ESCHERICHIA COLI 562 -11532546 7000685702 pykf pyruvate  
 kinase::fructose-1:6-bisphosphate dependent pyruvate kinase (cl:pyruvate  
 kinase) (ec:2.7.1.40) (db:pir1.dat) D64925 D64925 Escherichia coli 562  
 -11532546 295383 pykf pyruvate kinase (db:genpept-bct1) (ec:2.7.1.40)  
 (de:escherichia coli k-12 mg1655 genome, ribc-pykf region.) (nt:cg site  
 number 17620; alternate name pk-1) (le:13102) (re:14514) (di:direct)  
 ECU68703 U68703 g1549287 Escherichia coli 562 -11532546 239775 pykf  
 pyruvate kinase i formerly f:fructose (fn:enzyme; energy metabolism, carbon:  
 glycolysis) (db:genpept-bct2) (ec:2.7.1.40) (de:escherichia coli k-12 mg1655  
 section 152 of 400 of the completegenome.) (nt:o470; residues 1-450 are 100  
 pct identical) (le:9439) (re:10851) (di:direct) AE000262 AE000262 g1787965  
 Escherichia coli 562 -11532546 5000689946 (de:(ecoli\_1633) (pn:pyruvate  
 kinase i:formerly f, fructose stimulated) (gn:pykf) (gtcfc:1.1:1.8:2.4)  
 (ec:2.7.1.40) (kpy1\_ecoli) (keggfc:1.1:1.8:2.3) (rileyfc:1.2.1)  
 (db:gtc-escherichia coli)) ECOLI\_1633 ECOLI\_1633 Escherichia coli 562  
 10123419

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819809	7012	29168	183	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819810	7013	29169	300	99

Description

6500728689 pfkb:b1723 6-phosphofructokinase isozyme:6-phosphofructokinase isozyme 2:phosphofructokinase-2 (gtcfc:1.1:1.3:1.5:1.6) (ec:2.7.1.11) (keggfc:1.1:1.3:1.5:1.6) (rileyfc:1.2.1) (db:gtc-escherichia coli) b1723 b1723 Escherichia coli 562 -11532547 80263 pfkb (ec:2.7.1.11) (de:6-phosphofructokinase isozyme 2, (phosphofructokinase-2)) (db:swissprot) K6P2\_ECOLI P06999 ESCHERICHIA COLI 562 -11532547 7000685658 pfkb 6-phosphofructokinase:2:phosphofructokinase 1:isozyme 2:phosphohexokinase:isozyme 2 (cl:6-phosphofructokinase 2) (ec:2.7.1.11) (db:pir1.dat) (mp:38 min) KIECFB C64931 Escherichia coli 562 -11532547 7500884418 pfkb 6-phosphofructokinase ii:suppressor of pfka (fn:enzyme; energy metabolism, carbon: glycolysis) (db:genpept-bct2) (ec:2.7.1.11) (de:escherichia coli k-12 mg1655 section 157 of 400 of the completegenome.) (nt:o309; residues 39-309 are 93 pct identical to) (le:6353) (re:7282) (di:direct) AE000267 AE000267 g1788017 Escherichia coli 562 -11532547 5000689947 (de:(ecoli\_1680) (pn:6-phosphofructokinase ii; suppressor of pfka) (gn:pfkb) (gtcfc:1.1:1.3:1.5:1.6) (ec:2.7.1.11) (k6p2\_ecoli) (keggfc:1.1:1.3:1.5:1.6) (rileyfc:1.2.1) (db:gtc-escherichia coli)) ECOLI\_1680 ECOLI\_1680 Escherichia coli 562 10123435

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819812	7014	29170	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819813	7015	29171	687	228

Description

6500728690 celc:b1736 phosphoenolpyruvate dependent phosphotransferase enzyme iii-cellobiose:pts system:cellobiose-specific iia component:eiaa-cel:cellobiose-permease iia component:phosphotransferase enzyme ii:a component:eiii-cel (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b1736 b1736 Escherichia coli 562 -11532548 92138 celc (ec:2.7.1.69) (de:(ec 2.7.1.69) (eiii-cel)) (db:swissprot) PTCA\_ECOLI P17335 ESCHERICHIA COLI 562 -11532548 7000686209 celc phosphotransferase system enzyme ii::cellobiose-specific:factor iii:phosphotransferase system enzyme iii:phosphoenolpyruvate-dependent (cl:phosphotransferase system lactose-specific enzyme ii, factor iii) (ec:2.7.1.69) (db:pir2.dat) (mp:38 min) H64932 H64932 Escherichia coli 562 -11532548 224197 celc phosphotransferase system enzyme ii ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #325(38.9-39.2 min.)) (nt:orf\_id:o326#5; similar to (pir accession number) (le:12044) (re:12394) (di:complement) D90816 D90816 g1742833 Escherichia coli 562 -11532548 224205 celc phosphotransferase system enzyme ii ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #326(39.1-39.4 min.)) (nt:orf\_id:o326#5; similar to (pir accession number) (le:4815) (re:5165) (di:complement) D90817 D90817 g1742842 Escherichia coli 562 -11532548 233953 celc (sr:e.coli dna) (db:genpept-bct1) (de:e.coli cellobiose permease proteins cela, celb, celc, cellobioseoperon repressor protein celd and cellobiose phospho-b-glucosidaseprotein celf gene, complete cds.) (nt:putative) (le:2089) (re:2439) (di:direct) ECOCELA M64438 g145480 Escherichia coli 562 -11532548 233954 celc pts enzyme iii cel (sr:escherichia coli (individual\_isolate rm66c/human/iowa, strain eco) (db:genpept-bct1) (de:escherichia coli (strain ecor 6, isolate rm66c/human/iowa) ptsenzyme iii cel (celc) gene, complete cds.) (nt:putative) (le:1) (re:351) (di:direct) ECOCELCB M93575 g145486 Escherichia coli 562 -11532548 233955 celc pts enzyme iii cel (sr:escherichia coli (individual\_isolate rm52b/human/iowa, strain eco) (db:genpept-bct1) (de:escherichia coli (strain ecor 28, isolate rm52b/human/iowa) ptsenzyme iii cel (celc) gene, complete cds.) (nt:putative) (le:1) (re:351) (di:direct) ECOCELC C M93571 g145488 Escherichia coli 562 -11532548 233956 celc pts enzyme iii cel (sr:escherichia coli (individual\_isolate rm42b/human/iowa, strain eco) (db:genpept-bct1) (de:escherichia coli (strain ecor 35, isolate rm42b/human/iowa) ptsenzyme iii cel (celc) gene, complete cds.) (nt:putative) (le:1) (re:351) (di:direct) ECOCELCD M93572 g145490 Escherichia coli 562 -11532548 233958 celc pts enzyme iii cel (sr:escherichia coli (individual\_isolate rm44b/marmoset/washington zoo) (db:genpept-bct1) (de:escherichia coli (strain ecor 37, isolate rm44b/marmoset/washingtonzoo) pts enzyme iii cel (celc) gene, complete cds.) (nt:putative) (le:1) (re:351) (di:direct) ECOCELCE M93592 g145492 Escherichia coli 562 -11532548 233959 celc pts enzyme iii cel

Escherichia coli 562 -11532548 233959 celc pts enzyme iii cel  
 (sr:escherichia coli (individual isolate dd/human/massachusetts, strai)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819817	7016	29172	507	168

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819851	7017	29173	1533	511

Description

6500728691 celb:b1737 pts system:cellobiose-specific iic  
 component:eiic-cel:cellobiose-permease iic component:phosphotransferase  
 enzyme ii:c component (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69)  
 (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b1737  
 b1737 Escherichia coli 562 -11532549 92142 celb (de:permease iic component)  
 (phosphotransferase enzyme ii, c component)) (db:swissprot) PTCC\_ECOLI  
 P17334 ESCHERICHIA COLI 562 -11532549 7000686212 celb celb protein  
 (cl:phosphotransferase system enzyme ii factor ii,  
 phosphoenolpyruvate-dependent) (db:pir2.dat) A64933 A64933 Escherichia coli  
 562 -11532549 7500888933 celb pep-dependent phosphotransferase enzyme ii  
 for (fn:enzyme; transport of small molecules:) (db:genpept-bct2)  
 (de:escherichia coli k-12 mg1655 section 158 of 400 of the completegenome.)  
 (nt:f452; cg site no. 18487; residues 1-189 are 100 pct) (le:9763)  
 (re:11121) (di:complement) AE000268 AE000268 g1788032 Escherichia coli 562  
 -11532549 5000689949 (de:(ecoli\_1694) (pn:pep-dependent phosphotransferase  
 enzyme ii for cellobiose, arbutin, and salicin) (gn:celb)  
 (gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69) (ptcc\_ecoli)  
 (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3) (db:gtc-escheric) ECOLI\_1694  
 ECOLI\_1694 Escherichia coli 562 10123442

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819855	7018	29174	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819856	7019	29175	318	105
<u>Description</u>				
6500728692 cela:b1738 pts system:cellobiose-specific iib component:eiib-cel:cellobiose-permease iib component:phosphotransferase enzyme ii:b component (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b1738 b1738 Escherichia coli 562 -11532550 233947 cela (ec:2.7.1.69) (de:(ec 2.7.1.69)) (db:swissprot) PTCB_ECOLI P17409 ESCHERICHIA COLI 562 -11532550 162805 cela phosphotransferase system enzyme ii::cellobiose-specific factor iib (cl:phosphotransferase system enzyme ii cellobiose-specific factor iib) (ec:2.7.1.69) (db:pir2.dat) S10870 S10870 Escherichia coli 562 -11532550 224199 cela cela protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #325(38.9-39.2 min.)) (nt:orf_id:o326#7; similar to (pir accession number) (le:13888) (re:14208) (di:complement) D90816 D90816 g1742835 Escherichia coli 562 -11532550 224207 cela cela protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #326(39.1-39.4 min.)) (nt:orf_id:o326#7; similar to (pir accession number) (le:6659) (re:6979) (di:complement) D90817 D90817 g1742844 Escherichia coli 562 -11532550 300855 cela cela protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #327(39.2-39.5 min.)) (nt:orf_id:o326#7; similar to (pir accession number) (le:1027) (re:1347) (di:complement) D90818 D90818 g1742851 Escherichia coli 562 -11532550 300849 (db:genpept-bct1) (de:escherichia coli dna for cel operon including cela, celb, celc, celd and celf genes.) (nt:cela product, unknown) (le:286) (re:606) (di:direct) ECCELOPE X52890 g41097 Escherichia coli 562 -11532550 5000689950 cela (sr:e.coli dna) (db:genpept-bct1) (de:e.coli cellobiose permease proteins cela, celb, celc, cellobioseoperon repressor protein celd and cellobiose phospho-b-glucosidaseprotein celf gene, complete cds.) (nt:putative) (le:286) (re:606) (di:direct) ECOCELA M64438 g145478 Escherichia coli 562 -11532550 232506 cela pep-dependent phosphotransferase enzyme iv for (fn:enzyme; transport of small molecules:) (db:genpept-bct2) (ec:2.7.1.69) (de:escherichia coli k-12 mg1655 section 159 of 400 of the completegenome.) (nt:f106; 100 pct identical to ptcb_ecoli sw: p17409;) (le:73) (re:393) (di:complement) AE000269 AE000269 g1788034 Escherichia coli 562 -11532550 92140 cela (ec:2.7.1.69) (de:(ec 2.7.1.69)) (db:swissprot) PTCB_ECOLI P17409 ESCHERICHIA COLI 562 -11532550 224213 cela cela protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #327(39.2-39.5 min.)) (nt:orf_id:o326#7; similar to (pir accession number) (le:1027) (re:1347) (di:complement) D90818 D90818 g1742851 Escherichia coli 562 -11532550				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501819859	7020	29176	276	92
<u>Description</u>				
6500728693 gapa:b1779 glyceraldehyde 3-phosphate dehydrogenase a:gapdh-a (gtcfc:1.1:6.14:6.8) (ec:1.2.1.12) (keggfc:1.1:6.7) (rileyfc:1.2.1) (db:gtc-escherichia coli) b1779 b1779 Escherichia coli 562 -11532551 122633 gapa::gap glyceraldehyde-3-phosphate dehydrogenase:a (cl:glyceraldehyde-3-phosphate dehydrogenase) (ec:1.2.1.12) (db:pir1.dat) (mp:39 min) DEECG3 A25209 Escherichia coli 562 -11532551 224256 gap glyceraldehyde-3-phosphate dehydrogenase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #330(39.9-40.3 min.)) (nt:orf_id:o330#6; similar to (pir accession number) (le:10448) (re:11443) (di:direct) D90821 D90821 g1742897 Escherichia coli 562 -11532551 300898 (db:genpept-bct1) (de:e. coli gap gene for gapdh (glyceraldehyde-3-phosphatedehydrogenase).) (nt:put. gapdh (aa 1-332)) (le:484) (re:1479) (di:direct) ECGAP X02662 g41539 Escherichia coli 562 -11532551 232968 gapa glyceraldehyde-3-phosphate dehydrogenase a (fn:enzyme; energy metabolism, carbon: glycolysis) (db:genpept-bct2) (ec:1.2.1.12) (de:escherichia coli k-12 mg1655 section 163 of 400 of the completegenome.) (nt:o331; 100 pct identical to g3p1_ecoli sw: p06977;) (le:201) (re:1196) (di:direct) AE000273 AE000273 g1788079 Escherichia coli 562 -11532551 5000689951 (de:(ecoli_1736) (pn:glyceraldehyde-3-phosphate dehydrogenase) (gn:gapa) (gtcfc:1.1:6.14:6.8) (ec:1.2.1.12) (g3p1_ecoli) (keggfc:1.1:6.7) (rileyfc:1.2.1) (db:gtc-escherichia coli)) ECOLI_1736 ECOLI_1736 Escherichia coli 562 10065566				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819862	7021	29177	615	204
<u>Description</u>				
<p>6500728694 manx:ptsl:gptb:b1817 pts system:mannose-specific iiab component:eiab-mannose-permease iiab component:phosphotransferase enzyme ii:ab component:eiab-mannose (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b1817 b1817 Escherichia coli 562 -11532552 123809 manx:ptsl phosphotransferase system enzyme ii::mannose-specific:factor iii:mannose permease:factor iii:phosphotransferase system enzyme ii-a:mannose-specific:phosphotransferase system enzyme iii:mannose-specific:protein-npi-phosphohistidine--mannose phosphotransferase:factor iii:protein-npi-phosphohistidine--sugar phosphotransferase:mannose-specific enzyme iii (cl:phosphotransferase system mannose-specific enzyme ii, factor iii) (ec:2.7.1.69) (db:pir1.dat) (mp:40 min) WQECM3 A30286 Escherichia coli 562 -11532552 224306 manx:ptsl phosphotransferase system enzyme ii ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #334(40.6-41.0 min.)) (nt:orf_id:o334#10; similar to (pir accession number) (le:14754) (re:15725) (di:direct) D90825 D90825 g1736455 Escherichia coli 562 -11532552 300952 manx:ptsl phosphotransferase system enzyme ii ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #335(40.9-41.3 min.)) (nt:orf_id:o334#10; similar to (pir accession number) (le:3212) (re:4183) (di:direct) D90826 D90826 g1736462 Escherichia coli 562 -11532552 300947 ptsl mannose permease subunit iii-man (sr:e.coli dna, clone rp7029) (db:genpept-bct1) (de:e.coli ptsl, ptsp and ptsm genes encoding mannose permease subunitsiii-man, ii-p-man and ii-m-man, complete cds.) (le:376) (re:1347) (di:direct) ECOPTSLPM J02699 g147402 Escherichia coli 562 -11532552 235596 manx pts enzyme iiab:mannose-specific (fn:enzyme; transport of small molecules:) (db:genpept-bct2) (ec:2.7.1.69) (de:escherichia coli k-12 mg1655 section 166 of 400 of the completegenome.) (nt:o323; 100 pct identical to ptna_ecoli sw: p08186;) (le:3732) (re:4703) (di:direct) AE000276 AE000276 g1788120 Escherichia coli 562 -11532552 224312 manx:ptsl phosphotransferase system enzyme ii ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #335(40.9-41.3 min.)) (nt:orf_id:o334#10; similar to (pir accession number) (le:3212) (re:4183) (di:direct) D90826 D90826 g1736462 Escherichia coli 562 -11532552 5000689952 (de:(ecoli_1774) (pn:pts system, mannose-specific iiab component:eiab-mannose-permease iiab component:phosphotransferase enzyme ii, ab component:eiab-mannose) (gn:manx) (gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69) (ptna_ecoli) (ke) ECOLI_1774 ECOLI_1774 Escherichia coli 562 10065956</p>				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819865	7022	29178	447	148

Description

6500728695 pyka:b1854 pyruvate kinase a:pyruvate kinase ii:pk-2  
 (gtcfc:1.1:1.8:2.4) (ec:2.7.1.40) (keggfc:1.1:1.8:2.3) (rileyfc:1.2.1)  
 (db:gtc-escherichia coli) b1854 b1854 Escherichia coli 562 -11532553 138878  
 pyka pyruvate kinase:a:pyruvate kinase ii (cl:pyruvate kinase) (ec:2.7.1.40)  
 (db:pir2.dat) S29790 S29790 Escherichia coli 562 -11532553 224345 pyka  
 pyruvate kinase ec 2.7.1.40 (sr:escherichia coli (strain:k12) dna,  
 clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
 kohara clone #336gap(41.6-41.9 min.)) (nt:orf\_id:o336gap#7; similar to (pir  
 accession number) (le:7175) (re:8617) (di:direct) D90828 D90828 g1736497  
 Escherichia coli 562 -11532553 300985 pyka pyruvate kinase type ii  
 (sr:e.coli (strain k12) dna) (db:genpept-bct1) (de:e.coli pyruvate kinase  
 type ii (pyka) gene, complete cds.) (le:152) (re:1594) (di:direct) ECOPYKAA  
 M63703 g147459 Escherichia coli 562 -11532553 235635 pyka pyruvate kinase  
 ii:glucose stimulated (fn:enzyme; energy metabolism, carbon: glycolysis)  
 (db:genpept-bct2) (ec:2.7.1.40) (de:escherichia coli k-12 mg1655 section 169  
 of 400 of the completegenome.) (nt:o480; 100 pct identical to kpy2\_ecoli sw:  
 p21599;) (le:6865) (re:8307) (di:direct) AE000279 AE000279 g1788160  
 Escherichia coli 562 -11532553 5000689953 (de:(ecoli\_1811) (pn:pyruvate  
 kinase ii, glucose stimulated) (gn:pyka) (gtcfc:1.1:1.8:2.4) (ec:2.7.1.40)  
 (kpy2\_ecoli) (keggfc:1.1:1.8:2.3) (rileyfc:1.2.1) (db:gtc-escherichia coli))  
 ECOLI\_1811 ECOLI\_1811 Escherichia coli 562 10070964

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819876	7023	29179	570	189

Description

GTC ORF with score 519 to: (sr:t.reesei (strain vtt-d-80133) dna, clone w12;  
 and cdna to mrna) (db:genpept-pln1) (de:trichoderma reesei endoglucanase i  
 gene, complete cds.) (nt:endoglucanase i precursor) (le:11:851:1498)  
 (re:780:1440:1517) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819908	7024	29180	387	128

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819928	7025	29181	459	153

#### Description

6500728696 gatb:b2093 pts system:galactitol-specific iib component:eiib-gat:galacticol-permease iib component:phosphotransferase enzyme ii:b component (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b2093 b2093 Escherichia coli 562 -11532554 92209 gatb (ec:2.7.1.69) (de:(ec 2.7.1.69)) (db:swissprot) PTKB\_ECOLI P37188 ESCHERICHIA COLI 562 -11532554 7000686221 gatb pts system:galactitol-specific iib component (db:pir2.dat) D64976 D64976 Escherichia coli 562 -11532554 224639 gatb pts system:galactitol-specific iib component (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #358(46.6-46.9 min.)) (nt:orf\_id:o358#3; similar to (swissprot accession) (le:11677) (re:11961) (di:complement) D90847 D90847 g1736810 Escherichia coli 562 -11532554 301284 gatb pts system:galactitol-specific iib component (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #359(46.8-47.2 min.)) (nt:orf\_id:o358#3; similar to (swissprot accession) (le:1007) (re:1291) (di:complement) D90848 D90848 g1736816 Escherichia coli 562 -11532554 301279 gatb galactitol-specific enzyme iib of (fn:enzyme; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 188 of 400 of the completegenome.) (nt:f94; 95 pct identical to ptkb\_ecoli sw: p37188) (le:9236) (re:9520) (di:complement) AE000298 AE000298 g1788409 Escherichia coli 562 -11532554 224644 gatb pts system:galactitol-specific iib component (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #359(46.8-47.2 min.)) (nt:orf\_id:o358#3; similar to (swissprot accession) (le:1007) (re:1291) (di:complement) D90848 D90848 g1736816 Escherichia coli 562 -11532554 5000689954 (de:(ecoli\_2041) (pn:pts system, galactitol-specific iib component:eiib-gat:galacticol- permease iib component:phosphotransferase enzyme ii, b component) (gn:gatb) (gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69) (ptkb\_ecoli) (keggfc:1.) ECOLI\_2041 ECOLI\_2041 Escherichia coli 562 10120003

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819934	7026	29182	294	97

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819935	7027	29183	297	98

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819936	7028	29184	354	117

Description

6500728697 gata:b2094 pts system:galactitol-specific iia  
component:eiia-gat:galacticol-permease iia component:phosphotransferase  
enzyme ii:a component (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69)  
(keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b2094  
b2094 Escherichia coli 562 -11532555 92208 gata (ec:2.7.1.69) (de:(ec  
2.7.1.69)) (db:swissprot) PTKA\_ECOLI P37187 ESCHERICHIA COLI 562 -11532555  
7000686220 gata pts system:galactitol-specific iia component (db:pir2.dat)  
E64976 E64976 Escherichia coli 562 -11532555 7500888975 gata  
galactitol-specific enzyme iia of (fn:enzyme; transport of small molecules:)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 188 of 400 of the  
completegenome.) (nt:f150; 99 pct identical to ptka\_ecoli sw: p37187)  
(le:9551) (re:10003) (di:complement) AE000298 AE000298 g1788410 Escherichia  
coli 562 -11532555 5000689955 (de:(ecoli\_2042) (pn:pts system,  
galactitol-specific iia component:eiia-gat:galacticol- permease iia  
component:phosphotransferase enzyme ii, a component) (gn:gata)  
(gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69) (ptka\_ecoli) (keggfc:1.)  
ECOLI\_2042 ECOLI\_2042 Escherichia coli 562 10123564

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501819945	7029	29185	378	125

Description

6500728698 frua:ptsf:b2167 pts system:fructose-specific iibc  
component:eiibc-fru:fructose-permease iibc component:phosphotransferase  
enzyme ii:bc component:eii-fru (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2)  
(ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3)  
(db:gtc-escherichia coli) b2167 b2167 Escherichia coli 562 -11532556 92153  
frua:ptsf (ec:2.7.1.69) (de:(ec 2.7.1.69) (eii-fru)) (db:swissprot)  
PTFB\_ECOLI P20966 ESCHERICHIA COLI 562 -11532556 164326 frua:ptsf  
phosphotransferase system enzyme ii::fructose-specific  
(cl:phosphotransferase system enzyme ii,  
fructose-specific:phosphotransferase system mannitol-specific enzyme ii  
factor iii homology) (ec:2.7.1.69) (db:pir2.dat) (mp:47 min) A34962 A34962  
Escherichia coli 562 -11532556 234774 frua enzyme ii-fru (db:genpept-bct1)  
(de:e. coli phosphotransferase system enzyme ii (frua) gene, completecds.)  
(le:120) (re:1811) (di:direct) ECOFRUA M23196 g450372 Escherichia coli 562  
-11532556 7500888941 fructose-specific iibc component (sr:escherichia coli  
k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12  
bhb2600.) (le:67463) (re:69154) (di:complement) ECOHU47 U00007 g405893  
Escherichia coli 562 -11532556 234397 frua pts system:fructose-specific  
transport protein (fn:regulator; degradation of small molecules:)  
(db:genpept-bct2) (ec:2.7.1.69) (de:escherichia coli k-12 mg1655 section 196  
of 400 of the completegenome.) (nt:f563; 100 pct identical to ptfb\_ecoli sw:  
p20966) (le:2367) (re:4058) (di:complement) AE000306 AE000306 g1788492  
Escherichia coli 562 -11532556 5000689956 (de:(ecoli\_2116) (pn:pts system,  
fructose-specific iibc component:eiibc-fru:fructose- permease iibc  
component:phosphotransferase enzyme ii, bc component:eii-fru) (gn:frua)  
(gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69) (ptfb\_ecoli) (k)) ECOLI\_2116  
ECOLI\_2116 Escherichia coli 562 10034187

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819957	7030	29186	354	117

Description

6500728699 frub:fruf:fpr:b2169 pts system:fructose-specific iia/fpr  
component:eiaa-fru:fructose-permease iia/fpr component:phosphotransferase  
enzyme ii:a/fpr component:phosphotransferase fpr  
protein:pseudo-hpr:eiii-fru:fructose pts diphosphoryl transfer protein  
(gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1)  
(rileyfc:4.1.3) (db:gtc-escherichia coli) b2169 b2169 Escherichia coli 562  
-11532557 92148 frub:fruf:fpr (ec:2.7.1.69) (de:hpr) (eiii-fru) (fructose  
pts diphosphoryl transfer protein)) (db:swissprot) PTFA\_ECOLI P24217  
ESCHERICHIA COLI 562 -11532557 162936 frub phosphotransferase system enzyme  
ii::diphosphoryl transfer protein:pts system:fructose-specific iia/fpr  
component (cl:fructose phosphotransferase protein:phosphotransferase system  
mannitol-specific enzyme ii factor iii homology:phosphotransferase system  
phosphohistidine-containing protein homology) (ec:2.7.1.69) (db:pir2.dat)  
I53564 I53564 Escherichia coli 562 -11532557 258717 fructose-specific  
iia/fpr component (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47  
to 48 centisome region of e.coli k12 bhb2600.) (nt:phosphotransferase fpr  
protein (pseudo-hpr).) (le:70109) (re:71239) (di:complement) ECOHU47 U00007  
g453292 Escherichia coli 562 -11532557 7500888937 frub dtp  
(db:genpept-bct1) (de:47-48 centisome region: frub=dtp (escherichia coli,  
genomic, 1314nt).) (nt:phosphoenolpyruvate: sugar phosphotransferase)  
(le:181) (re:1311) (di:direct) S72443 S72443 g619247 Escherichia coli 562  
-11532557 234776 frub pts system:fructose-specific iia/fpr component  
(fn:enzyme; transport of small molecules:) (db:genpept-bct2) (ec:2.7.1.69)  
(de:escherichia coli k-12 mg1655 section 196 of 400 of the completegenome.)  
(nt:f376; 100 pct identical to ptfa\_ecoli sw: p24217) (le:5013) (re:6143)  
(di:complement) AE000306 AE000306 g1788494 Escherichia coli 562 -11532557  
5000689957 (de:(ecoli\_2118) (pn:pts system, fructose-specific iia)  
(gn:frub) (gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69) (ptfa\_ecoli)  
(keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3) (db:gtc-escherichia coli))  
ECOLI\_2118 ECOLI\_2118 Escherichia coli 562 10034182

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501819958	7031	29187	537	178

Description

6500728700 glk:b2388 glucokinase:glucose kinase  
(gtcf:1.1:1.3:1.4:1.5:1.6:7.2) (ec:2.7.1.2) (keggfc:1.1:1.3:1.5:1.6:7.1)  
(rileyfc:1.1.1) (db:gtc-escherichia coli) b2388 b2388 Escherichia coli 562  
-11532558 7500883661 glk (ec:2.7.1.2) (de:glucokinase, (glucose kinase))  
(db:swissprot) HXKG\_ECOLI P46880 ESCHERICHIA COLI 562 -11532558 7000690890  
glk glucokinase (cl:glucokinase) (ec:2.7.1.2) (db:pir2.dat) A65013 A65013  
Escherichia coli 562 -11532558 224945 glk glucokinase ec 2.7.1.2 .  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #414(53.8-54.2  
min.)) (nt:similar to (swissprot accession number p46880)) (le:16937)  
(re:17902) (di:complement) D90868 D90868 g1799799 Escherichia coli 562  
-11532558 7500883663 glk glucokinase ec 2.7.1.2 . (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #416(54.1-54.5 min.)) (nt:similar to  
(swissprot accession number p46880)) (le:1305) (re:2270) (di:complement)  
D90869 D90869 g1799803 Escherichia coli 562 -11532558 7500883664 glk  
glucokinase (fn:enzyme; degradation of small molecules: carbon)  
(db:genpept-bct2) (ec:2.7.1.2) (de:escherichia coli k-12 mg1655 section 217  
of 400 of the completegenome.) (nt:f321; 98 pct identical to hxkg\_ecoli sw:  
p46880) (le:140) (re:1105) (di:complement) AE000327 AE000327 g1788732  
Escherichia coli 562 -11532558 224948 glk glucokinase ec 2.7.1.2 .  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #414(53.8-54.2  
min.)) (nt:similar to (swissprot accession number p46880)) (le:16937)  
(re:17902) (di:complement) D90868 D90868 g1799799 Escherichia coli 562  
-11532558 5000689958 (de:(ecoli\_2335) (pn:glucokinase) (gn:glk)  
(gtcf:1.1:1.3:1.5:1.6:7.2) (ec:2.7.1.2) (hxkg\_ecoli)  
(keggfc:1.1:1.3:1.5:1.6:7.1) (rileyfc:1.1.1) (db:gtc-escherichia coli))  
ECOLI\_2335 ECOLI\_2335 Escherichia coli 562 10120169

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501819963	7032	29188	414	137

Description

6500728701 ptsh:hpr:b2415 phosphocarrier protein hpr:histidine-containing protein (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b2415 b2415 Escherichia coli 562 -11532559 263393 ptsh:hpr (de:phosphocarrier protein hpr (histidine-containing protein)) (db:swissprot) PTHP\_ECOLI P07006 ESCHERICHIA COLI 562 -11532559 7502851775 ptsh:hpr (de:phosphocarrier protein hpr (histidine-containing protein)) (db:swissprot) PTHP\_ECOLI P07006 SALMONELLA TYPHIMURIUM 602 -11532559 7500888954 ptsh phosphotransferase system phosphohistidine-containing protein:phosphotransferase system hpr (cl:phosphotransferase system phosphohistidine-containing protein:phosphotransferase system phosphohistidine-containing protein homology) (db:pir1.dat) (mp:52 min) WQECPH A29785 Escherichia coli 562 -11532559 130682 ptsh phosphotransferase system phosphohistidine-containing protein:phosphocarrier protein hpr (cl:phosphotransferase system phosphohistidine-containing protein:phosphotransferase system phosphohistidine-containing protein homology) (db:pir1.dat) (mp:49 min) WQEBPH C28181 Salmonella typhimurium 602 -11532559 7500888955 hpr phosphocarrier protein hpr histidine-containing (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #418(54.6-54.9 min.)) (nt:similar to (swissprot accession number p07006)) (le:2132) (re:2389) (di:direct) D90871 D90871 g1799834 Escherichia coli 562 -11532559 234112 (sr:e.coli (k12 strain c600) dna, clone pab101) (db:genpept-bct1) (de:e.coli cysz, cysk, ptsh, and ptsi genes, complete cds.) (nt:ptsh protein) (le:2133) (re:2390) (di:direct) ECOCYSPTS M21451 g145687 Escherichia coli 562 -11532559 235487 (sr:e.coli (strain tp2110) dna, clone pdia3206) (db:genpept-bct1) (de:e.coli cysk gene, 3' end, ptsh, ptsi, and crr phototransferasesystem genes, complete cds.) (nt:hpr protein (ec 2.7.1.68)) (le:417) (re:674) (di:direct) ECOPHOSYS M21994 g147263 Escherichia coli 562 -11532559 235591 ptsh (sr:e.coli k-12 dna, clone pdia3204) (db:genpept-bct1) (de:e.coli ptsh gene coding for histidine-containing protein (hpr), complete cds, and ptsi gene encoding enzyme i of the pts system(phosphoenolpyruvate-dependent glyose phosphotransferase system).)... ECOPTSH M10425 g147395 Escherichia coli 562 -11532559 235593 ptsh (sr:e.coli dna, clone pds20) (db:genpept-bct1) (de:e.coli ptsh, ptsi and crr genes encoding cytoplasmic proteins ofthe phosphoenolpyruvate:glyose phosphotransferase system (hpr,enzymes i and glc-iii), complete cds.) (nt:hpr) (le:214) (re:471) (di:direct) ECOPTSHI J02796 g147398 Escherichia coli 562 -11532559 264136 (db:genpept-bct1) (de:salmonella typhimurium pts operon partial sequence.) (nt:hpr (aa 1-83)) (le:215) (re:472) (di:direct) STPTSOP X14737 g47845 Salmonella typhimurium 602 -11532559 7502851776 (sr:s.typhimurium (strain lt2) dna, clone prsm28) (db:genpept-bct1) (de:s.typhimurium cysz, cysk, ptsh, and ptsi genes, complete cds.) (nt:ptsh protein) (le:2610) (re:2867) (di:direct) STYCYSPTS M21450 g153936 Salmonella typhimurium 602 -11532559 224977 ptsh pts system protein hpr (fn:enzyme; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 219 of 400 of the completegenome.)



(de:escherichia coli k-12 mg1655 section 219 of 400 of the completegenome.)  
~~(nt:085; 100 pct identical to pthp\_ecoli sw: p07006;) (le:3583) (re:3840)~~

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501819984	7033	29189	990	329

# Description

6500728702 crr:gsr:ies:tgs:tred:b2417 pts system:glucose-specific iia component:eiia-glc:glucose-permease iia component:phosphotransferase enzyme ii:a component:eiia-glc (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b2417 b2417 Escherichia coli 562 -11532560 123817 crr phosphotransferase system enzyme ii::glucose-specific:factor iii:phosphotransferase system:enzyme iii-glc (cl:phosphotransferase system glucose-specific enzyme ii, factor iii:phosphotransferase system glucose-specific enzyme ii, factor iii homology) (ec:2.7.1.69) (db:pir1.dat) (mp:52 min) WQEC3 C29785 Escherichia coli 562 -11532560 224979 crr phosphotransferase system enzyme ii ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #418(54.6-54.9 min.)) (nt:similar to (pir accession number c29785)) (le:4202) (re:4711) (di:direct) D90871 D90871 g1799836 Escherichia coli 562 -11532560 234047 crr pts enzyme iii glc (sr:escherichia coli (individual\_isolate rm74a/human/iowa, strain eco) (db:genpept-bct1) (de:escherichia coli (strain ecor 1, isolate rm74a/human/iowa) ptsenzyme iii glc (crr) gene, complete cds.) (nt:putative) (le:1) (re:510) (di:direct) ECOCRRA M93578 g145603 Escherichia coli 562 -11532560 234048 crr pts enzyme iii glc (sr:escherichia coli (individual\_isolate rm66c/human/iowa, strain eco) (db:genpept-bct1) (de:escherichia coli (strain ecor 6, isolate rm66c/human/iowa) ptsenzyme iii glc (crr) gene, complete cds.) (nt:putative) (le:1) (re:510) (di:direct) ECOCRRB M93580 g145605 Escherichia coli 562 -11532560 234049 crr pts enzyme iii glc (sr:escherichia coli (individual\_isolate rm52b/human/iowa, strain eco) (db:genpept-bct1) (de:escherichia coli (strain ecor 28, isolate rm52b/human/iowa) ptsenzyme iii glc (crr) gene, complete cds.) (nt:putative) (le:1) (re:510) (di:direct) ECOCRRC M93582 g145607 Escherichia coli 562 -11532560 234050 crr pts enzyme iii glc (sr:escherichia coli (individual\_isolate rm42b/human/iowa, strain eco) (db:genpept-bct1) (de:escherichia coli (strain ecor 35, isolate rm42b/human/iowa) ptsenzyme iii glc (crr) gene, complete cds.) (nt:putative) (le:1) (re:510) (di:direct) ECOCRRD M93579 g145609 Escherichia coli 562 -11532560 234051 crr pts enzyme iii glc (sr:escherichia coli (individual\_isolate rm44b/marmoset/washington zoo) (db:genpept-bct1) (de:escherichia coli (strain ecor 37, isolate rm44b/marmoset/washingtonzoo) pts enzyme iii glc (crr) gene, complete cds.) (nt:putative) (le:1) (re:510) (di:direct) ECOCRRE M93581 g145611 Escherichia coli 562 -11532560 234052 crr pts enzyme iii glc (sr:escherichia coli (individual\_isolate p97/human/sweden, strain eco) (db:genpept-bct1) (de:escherichia coli (strain ecor 50, isolate p97/human/sweden) ptsenzyme iii glc (crr) gene, complete cds.) (nt:putative) (le:1) (re:510) (di:direct) ECOCRRF M93594 g145613 Escherichia coli 562 -11532560 234053 crr pts enzyme iii glc (sr:escherichia coli (individual\_isolate dd/human/massachusetts, strai) (db:genpept-bct1) (de:escherichia coli (strain ecor 51, isolate dd/human/massachusetts)pts enzyme iii glc (crr) gene, complete cds.) (nt:putative) (le:1) (re:510) (di:direct) ECOCRRG M93595 g145615 Escherichia

(nt:putative) (le:1) (re:510) (di:direct) ECOCRRG M93595 g145615 Escherichia coli 562 -11532560 234054 crr pts enzyme iii glc (sr:escherichia coli

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501819985	7034	29190	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820031	7035	29191	1815	604

Description

6500728703 srla\_1:b2702 pts system:glucitol/sorbitol-specific iibc component (gtcfc:12.2:1.1) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2702 b2702 Escherichia coli 562 -11532561 7500960413 srla pts system:glucitol/sorbitol-specific iic (fn:transport; transport of small molecules:) (db:genpept-bct2) (ec:2.7.1.69) (de:escherichia coli k-12 mg1655 section 244 of 400 of the completegenome.) (nt:o187; frameshift disrupts match to pthb\_ecoli) (le:3788) (re:4351) (di:direct) AE000354 AE000354 g1789054 Escherichia coli 562 -11532561 7000691885 srla\_1 phosphotransferase system enzyme ii::sorbitol-specific:factor iibc (ec:2.7.1.69) (db:pir) B65050 B65050 Escherichia coli 562 -11532561 5000689961 (de:(ecoli\_2630) (pn:pts system, glucitol) (gn:srla) (gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69) (pthb\_ecoli) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2630 ECOLI\_2630 Escherichia coli 562 10123782

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820032	7036	29192	1260	419

Description

6500728704 srla\_2:b2703 (gtcfc:14.3) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2703 b2703 Escherichia coli 562 -11532562 7500974863 srle pts system:glucitol/sorbitol-specific iib (fn:transport; transport of small molecules:) (db:genpept-bct2) (ec:2.7.1.69) (de:escherichia coli k-12 mg1655 section 244 of 400 of the completegenome.) (nt:o319; frameshift disrupts match to pthb\_ecoli) (le:4348) (re:5307) (di:direct) AE000354 AE000354 g1789055 Escherichia coli 562 -11532562 5000689962 (de:(ecoli\_2631) (pn:pts system, glucitol) (gn:srla) (gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69) (pthb\_ecoli) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2631 ECOLI\_2631 Escherichia coli 562 -11532562 7000691884 c65050 (de:(pn:phosphotransferase system enzyme ii, srla\_2) (gn:srla\_2) (ec:2.7.1.69) (db:pir)) C65050 C65050 Escherichia coli 562 10123783

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820041	7037	29193	1221	407

Description

6500728705 srlb:gutb:b2704 pts system:glucitol/sorbitol-specific iia  
component:eiia-gut:glucitol/sorbitol-permease iia  
component:phosphotransferase enzyme ii:a component:eiia-gut (gtcfc:12.2:1.1)  
(ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:5.8.0)  
(db:gtc-escherichia coli) b2704 b2704 Escherichia coli 562 -11532563 92170  
srlb:gutb (ec:2.7.1.69) (de:ii, a component), (eiia-gut)) (db:swissprot)  
PTHA\_ECOLI P05706 ESCHERICHIA COLI 562 -11532563 123819 gutb:srlb  
phosphotransferase system enzyme ii::sorbitol-specific:factor  
iii:phosphotransferase enzyme iii:glucitol-specific:protein-n pi  
-phosphohistidine-glucitol phosphotransferase:factor iii  
(cl:phosphotransferase system sorbitol-specific enzyme ii, factor iii)  
(ec:2.7.1.69) (db:pir1.dat) (mp:58 min) WQEC3S B26725 Escherichia coli 562  
-11532563 234600 (db:genpept-bct1) (de:e.coli glucitol (gut) operon:  
glucitol-specific enzyme ii (guta), and iii (gutb), glucitol-6-phosphate  
dehydrogenase (gutd), activator (gutm) and repressor (gutr) genes, complete  
cds.) (nt:glucitol-specific enzyme iii (gutb)) (le:20... ECOGUT J02708  
g146279 Escherichia coli 562 -11532563 7500888953 gutb pts enzyme iii  
glucitol (sr:escherichia coli (individual\_isolate rm74a/human/iowa, strain  
eco) (db:genpept-bct1) (de:escherichia coli (strain ecor 1, isolate  
rm74a/human/iowa) ptsenzyme iii glucitol (gutb) gene, complete cds.)  
(nt:putative) (le:1) (re:372) (di:direct) ECOGUTBA M93583 g146284  
Escherichia coli 562 -11532563 234596 srlb pts  
system:glucitol/sorbitol-specific enzyme (fn:enzyme; transport of small  
molecules:) (db:genpept-bct2) (ec:2.7.1.69) (de:escherichia coli k-12 mg1655  
section 244 of 400 of the completegenome.) (nt:ol23; 100 pct identical to  
ptha\_ecoli sw: p05706;) (le:5318) (re:5689) (di:direct) AE000354 AE000354  
g1789056 Escherichia coli 562 -11532563 5000689963 (de:(ecoli\_2632)  
(pn:d-glucitol:sorbitol-specific enzyme ii of phosphotransferase system)  
(gn:srlb) (gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69) (ptha\_ecoli)  
(keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:5.7.0) (db:gtc-escherichia coli))  
ECOLI\_2632 ECOLI\_2632 Escherichia coli 562 10034204

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820066	7038	29194	276	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820068	7039	29195	852	283

#### Description

6500728706 ascf:b2715 phosphotransferase enzyme iiabc-asc:pts  
system:arbutin-cellobiose-and salicin-specific iiabc  
component:eiiabc-asc:arbutin-cellobiose-and salicin-permease iiabc  
component:phosphotransferase enzyme ii:abc component:eii-asc  
(gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1)  
(rileyfc:4.1.3) (db:gtc-escherichia coli) b2715 b2715 Escherichia coli 562  
-11532564 92144 ascf (ec:2.7.1.69) (de:(ec 2.7.1.69) (eii-asc))  
(db:swissprot) PTDA\_ECOLI\_P24241 ESCHERICHIA COLI 562 -11532564 7000686213  
ascf phosphotransferase system enzyme ii:asc (cl:phosphotransferase system  
sucrose-specific enzyme ii, factor ii) (ec:2.7.1.69) (db:pir2.dat) G65051  
G65051 Escherichia coli 562 -11532564 7500888934 ascf phosphotransferase  
enzyme iiabc-asc (db:genpept-bct1) (de:escherichia coli k-12 genome;  
approximately 61 to 62 minutes.) (nt:cg site no. 33233) (le:11828)  
(re:13285) (di:direct) ECU29579 U29579 g882608 Escherichia coli 562  
-11532564 239289 ascf pts system enzyme ii abc asc:cryptic (fn:enzyme;  
transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12  
mg1655 section 245 of 400 of the completegenome.) (nt:o485; 98 pct identical  
to ptda\_ecoli sw: p24241; cg) (le:7134) (re:8591) (di:direct) AE000355  
AE000355 g1789069 Escherichia coli 562 -11532564 5000689964  
(de:(ecoli\_2644) (pn:phosphotransferase enzyme ii:asc, cryptic, transports  
specific beta-glucosides) (gn:ascf) (gtcfc:1.1:1.5:1.6:7.1:7.2)  
(ec:2.7.1.69) (ptda\_ecoli) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3)  
(db:gtc-escherich) ECOLI\_2644 ECOLI\_2644 Escherichia coli 562 10123791

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820103	7040	29196	381	126

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820114	7041	29197	420	139
<u>Description</u>				
6500728707 eno:b2779 lase:2-phosphoglycerate dehydratase:2-phospho-d-glycerate hydro-lyase (gtcfc:1.1) (ec:4.2.1.11) (keggfc:1.1) (rileyfc:1.2.1) (db:gtc-escherichia coli) b2779 b2779 Escherichia coli 562 -11532565 7000688892 eno phosphopyruvate hydratase::2-phosphoglycerate dehydratase:enolase (cl:enolase) (ec:4.2.1.11) (db:pir1.dat) (mp:60 min) NOEC G65059 Escherichia coli 562 -11532565 7500953340 eno enolase (db:genpept-bct1) (ec:4.2.1.11) (de:escherichia coli k-12 genome; approximately 62 minute region.) (nt:cg site no. 823) (le:4508) (re:5806) (di:complement) ECU29580 U29580 g882673 Escherichia coli 562 -11532565 239353 eno enolase (fn:enzyme; energy metabolism, carbon: glycolysis) (db:genpept-bct2) (ec:4.2.1.11) (de:escherichia coli k-12 mg1655 section 251 of 400 of the completegenome.) (nt:f432; 99 pct identical to 419 aa of eno_ecoli) (le:7220) (re:8518) (di:complement) AE000361 AE000361 g1789141 Escherichia coli 562 -11532565 5000689965 (de:(ecoli_2710) (pn:lase) (gn:eno) (gtcfc:1.1) (ec:4.2.1.11) (eno_ecoli) (keggfc:1.1) (rileyfc:1.2.1) (db:gtc-escherichia coli)) ECOLI_2710 ECOLI_2710 Escherichia coli 562 10123829				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820123	7042	29198	612	203

Description

6500728708 fba:fda:b2925 fructose 1:6-bisphosphate  
aldolase:fructose-bisphosphate aldolase (gtcfc:1.1:1.3:1.5:2.4)  
(ec:4.1.2.13) (keggfc:1.1:1.3:1.5:2.3) (rileyfc:1.2.1) (db:gtc-escherichia  
coli) b2925 b2925 Escherichia coli 562 -11532566 125509 fba:fda  
fructose-bisphosphate aldolase:ii:metal-dependent fructose-bisphosphate  
aldolase (cl:fructose-bisphosphate aldolase ii) (ec:4.1.2.13) (db:pir1.dat)  
(mp:63 min) ADEC2A S02177 Escherichia coli 562 -11532566 239138  
(db:genpept-bct1) (de:escherichia coli fda, pgk and gapb genes for  
fructose1,6-biphosphate aldolase (class ii), phosphoglycerate kinase  
andglyceraldehyde 3-phosphate dehydrogenase.) (nt:fructose 1,6-biphosphate  
aldolase (aa 1-359)) (le:4401) (re:5480) ... ECFDAPGK X14436 g41423  
Escherichia coli 562 -11532566 7500953325 fba fructose 1:6-bisphosphate  
aldolase (db:genpept-bct1) (ec:4.1.2.13) (de:escherichia coli k-12 genome;  
approximately 65 to 68 minutes.) (nt:cg site no. 786; alternate name alc,  
fda) (le:24556) (re:25635) (di:complement) ECU28377 U28377 g882454  
Escherichia coli 562 -11532566 232836 fba fructose-bisphosphate  
aldolase:class ii (fn:enzyme; energy metabolism, carbon: glycolysis)  
(db:genpept-bct2) (ec:4.1.2.13) (de:escherichia coli k-12 mg1655 section 266  
of 400 of the completegenome.) (nt:f359; 100 pct identical to alf\_ecoli sw:  
p11604; cg) (le:209) (re:1288) (di:complement) AE000376 AE000376 g1789293  
Escherichia coli 562 -11532566 5000689966 (de:(ecoli\_2847)  
(pn:fructose-bisphosphate aldolase, class ii) (gn:fba)  
(gtcfc:1.1:1.3:1.5:2.4) (ec:4.1.2.13) (alf\_ecoli) (keggfc:1.1:1.3:1.5:2.3)  
(rileyfc:1.2.1) (db:gtc-escherichia coli)) ECOLI\_2847 ECOLI\_2847 Escherichia  
coli 562 10066349

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820129	7043	29199	237	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820137	7044	29200	351	116

Description

6500728709 pgk:b2926 phosphoglycerate kinase (gtcfc:1.1:2.4) (ec:2.7.2.3) (keggfc:1.1:2.3) (rileyfc:1.2.1) (db:gtc-escherichia coli) b2926 b2926 Escherichia coli 562 -11532567 123857 pgk phosphoglycerate kinase (cl:phosphoglycerate kinase) (ec:2.7.2.3) (db:pir1.dat) (mp:63 min) TVECG S04733 Escherichia coli 562 -11532567 239139 (db:genpept-bct1) (de:escherichia coli fda, pgk and gapb genes for fructose1,6-biphosphate aldolase (class ii), phosphoglycerate kinase andglyceraldehyde 3-phosphate dehydrogenase.) (nt:phosphoglycerate kinase (aa 1-387)) (le:3023) (re:4186) (di:direct) ECFDAPGK X14436 g41422 Escherichia coli 562 -11532567 7500953264 pgk phosphoglycerate kinase (db:genpept-bct1) (ec:2.7.2.3) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:cg site no. 408) (le:25850) (re:27013) (di:complement) ECU28377 U28377 g882455 Escherichia coli 562 -11532567 232835 pgk phosphoglycerate kinase (fn:enzyme; energy metabolism, carbon: glycolysis) (db:genpept-bct2) (ec:2.7.2.3) (de:escherichia coli k-12 mgl655 section 266 of 400 of the completegenome.) (nt:f387; 100 pct identical to pgk\_ecoli sw: p11665; cg) (le:1503) (re:2666) (di:complement) AE000376 AE000376 g1789294 Escherichia coli 562 -11532567 5000689967 (de:(ecoli\_2848) (pn:phosphoglycerate kinase) (gn:pgk) (gtcfc:1.1:2.4) (ec:2.7.2.3) (pgk\_ecoli) (keggfc:1.1:2.3) (rileyfc:1.2.1) (db:gtc-escherichia coli)) ECOLI\_2848 ECOLI\_2848 Escherichia coli 562 10065976

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820141	7045	29201	933	310

Description

GTC ORF with score 122 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid t17h7.) (nt:short region of weak similarity to collagen) (le:13101:13401:13635) (re:13355:13586:15242) (di:directjoin)



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820143	7046	29202	864	288

Description

6500728710 cmta:b2933 protein-n:pi-phosphohistidine-sugar  
phosphotransferase:pts system:mannitol:cryptic-specific iibc  
component:eiibc-:cmt1:mannitol:cryptic-permease iibc  
component:phosphotransferase enzyme ii:bc component  
(gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1)  
(rileyfc:4.1.3) (db:gtc-escherichia coli) b2933 b2933 Escherichia coli 562  
-11532568 92348 cmta (ec:2.7.1.69) (de:enzyme ii, bc component),)  
(db:swissprot) PTYC\_ECOLI P32059 ESCHERICHIA COLI 562 -11532568 7000686237  
cmta phosphotransferase system enzyme ii:factor  
ii:mannitol-specific:cryptic:protein-npi-phosphohistidine--sugar  
phosphotransferase (cl:phosphotransferase system mannitol-specific enzyme ii  
factor ii:phosphotransferase system mannitol-specific enzyme ii factor ii  
homology) (ec:2.7.1.69) (db:pir1.dat) S36123 D65078 Escherichia coli 562  
-11532568 7500889026 cmta protein-n pi -phosphohistidine-sugar (fn:cryptic  
mannitol transport; putative enzyme ii) (db:genpept-bct1) (ec:2.7.1.69)  
(de:escherichia coli k-12 genome; approximately 65 to 68 minutes.)  
(nt:alternate name tolm) (le:31861) (re:33249) (di:complement) ECU28377  
U28377 g882462 Escherichia coli 562 -11532568 239146 cmta pts  
system:mannitol-specific enzyme ii (fn:enzyme; transport of small  
molecules:) (db:genpept-bct2) (ec:2.7.1.69) (de:escherichia coli k-12 mg1655  
section 266 of 400 of the completegenome.) (nt:f462; residues 1-415 99 pct  
identical (1 gap)) (le:7514) (re:8902) (di:complement) AE000376 AE000376  
g1789301 Escherichia coli 562 -11532568 5000689968 (de:(ecoli\_2855)  
(pn:pep-dependent phosphotransferase enzyme iibc for mannitol) (gn:cmta)  
(gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69) (ptyc\_ecoli)  
(keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3) (db:gtc-escherichia coli))  
ECOLI\_2855 ECOLI\_2855 Escherichia coli 562 10034380

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820149	7047	29203	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820151	7048	29204	633	210
<u>Description</u>				
6500728711 cmtb:b2934 protein-n:pi-phosphohistidine-sugar phosphotransferase:pts system:mannitol:cryptic-specific iia component:eiia-:cmtl:mannitol:cryptic-permease iia component:phosphotransferase enzyme ii:a component (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b2934 b2934 Escherichia coli 562 -11532569 239147 cmtb (ec:2.7.1.69) (de:enzyme ii, a component),) (db:swissprot) PTYA_ECOLI P32058 ESCHERICHIA COLI 562 -11532569 164322 cmtb phosphotransferase system enzyme ii:factor iii:mannitol-specific:protein-npi-phosphohistidine--sugar phosphotransferase (cl:probable phosphotransferase protein yjfu:phosphotransferase system mannitol-specific enzyme ii factor iii homology) (ec:2.7.1.69) (db:pir2.dat) S36122 S36122 Escherichia coli 562 -11532569 5000689969 cmtb cryptic ...:transport protein-n pi -phosphohistidine-sugar (db:genpept-bct1) (ec:2.7.1.69) (de:e.coli genes cmtb and cmta.) (nt:putative enzyme iii of pep-phosphotranferase system) (le:31) (re:474) (di:direct) ECCMT X72677 g312762 Escherichia coli 562 -11532569 7500889025 cmtb protein-n pi -phosphohistidine-sugar (fn:cryptic mannitol transport; putative enzyme iii) (db:genpept-bct1) (ec:2.7.1.69) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:alternate name tolm) (le:33277) (re:33720) (di:complement) ECU28377 U28377 g882463 Escherichia coli 562 -11532569 232524 cmtb pts system:mannitol-specific enzyme ii (fn:transport; transport of small molecules:) (db:genpept-bct2) (ec:2.7.1.69) (de:escherichia coli k-12 mg1655 section 266 of 400 of the completegenome.) (nt:fl47; 100 pct identical to ptya_ecoli sw: p32058;) (le:8930) (re:9373) (di:complement) AE000376 AE000376 g1789302 Escherichia coli 562 -11532569 92347 cmtb (ec:2.7.1.69) (de:enzyme ii, a component),) (db:swissprot) PTYA_ECOLI P32058 ESCHERICHIA COLI 562 -11532569				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820161	7049	29205	810	269
<u>Description</u>				
6500728712 agav:b3133 pts system:n-acetylgalactosamine-specific iib component 2 (gtcfc:12.2:1.1) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3133 b3133 Escherichia coli 562 -11532570 7000691902 agav pts system:n-acetylgalactosamine-specific iib component 2 (cl:phosphotransferase system mannose-specific enzyme ii, factor iii) (db:pir2.dat) A65103 A65103 Escherichia coli 562 -11532570 7500960440 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o169) (le:60934) (re:61443) (di:direct) ECOUW67 U18997 g606073 Escherichia coli 562 -11532570 236372 agav pts system:cytoplasmic (fn:enzyme; central intermediary metabolism: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 284 of 400 of the completegenome.) (nt:o169; 100 pct identical to 157 amino acids) (le:10579) (re:11088) (di:direct) AE000394 AE000394 g1789521 Escherichia coli 562 -11532570 5000689970 (de:(ecoli_3057) (pn:pts system, n-acetylgalactosamine-specific iib component 2:iib-aga":n-acetylgalactosamine-permease iib component 2:phosphotransferase enzyme ii, b component 2) (gn:agav) (gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69)) ECOLI_3057 ECOLI_3057 Escherichia coli 562 10123982				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820164	7050	29206	420	139

Description

6500728713 agab:b3138 pts system:n-acetylgalactosamine-specific iib component 1:eiib-aga:n-acetylgalactosamine-permease iib component 1:phosphotransferase enzyme ii:b component 1 (gtcfc:12.2:1.1) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3138 b3138 Escherichia coli 562 -11532571 92277 agab (ec:2.7.1.69) (de:enzyme ii, b component 1),) (db:swissprot) PTPB\_ECOLI P42909 ESCHERICHIA COLI 562 -11532571 7000686225 agab pts system:n-acetylgalactosamine-specific iib component 1 (cl:phosphotransferase system mannose-specific enzyme ii, factor iii) (db:pir2.dat) F65103 F65103 Escherichia coli 562 -11532571 7500888988 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf\_o158) (le:64922) (re:65398) (di:direct) ECOUW67 U18997 g606078 Escherichia coli 562 -11532571 236377 agab pts system:cytoplasmic (fn:enzyme; central intermediary metabolism: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 285 of 400 of the completengenome.) (nt:o158; 100 pct identical amino acid sequence and) (le:2405) (re:2881) (di:direct) AE000395 AE000395 g1789527 Escherichia coli 562 -11532571 5000689971 (de:(ecoli\_3062) (pn:pts system, n-acetylgalactosamine-specific iib component 1:eiib-aga:n-acetylgalactosamine-permease iib component 1:phosphotransferase enzyme ii, b component 1) (gn:agab) (gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69)) ECOLI\_3062 ECOLI\_3062 Escherichia coli 562 10034309

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820176	7051	29207	699	232

Description

GTC ORF with score 236 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome 1 bac f20d22 sequence, completesequence.) (nt:contains similarity to myosin ib heavy chain) (le:19889:20589) (re:20488:21254) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820177	7052	29208	555	184

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820213	7053	29209	1389	462

#### Description

6500728714 ptsn:rpop:b3204 enzyme iiantr:nitrogen regulatory iia protein:enzyme iia-ntr:phosphotransferase enzyme ii:a component (gtcfc:12.5:2.6) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_):energy metabolism-nitrogen metabolism) b3204 b3204 Escherichia coli 562 -11532572 238606 ptsn:rpop (ec:2.7.1.69) (de:(phosphotransferase enzyme ii, a component)) (db:swissprot) PTSN\_ECOLI P31222 ESCHERICHIA COLI 562 -11532572 164440 ptsn phosphotransferase system enzyme ii::iiantr:ptsn protein (cl:phosphotransferase system enzyme ii:phosphotransferase system mannitol-specific enzyme ii factor iii homology) (ec:2.7.1.69) (db:pir2.dat) I76720 I76720 Escherichia coli 562 -11532572 236442 rpon orf4 (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e. coli rpon gene.) (le:2924) (re:3415) (di:direct) ECORPON D12938 g285783 Escherichia coli 562 -11532572 238258 ptsn enzyme iiantr (fn:pts related carbon and organic nitrogen) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (le:127329) (re:127820) (di:direct) ECOUW67 U18997 g606143 Escherichia coli 562 -11532572 5000689972 (db:genpept-bct1) (de:e.coli(k12) rpon gene for sigma factor 54.) (nt:orfiii) (le:1954) (re:2445) (di:direct) ECSIG540 Z27094 g414887 Escherichia coli 562 -11532572 7500889006 ptsn enzyme iiantr (fn:pts related carbon and organic nitrogen) (db:genpept-bct1) (de:escherichia coli rpon operon and adjoining regions includingorf185, orf241, sigma-54 (rpon), orf95, iiantr (ptsn), orf284, andnpr (npr) genes, complete cds.) (le:3339) (re:3830) (di:dir... ECU12684 U12684 g551340 Escherichia coli 562 -11532572 235893 ptsn phosphotransferase system enzyme iia:regulates (fn:enzyme; transport of small molecules: amino) (db:genpept-bct2) (ec:2.7.1.69) (de:escherichia coli k-12 mg1655 section 290 of 400 of the completegenome.) (nt:o163; 100 pct identical amino acid sequence and) (le:108) (re:599) (di:direct) AE000400 AE000400 g1789597 Escherichia coli 562 -11532572 92326 ptsn:rpop (ec:2.7.1.69) (de:(phosphotransferase enzyme ii, a component)) (db:swissprot) PTSN\_ECOLI P31222 ESCHERICHIA COLI 562 -11532572

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820235	7054	29210	225	74

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820237	7055	29211	198	65

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820251	7056	29212	264	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820264	7057	29213	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820265	7058	29214	291	96

Description

6500728715 mtla:b3599 mannitol-specific enzyme ii of phosphotransferase system:pts system:mannitol-specific iiabc component:eiiabc-mtl:mannitol-permease iiabc component:phosphotransferase enzyme ii:abc component:eii-mtl (gtcfc:12.2:1.5) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3599 b3599 Escherichia coli 562 -11532573 236836 mtla (ec:2.7.1.69) (de:component), (eii-mtl)) (db:swissprot) PTMA\_ECOLI P00550 ESCHERICHIA COLI 562 -11532573 123810 mtla phosphotransferase system enzyme ii::mannitol-specific:mannitol permease:protein-n pi -phosphohistidine-mannitol phosphotransferase (cl:phosphotransferase system mannitol-specific enzyme ii:phosphotransferase system mannitol-specific enzyme ii factor ii homology:phosphotransferase system mannitol-specific enzyme ii factor iii homology) (ec:2.7.1.69) (db:pir1.dat) (mp:81 min) WQEC2M A00661 Escherichia coli 562 -11532573 5000689973 mtla mannitol permease (db:genpept-bct1) (de:e. coli gene mtla encoding mannitol permease. this is part of thephosphotransferase system. mannitol permease is enzyme ii of thatsistem.) (le:138) (re:2051) (di:direct) ECMTLA V01503 g42034 Escherichia coli 562 -11532573 7500888981 mtla mannitol-specific enzyme ii of (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 481) (le:186533) (re:188446) (di:direct) ECOUW76 U00039 g466737 Escherichia coli 562 -11532573 233417 mtla pts system:mannitol-specific enzyme iiabc (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 328 of 400 of the completegenome.) (nt:o637; 100 pct identical to ptma\_ecoli sw: p00550;) (le:77) (re:1990) (di:direct) AE000438 AE000438 g1790027 Escherichia coli 562 -11532573 92221 mtla (ec:2.7.1.69) (de:component), (eii-mtl)) (db:swissprot) PTMA\_ECOLI P00550 ESCHERICHIA COLI 562 -11532573

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820267	7059	29215	651	217

Description

6500728716 yibo:b3612 putative 2:3-bisphosphoglycerate-independent phosphoglycerate:putative 2:3-bisphosphoglycerate-independent phosphoglycerate mutase:phosphoglyceromutase:bpg-independent pgam (gtcfc:1.1:8.4:8.1) (ec:5.4.2.1) (keggfc:1.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3612 b3612 Escherichia coli 562 -11532574 90087 yibo (ec:5.4.2.1) (de:(ec 5.4.2.1) (phosphoglyceromutase) (bpg-independent pgam)) (db:swissprot) PMGI\_ECOLI P37689 ESCHERICHIA COLI 562 -11532574 163854 yibo probable phosphoglycerate mutase::2:3-diphosphoglycerate-independent:hypothetical protein o514 (cl:phosphoglycerate mutase, 2, 3-bisphosphoglycerate-independent) (ec:5.4.2.1) (db:pir2.dat) S47833 S47833 Escherichia coli 562 -11532574 7500888191 (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:199510) (re:201054) (di:direct) ECOUW76 U00039 g466750 Escherichia coli 562 -11532574 236849 yibo putative 2:3-bisphosphoglycerate-independent (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 329 of 400 of the completegenome.) (nt:o514; 100 pct identical amino acid sequence and) (le:2688) (re:4232) (di:direct) AE000439 AE000439 g1790041 Escherichia coli 562 -11532574 5000689974 (de:(ecoli\_3532) (pn:putative 2,3-bisphosphoglycerate-independent phosphoglycerate mutase:phosphoglyceromutase:bpg-independent pgam) (gn:yibo) (gtcfc:1.1) (ec:5.4.2.1) (pmgi\_ecoli) (keggfc:1.1) (rileyfc:5.7.0) (db:gtc-escherichi) ECOLI\_3532 ECOLI\_3532 Escherichia coli 562 10032207

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820269	7060	29216	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820278	7061	29217	261	86

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820279	7062	29218	1188	395
<u>Description</u>				
6500728717 glvb:b3682 pts system:arbutin-like iib component:phosphotransferase enzyme ii:b component (gtcfc:1.1:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3682 b3682 Escherichia coli 562 -11532575 92206 glvb (ec:2.7.1.69) (de:ii, b component),) (db:swissprot) PTIB_ECOLI P31451 ESCHERICHIA COLI 562 -11532575 7000686219 glvb pts system:arbutin-like iib component (db:pir2.dat) C65170 C65170 Escherichia coli 562 -11532575 7500888973 f161 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ecl4-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:similar to beta-glucoside transport protein) (le:51381) (re:51866) (di:complement) ECOUW82 L10328 g290531 Escherichia coli 562 -11532575 236919 glvb pts system:arbutin-like iib component (fn:enzyme; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 335 of 400 of the completegenome.) (nt:f161; 100 pct identical amino acid sequence and) (le:9162) (re:9647) (di:complement) AE000445 AE000445 g1790116 Escherichia coli 562 -11532575 5000689975 (de:(ecoli_3601) (pn:pts system, arbutin-like iib component:phosphotransferase enzyme ii, b component) (gn:glvb) (gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69) (ptib_ecoli) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3) (db:gtc-escheri) ECOLI_3601 ECOLI_3601 Escherichia coli 562 10034239				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820294	7063	29219	798	265
<u>Description</u>				
6500728718 bglf:bglc:bglb:b3722 transport protein:pts system:beta-glucosides-specific iiabc component:eiiabc-bgl:beta-glucosides-permease iiabc component:phosphotransferase enzyme ii:abc component:eii-bgl (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:12.2:11.1:1.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3722 b3722 Escherichia coli 562 -11532576 92130 bglf:bglc:bglb (ec:2.7.1.69) (de:enzyme ii, abc component), (eii-bgl) (db:swissprot) PTBA_ECOLI P08722 ESCHERICHIA COLI 562 -11532576 164325 bglf:bglb phosphotransferase system enzyme ii::beta-glucoside-specific (cl:phosphotransferase system enzyme ii sucrose-specific:phosphotransferase system glucose-specific enzyme ii, factor iii homology) (ec:2.7.1.69) (db:pir2.dat) C25977 C25977 Escherichia coli 562 -11532576 233906 bglc (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli bglc protein gene, complete cds, and flanking open readingframes, partial cds.) (le:182) (re:2059) (di:direct) ECOBGLC M15746 g145413 Escherichia coli 562 -11532576 7500888926 bglb transport protein (sr:e.coli k12 dna, clone pfdx733) (db:genpept-bct1) (de:e.coli bgl operon encoding a positive regulatory protein, atransport protein, and phospho-beta-glucosidase, complete cds, andphou gene, 3' end.) (le:1552) (re:3429) (di:direct) ECOBGLO M16487 g145418 Escherichia coli 562 -11532576 233901 bglf pts system beta-glucosides:enzyme ii:cryptic (fn:enzyme; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 339 of 400 of the completengenome.) (nt:f625; 99 pct identical amino acid sequence and) (le:5104) (re:6981) (di:complement) AE000449 AE000449 g1790159 Escherichia coli 562 -11532576 5000689976 (de:(ecoli_3640) (pn:pts system, beta-glucosides-specific iiabc component:eiiabc- bgl:beta-glucosides-permease iiabc component:phosphotransferase enzyme ii, abc component:eii-bgl) (gn:bglf) (gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69) ( ) ECOLI_3640 ECOLI_3640 Escherichia coli 562 10034164				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820295	7064	29220	276	91
<u>Description</u>				
6500728719 frvb:b3899 phosphotransferase:pts system:fructose-like-1 iibc component:phosphotransferase enzyme ii:bc component (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3899 b3899 Escherichia coli 562 -11532577 92341 frvb (ec:2.7.1.69) (de:ii, bc component),) (db:swissprot) PTVB_ECOLI P32154 ESCHERICHIA COLI 562 -11532577 163670 frvb pts system:fructose-like-1 iibc component phosphotransferase:hypothetical protein f485 (cl:phosphotransferase system, fructose-like component iib) (db:pir2.dat) S40843 S40843 Escherichia coli 562 -11532577 7500889014 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:similar to fructose-specific phosphotransferase) (le:52555) (re:54012) (di:complement) ECOUW87 L19201 g305003 Escherichia coli 562 -11532577 237117 frvb pts system:fructose-like enzyme iibc component (fn:enzyme; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 355 of 400 of the completegenome.) (nt:f485; 100 pct identical amino acid sequence and) (le:5093) (re:6550) (di:complement) AE000465 AE000465 g1790333 Escherichia coli 562 -11532577 5000689977 (de:(ecoli_3798) (pn:pts system, fructose-like-1 iibc component:phosphotransferase enzyme ii, bc component) (gn:frvb) (gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69) (ptvb_ecoli) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3) (db:gtc-es) ECOLI_3798 ECOLI_3798 Escherichia coli 562 10034373				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820296	7065	29221	624	208

#### Description

6500728720 frva:b3900 pts system:fructose-like-1 iia  
 component:phosphotransferase enzyme ii:a component (gtcfc:1.5:12.2)  
 (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:4.1.3)  
 (db:gtc-escherichia coli) b3900 b3900 Escherichia coli 562 -11532578  
 7500889013 frva (ec:2.7.1.69) (de:ii, a component),) (db:swissprot)  
 PTVA\_ECOLI P32155 ESCHERICHIA COLI 562 -11532578 163422 frva frva  
 protein:hypothetical protein f147 rhad 3 region (db:pir2.dat) D48649 D48649  
 Escherichia coli 562 -11532578 7502851779 (db:genpept-bct1) (de:e.coli  
 rhab, rha, rhad genes for rhamnulokinase, l-rhamnoseisomerase, and  
 ramnulose-1-phosphate aldolase.) (nt:unknown translated region) (le:4867)  
 (re:5313) (di:direct) ECRHABAD X60472 g396682 Escherichia coli 562 -11532578  
 238065 frva pts system:fructose-specific iia component (fn:enzyme;  
 transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12  
 mg1655 section 355 of 400 of the completegenome.) (nt:f147; this 147 aa orf  
 is 96 pct identical (1 gap)) (le:6555) (re:7001) (di:complement) AE000465  
 AE000465 g2367327 Escherichia coli 562 -11532578 92340 frva (ec:2.7.1.69)  
 (de:ii, a component),) (db:swissprot) PTVA\_ECOLI P32155 ESCHERICHIA COLI 562  
 -11532578

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820315	7066	29222	207	69

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820324	7067	29223	867	288

#### Description

GTC ORF with score 124 to: (sr:caenorhabditis elegans strain=bristol n2)  
 (db:genpept-inv) (de:caenorhabditis elegans cosmid r144.) (nt:weakly similar  
 to gastrula zinc finger protein) (le:23379:23566:23729:24316)  
 (re:23516:23680:23953:24354) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820327	7068	29224	225	74

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820330	7069	29225	270	89
<u>Description</u>				
6500728721 pfka:b3916 6-phosphofructokinase:6-phosphofructokinase isozyme i:phosphofructokinase-1:phosphohexokinase-1 (gtcfc:1.5) (ec:2.7.1.11) (keggfc:1.1:1.3:1.5:1.6) (rileyfc:1.2.1) (db:gtc-escherichia coli) b3916 b3916 Escherichia coli 562 -11532579 7000688863 pfka 6-phosphofructokinase:1:phosphofructokinase 1:isozyme 1:phosphohexokinase:isozyme 1 (cl:6-phosphofructokinase:6-phosphofructokinase 1 homology) (ec:2.7.1.11) (db:pir1.dat) (mp:88 min) KIECFA G65197 Escherichia coli 562 -11532579 7500953247 pfka 6-phosphofructokinase (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 413) (le:69185) (re:70147) (di:direct) ECOUW87 L19201 g305019 Escherichia coli 562 -11532579 237133 pfka 6-phosphofructokinase i (fn:enzyme; energy metabolism, carbon: glycolysis) (db:genpept-bct2) (ec:2.7.1.11) (de:escherichia coli k-12 mg1655 section 356 of 400 of the completegenome.) (nt:o320; 98 pct identical amino acid sequence and) (le:4828) (re:5790) (di:direct) AE000466 AE000466 g1790350 Escherichia coli 562 -11532579 5000689979 (de:(ecoli_3814) (pn:6-phosphofructokinase i) (gn:pfka) (gtcfc:1.1:1.3:1.5:1.6) (ec:2.7.1.11) (k6p1_ecoli) (keggfc:1.1:1.3:1.5:1.6) (rileyfc:1.2.1) (db:gtc-escherichia coli)) ECOLI_3814 ECOLI_3814 Escherichia coli 562 10124121				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820340	7070	29226	393	130

Description

6500728722 tpia:tpi:b3919 triosephosphate isomerase:tim  
 (gtcfc:1.1:1.5:2.4:8.1) (ec:5.3.1.1) (keggfc:1.1:1.5:2.3:8.1)  
 (rileyfc:1.2.1) (db:gtc-escherichia coli) b3919 b3919 Escherichia coli 562  
 -11532580 101908 tpia:tpi (ec:5.3.1.1) (de:triosephosphate isomerase,  
 (tim)) (db:swissprot) TPIS\_ECOLI P04790 ESCHERICHIA COLI 562 -11532580  
 7000686819 tpia triose-phosphate isomerase::phosphotriose  
 isomerase:triosephosphate mutase (cl:triose-phosphate isomerase)  
 (ec:5.3.1.1) (db:pir1.dat) (mp:88 min) ISECT B65198 Escherichia coli 562  
 -11532580 7500893310 tpia triosephosphate isomerase (sr:escherichia coli  
 (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e.  
 coli chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 88)  
 (le:72373) (re:73140) (di:complement) ECOUW87 L19201 g305022 Escherichia  
 coli 562 -11532580 237136 tpia triosephosphate isomerase (fn:enzyme; energy  
 metabolism, carbon: glycolysis) (db:genpept-bct2) (ec:5.3.1.1)  
 (de:escherichia coli k-12 mg1655 section 356 of 400 of the completegenome.)  
 (nt:f255; 100 pct identical to tpis\_ecoli sw: p04790;) (le:8016) (re:8783)  
 (di:complement) AE000466 AE000466 g1790353 Escherichia coli 562 -11532580  
 5000689980 (de:(ecoli\_3817) (pn:triosephosphate isomerase) (gn:tpia)  
 (gtcfc:1.1:1.5:2.4:8.1) (ec:5.3.1.1) (tpis\_ecoli) (keggfc:1.1:1.5:2.3:8.1)  
 (rileyfc:1.2.1) (db:gtc-escherichia coli)) ECOLI\_3817 ECOLI\_3817 Escherichia  
 coli 562 10043735

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820345	7071	29227	747	248

Description

6500728723 frwb:b3950 phosphotransfera:pts system:fructose-like-2 iib  
component 1:phosphotransferase enzyme ii:b component (gtcfc:1.5:12.2)  
(ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:5.8.0)  
(db:gtc-escherichia coli) b3950 b3950 Escherichia coli 562 -11532581 92342  
frwb (ec:2.7.1.69) (de:ii, b component),) (db:swissprot) PTWB\_ECOLI P32673  
ESCHERICHIA COLI 562 -11532581 7000686234 frwb pts system:fructose-like-2  
iib component 1 (cl:phosphotransferase system, fructose-like component iib)  
(db:pir2.dat) A65202 A65202 Escherichia coli 562 -11532581 237168 frwb pts  
system fructose-like iib component 1 (fn:enzyme; degradation of small  
molecules: carbon) (db:genpept-bct2) (de:escherichia coli k-12 mg1655  
section 359 of 400 of the completegenome.) (nt:o106; 100 pct identical amino  
acid sequence and) (le:1392) (re:1712) (di:direct) AE000469 AE000469  
g1790387 Escherichia coli 562 -11532581 7500889015 (sr:escherichia coli  
(sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e.  
coli chromosomal region from 89.2 to 92.8 minutes.) (nt:similar to  
phosphotransferase system enzyme ii) (le:8865) (re:9185) (di:direct) ECOUW89  
U00006 g396297 Escherichia coli 562 -11532581 5000689981 (de:(ecoli\_3848)  
(pn:pts system, fructose-like-2 iib component 1:phosphotransferase enzyme  
ii, b component) (gn:frwb) (gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69)  
(ptwb\_ecoli) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:5.7.0) (db:gtc-es)  
ECOLI\_3848 ECOLI\_3848 Escherichia coli 562 10034374

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820360	7072	29228	1713	570

Description

6500728724 frwd:b3953 phosphotransferase:pts system:fructose-like-2 iib component 2:phosphotransferase enzyme ii:b component (gtcfc:1.5:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3953 b3953 Escherichia coli 562 -11532582 92344 frwd (ec:2.7.1.69) (de:ii, b component),) (db:swissprot) PTWX\_ECOLI P32676 ESCHERICHIA COLI 562 -11532582 7000686236 frwd pts system:fructose-like-2 iib component 2 phosphotransferase (cl:phosphotransferase system, fructose-like component iib) (db:pir2.dat) D65202 D65202 Escherichia coli 562 -11532582 237171 frwd pts system fructose-like iib component 2 (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 359 of 400 of the completegenome.) (nt:ol13; 100 pct identical amino acid sequence and) (le:4906) (re:5247) (di:direct) AE000469 AE000469 g1790390 Escherichia coli 562 -11532582 7500889017 (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:similar to phosphotransferase system enzyme ii) (le:12379) (re:12720) (di:direct) ECOUW89 U00006 g396300 Escherichia coli 562 -11532582 5000689982 (de:(ecoli\_3851) (pn:pts system, fructose-like-2 iib component 2:phosphotransferase enzyme ii, b component) (gn:frwd) (gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69) (ptwx\_ecoli) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:5.7.0) (db:gtc-es) ECOLI\_3851 ECOLI\_3851 Escherichia coli 562 10034376

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820371	7073	29229	981	326
<u>Description</u>				
6500728725 pgi:b4025 glucose-6-phosphate isomerase:gpi:phosphoglucose isomerase:pgi:phosphohexose isomerase:phi (gtcfc:1.1:1.3:7.2) (ec:5.3.1.9) (keggfc:1.1:1.3:7.1) (rileyfc:1.2.1) (db:gtc-escherichia coli) b4025 b4025 Escherichia coli 562 -11532583 7000688903 pgi glucose-6-phosphate isomerase::phosphoglucose isomerase:phosphohexose isomerase (cl:glucose-6-phosphate isomerase) (ec:5.3.1.9) (db:pir1.dat) (mp:91 min) NUC H65209 Escherichia coli 562 -11532583 237231 pgi glucosephosphate isomerase (fn:enzyme; energy metabolism, carbon: glycolysis) (db:genpept-bct2) (ec:5.3.1.9) (de:escherichia coli k-12 mg1655 section 366 of 400 of the completegenome.) (nt:o549a; 99 pct identical amino acid sequence and) (le:469) (re:2118) (di:direct) AE000476 AE000476 g1790457 Escherichia coli 562 -11532583 7500953353 pgi glucose-6-phosphate isomerase (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (ec:5.3.1.9) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 409) (le:99000) (re:100649) (di:direct) ECUW89 U00006 g396360 Escherichia coli 562 -11532583 5000689983 (de:(ecoli_3911) (pn:glucosephosphate isomerase) (gn:pgi) (gtcfc:1.1:1.3:7.2) (ec:5.3.1.9) (g6pi_ecoli) (keggfc:1.1:1.3:7.1) (rileyfc:1.2.1) (db:gtc-escherichia coli)) ECOLI_3911 ECOLI_3911 Escherichia coli 562 10124135				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820373	7074	29230	708	235
<u>Description</u>				
6500728726 yjft:sgab:b4194 hypothetical 10.9 kd protein in aidb-rpsf intergenic region:unknown pentitol phosphotransferase enzyme ii:b component (gtcfc:1.3:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4194 b4194 Escherichia coli 562 -11532584 113731 sgab (ec:2.7.1.69) (de:(ec 2.7.1.69)) (db:swissprot) PTXB_ECOLI P39302 ESCHERICHIA COLI 562 -11532584 163705 yjft hypothetical 10.9k protein aidb-rpsf intergenic region:hypothetical protein o101 (db:pir2.dat) S56419 S56419 Escherichia coli 562 -11532584 7500889024 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o101) (le:112224) (re:112529) (di:direct) ECUW93 U14003 g537035 Escherichia coli 562 -11532584 237399 sgab orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 381 of 400 of the completegenome.) (nt:o101; formerly designated yjft) (le:5059) (re:5364) (di:direct) AE000491 AE000491 g1790638 Escherichia coli 562 -11532584 5000693934 (de:(ecoli_4077) (pn:hypothetical 10) (gn:yjft) (gtcfc:13.7:14.1) (ec:) (yjft_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4077 ECOLI_4077 Escherichia coli 562 10055459				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820380	7075	29231	390	129

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820391	7076	29232	474	157

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820394	7077	29233	405	134

Description

6500728727 ptxa:sgaa:b4195 hypothetical phosphotransferase enzyme ii:unknown pentitol phosphotransferase enzyme ii:a component (gtcfc:1.3:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4195 b4195 Escherichia coli 562 -11532585 7500889020 sgaa (ec:2.7.1.69) (de:(ec 2.7.1.69)) (db:swissprot) PTXA\_ECOLI P39303 ESCHERICHIA COLI 562 -11532585 7000690980 ptxa hypothetical phosphotransferase enzyme ii:hypothetical protein o158 (cl:probable phosphotransferase protein yjfu:phosphotransferase system mannitol-specific enzyme ii factor iii homology) (db:pir2.dat) F65230 F65230 Escherichia coli 562 -11532585 7500889022 ptxa putative pts system enzyme ii a component (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 381 of 400 of the completegenome.) (nt:o154; formerly designated yjfu) (le:5374) (re:5838) (di:direct) AE000491 AE000491 g2367359 Escherichia coli 562 -11532585

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820405	7078	29234	939	312

#### Description

6500728728 fbp:fdp:b4232  
fructose-1:6-bisphosphatase:d-fructose-1:6-bisphosphate  
1-phosphohydrolase:fbpase (gtcfc:1.5:1.3:1.5:2.4) (ec:3.1.3.11)  
(keggfc:1.1:1.3:1.5:2.3) (rileyfc:1.3.2) (db:gtc-escherichia coli) b4232  
b4232 Escherichia coli 562 -11532586 237438 fbp:fdp (ec:3.1.3.11)  
(de:1-phosphohydrolase) (fbpase)) (db:swissprot) F16P\_ECOLI P09200  
ESCHERICHIA COLI 562 -11532586 124282 fbp  
fructose-bisphosphatase::fructose-1:6-bisphosphatase  
(cl:fructose-bisphosphatase) (ec:3.1.3.11) (db:pir1.dat) PAEC S01383  
Escherichia coli 562 -11532586 5000689985 (db:genpept-bct1) (de:e.coli mrna  
for fructose-1,6-bisphosphatase (ec 3.1.3.11).)  
(nt:fructose-1,6-bisphosphatase (aa 1-332)) (le:353) (re:1351) (di:direct)  
ECFBPASE X12545 g41416 Escherichia coli 562 -11532586 7500881278 fbp  
fructose-1:6-bisphosphatase (db:genpept-bct1) (ec:3.1.3.11) (de:escherichia  
coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no.  
784; alternate gene name fdp) (le:145440) (re:146438) (di:complement)  
ECOUW93 U14003 g537074 Escherichia coli 562 -11532586 232830 fbp  
fructose-bisphosphatase (fn:enzyme; central intermediary metabolism:)  
(db:genpept-bct2) (ec:3.1.3.11) (de:escherichia coli k-12 mg1655 section 384  
of 400 of the completegenome.) (nt:f332; 100 pct identical to f16p\_ecoli sw:  
p09200;) (le:6295) (re:7293) (di:complement) AE000494 AE000494 g1790679  
Escherichia coli 562 -11532586 70895 fbp:fdp (ec:3.1.3.11)  
(de:1-phosphohydrolase) (fbpase)) (db:swissprot) F16P\_ECOLI P09200  
ESCHERICHIA COLI 562 -11532586

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820409	7079	29235	1683	561

#### Description

6500728729 treb:b4240 phosphotransferase system trehalose permease:pts  
system:trehalose-specific iibc component:eiibc-tre:trehalose-permease iibc  
component:phosphotransferase enzyme ii:bc component:eii-tre  
(gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1)  
(rileyfc:4.1.3) (db:gtc-escherichia coli) b4240 b4240 Escherichia coli 562  
-11532587 7500889010 treb (ec:2.7.1.69) (de:(ec 2.7.1.69) (eii-tre))  
(db:swissprot) PTTB\_ECOLI P36672 ESCHERICHIA COLI 562 -11532587 7000691886  
treb phosphotransferase system trehalose permease (cl:phosphotransferase  
system sucrose-specific enzyme ii, factor ii) (db:pir2.dat) C65236 C65236  
Escherichia coli 562 -11532587 7500889012 treb pts system enzyme  
ii:trehalose specific (fn:transport; transport of small molecules:)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 385 of 400 of the  
completegenome.) (nt:f473; 98 pct identical to pttb\_ecoli sw: p36672)  
(le:5401) (re:6822) (di:complement) AE000495 AE000495 g2367362 Escherichia  
coli 562 -11532587

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820430	7080	29236	1869	623

#### Description

6500728730 sgca:b4302 yjhl:putative phosphotransferase enzyme ii:a component sgca (gtcfc:1.1:1.5:12.6) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:5.9.0) (db:gtc-escherichia coli) b4302 b4302 Escherichia coli 562 -11532588 113800 sgca (ec:2.7.1.69) (de:putative phosphotransferase enzyme ii, a component sgca,) (db:swissprot) SGCA\_ECOLI P39363 ESCHERICHIA COLI 562 -11532588 7000686597 yjhl yjhl protein (cl:probable phosphotransferase protein yjfu:phosphotransferase system mannitol-specific enzyme ii factor iii homology) (db:pir2.dat) H65243 H65243 Escherichia coli 562 -11532588 7500891597 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf\_f143) (le:218381) (re:218812) (di:complement) ECOUW93 U14003 g1263174 Escherichia coli 562 -11532588 237507 sgca putative pts system enzyme ii a component (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 390 of 400 of the completegenome.) (nt:f143; formerly designated yjhl) (le:10859) (re:11290) (di:complement) AE000500 AE000500 g1790755 Escherichia coli 562 -11532588 5000689987 (de:(ecoli\_4185) (pn:hypothetical phosphotransferase enzyme ii, a component in feci-fimb intergenic region:f143) (gn:yjhl) (gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69) (yjhl\_ecoli) (keggfc:1.1:1.5:1.6:4.4:7.1) (rileyfc:5.7.0) (db:g) ECOLI\_4185 ECOLI\_4185 Escherichia coli 562 10055528

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820433	7081	29237	1338	445

#### Description

6500728731 gpmb:b4395 probable phosphoglycerate mutase 2:phosphoglyceromutase 2:pgam 2:bpg-dependent pgam 2 (gtcfc:1.1) (ec:5.4.2.1) (keggfc:1.1) (rileyfc:5.9.0) (db:gtc-escherichia coli) b4395 b4395 Escherichia coli 562 -11532589 163767 gpmb gpmb protein:hypothetical protein o215b (cl:phosphoglycerate mutase homology) (db:pir2.dat) S56619 S56619 Escherichia coli 562 -11532589 7500959757 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:kenn rudd identifies as gpmb) (le:324630) (re:325277) (di:direct) ECOUW93 U14003 g537235 Escherichia coli 562 -11532589 237600 gpmb phosphoglyceromutase 2 (fn:enzyme; energy metabolism, carbon: glycolysis) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 399 of 400 of the completegenome.) (le:8985) (re:9632) (di:direct) AE000509 AE000509 g1790856 Escherichia coli 562 -11532589 5000694062 (de:(ecoli\_4277) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_4277 ECOLI\_4277 Escherichia coli 562 10087044

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820446	7082	29238	1185	394

Description

6500728732 frul:b0079 frur-shl operon leader peptide:frur/shl operon leader peptide (gtcfc:1.1:1.5) (keggfc:14.2) (rileyfc:1.2.1) (db:gtc-escherichia coli) b0079 b0079 Escherichia coli 562 -11532590 227986 frul (de:very hypothetical frur/shl operon leader peptide) (db:swissprot) LPFS\_ECOLI P22183 ESCHERICHIA COLI 562 -11532590 164611 frul frur-shl operon leader peptide (cl:unassigned leader peptides) (db:pir2.dat) (mp:2 min) JU0297 JU0297 Escherichia coli 562 -11532590 304523 shl operon leader peptide (db:genpept-bct1) (de:e. coli 2 minute region.) (le:4390) (re:4476) (di:direct) EC2MIN X55034 g40847 Escherichia coli 562 -11532590 7502851780 (sr:e.coli (strain k12) dna) (db:genpept-bct1) (de:e.coli shl gene, complete cds, and acetolactate synthase ii (ilvh)gene, 3' end.) (nt:leader protein) (le:117) (re:203) (di:direct) ECOSHL M35034 g147817 Escherichia coli 562 -11532590 235979 frul frur leader peptide (fn:leader; energy metabolism, carbon: glycolysis) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 8 of 400 of the completegenome.) (nt:o28; 100 pct identical to lpfs\_ecoli sw: p22183) (le:4315) (re:4401) (di:direct) AE000118 AE000118 g1786267 Escherichia coli 562 -11532590 82385 frul (de:very hypothetical frur/shl operon leader peptide) (db:swissprot) LPFS\_ECOLI P22183 ESCHERICHIA COLI 562 -11532590

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820447	7083	29239	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820453	7084	29240	186	61

Description

6500728733 frur:cra:shl:fruc:b0080 fructose repressor (gtcfc:1.1:1.5) (keggfc:14.2) (rileyfc:1.2.1) (db:gtc-escherichia coli) b0080 b0080 Escherichia coli 562 -11532591 233606 frur:cra:shl:fruc (de:fructose repressor (catabolite repressor/activator)) (db:swissprot) FRUR\_ECOLI P21168 ESCHERICHIA COLI 562 -11532591 164247 frur:shl:cra:fruc transcription regulator frur:pep--fructosephosphotransferase system repressor:regulatory protein shl (db:pir2.dat) (mp:2 min) JU0298 JU0298 Escherichia coli 562 -11532591 227987 shl shl protein (db:genpept-bct1) (de:e. coli 2 minute region.) (le:4558) (re:5562) (di:direct) EC2MIN X55034 g581031 Escherichia coli 562 -11532591 304524 frur pep:fructose phosphotransferase system (db:genpept-bct1) (de:e.coli frur gene for pep:fructose phosphotransferase systemrepressor.) (le:285) (re:1289) (di:direct) ECFRURG X55457 g581090 Escherichia coli 562 -11532591 235980 shl regulatory protein shl (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (le:87681) (re:88685) (di:direct) ECO110K D10483 g285767 Escherichia coli 562 -11532591 7502851781 (sr:e.coli (strain k12) dna) (db:genpept-bct1) (de:e.coli shl gene, complete cds, and acetolactate synthase ii (ilvh)gene, 3' end.) (nt:shl protein) (le:285) (re:1289) (di:direct) ECOSHL M35034 g147818 Escherichia coli 562 -11532591 232917 frur transcriptional repressor of fru operon and (fn:regulator; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 8 of 400 of the completegenome.) (nt:o334; 100 pct identical to frur\_ecoli sw: p21168) (le:4483) (re:5487) (di:direct) AE000118 AE000118 g1786268 Escherichia coli 562 -11532591 72374 frur:cra:shl:fruc (de:fructose repressor (catabolite repressor/activator)) (db:swissprot) FRUR\_ECOLI P21168 ESCHERICHIA COLI 562 -11532591

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820457	7085	29241	732	243

Description

GTC ORF with score 158 to: (sr:human) (db:genpept-pri1) (de:human dna sequence from cosmid cu120e2, on chromosome x containslowe oculocerebrorenal syndrome (ocrl) ests and sts.) (le:<2175:3657:5667:11543) (re:2286:3766:5802:11653) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820465	7086	29242	300	99

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820484	7087	29243	1653	550

Description

6500728734 fruk:fpk:b2168 1-phosphofructokinase:fructose 1-phosphate kinase  
(gtcfc:1.1:1.5:1.6) (ec:2.7.1.56) (keggfc:1.5:1.6) (rileyfc:1.2.1)  
(db:gtc-escherichia coli) b2168 b2168 Escherichia coli 562 -11532592 234775  
fruk:fpk (ec:2.7.1.56) (de:1-phosphofructokinase, (fructose 1-phosphate  
kinase)) (db:swissprot) K1PF\_ECOLI P23539 ESCHERICHIA COLI 562 -11532592  
162583 fruk 1-phosphofructokinase (cl:6-phosphofructokinase 2)  
(ec:2.7.1.56) (db:pir2.dat) B37245 B37245 Escherichia coli 562 -11532592  
224661 fruk:fpk 1-phosphofructokinase ec 2.7.1.56 fructose (sr:escherichia  
coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #369(48.6-49.0 min..))  
(nt:orf\_id:o368#6; similar to (swissprot accession) (le:1112) (re:2050)  
(di:complement) D90849 D90849 g1736834 Escherichia coli 562 -11532592  
5000690079 fruk 1-phosphofructokinase (db:genpept-bct1) (ec:2.7.1.56)  
(de:e. coli fruk gene for 1-phosphofructokinase.) (le:313) (re:1251)  
(di:direct) ECFRUK X53948 g41487 Escherichia coli 562 -11532592 301301  
1-phosphofructokinase (sr:escherichia coli k12 bhb2600) (db:genpept-bct1)  
(de:47 to 48 centisome region of e.coli k12 bhb2600.) (le:69171) (re:70109)  
(di:complement) ECOHU47 U00007 g405894 Escherichia coli 562 -11532592  
232916 fruk fructose-1-phosphate kinase (fn:enzyme; energy metabolism,  
carbon: glycolysis) (db:genpept-bct2) (ec:2.7.1.56) (de:escherichia coli  
k-12 mg1655 section 196 of 400 of the completegenome.) (nt:f312; 100 pct  
identical to klpf\_ecoli sw: p23539) (le:4075) (re:5013) (di:complement)  
AE000306 AE000306 g1788493 Escherichia coli 562 -11532592 80221 fruk:fpk  
(ec:2.7.1.56) (de:1-phosphofructokinase, (fructose 1-phosphate kinase))  
(db:swissprot) K1PF\_ECOLI P23539 ESCHERICHIA COLI 562 -11532592

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820489	7088	29244	879	292
<u>Description</u>				
6500728735 ppsa:pps:b1702 phosphoenolpyruvate synthase:pyruvate:water dikinase:pep synthase (gtcfc:1.1:1.8:2.5) (ec:2.7.9.2) (keggfc:1.8:2.4) (rileyfc:1.3.2) (db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-glycolysis--gluconeogenesis:carbohydrate metabolism-pyruvate and acetyl-coa metabolism:energy metabolism-reductive carboxylate cy... b1702 b1702 Escherichia coli 562 -11532593 164450 ppsa pyruvate:water dikinase::phosphoenolpyruvate synthase (ec:2.7.9.2) (db:pir2.dat) S20554 S20554 Escherichia coli 562 -11532593 224150 pps pyruvate:water dikinase ec 2.7.9.2 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #322(38.4-38.8 min.)) (nt:orf_id:o322#2; similar to (pir accession number) (le:1479) (re:3857) (di:complement) D90813 D90813 g1742783 Escherichia coli 562 -11532593 300819 pps phosphoenolpyruvate synthase (db:genpept-bct1) (ec:2.7.9.2) (de:e.coli pps gene for phosphoenolpyruvate synthase.) (nt:pyruvate,water dikinase) (le:655) (re:3033) (di:direct) ECPPSGENE X59381 g42481 Escherichia coli 562 -11532593 237869 ppsa phosphoenolpyruvate synthase (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:2.7.9.2) (de:escherichia coli k-12 mg1655 section 155 of 400 of the completegenome.) (nt:f792; 100 pct identical to pir: s20554; cg site) (le:5353) (re:7731) (di:complement) AE000265 AE000265 g1787994 Escherichia coli 562 -11532593 90817 ppsa:pps (ec:2.7.9.2) (de:(pep synthase)) (db:swissprot) PPSA_ECOLI P23538 ESCHERICHIA COLI 562 -11532593 5000690105 (de:(ecoli_1659) (pn:phosphoenolpyruvate synthase) (gn:pps) (gtcfc:1.8:2.5) (ec:2.7.9.2) (pps_a_ecoli) (keggfc:1.8:2.4) (rileyfc:1.3.2) (db:gtc-escherichia coli)) ECOLI_1659 ECOLI_1659 Escherichia coli 562 10087321				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820490	7089	29245	225	74
<u>Description</u>				
6500728736 pcka:b3403 phosphoenolpyruvate carboxykinase:atp (gtcfc:1.1:1.2:1.8:2.4) (ec:4.1.1.49) (keggfc:1.2:1.8:2.3) (rileyfc:1.3.2) (db:gtc-escherichia coli) b3403 b3403 Escherichia coli 562 -11532594 90741 pcka (ec:4.1.1.49) (de:phosphoenolpyruvate carboxykinase (atp),) (db:swissprot) PPCK_ECOLI P22259 ESCHERICHIA COLI 562 -11532594 7000686162 pcka phosphoenolpyruvate carboxykinase atp (cl:phosphoenolpyruvate carboxykinase (atp)) (ec:4.1.1.49) (db:pir2.dat) F65135 F65135 Escherichia coli 562 -11532594 7500888350 pcka phosphoenolpyruvate carboxykinase (db:genpept-bct1) (ec:4.1.1.49) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:ends differs from ecopcka due to several sequence) (le:313566) (re:315188) (di:direct) ECOUW67 U18997 g606337 Escherichia coli 562 -11532594 236636 pcka phosphoenolpyruvate carboxykinase (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:4.1.1.49) (de:escherichia coli k-12 mg1655 section 306 of 400 of the completegenome.) (nt:o540; end differs from ecopcka due to) (le:75) (re:1697) (di:direct) AE000416 AE000416 g1789807 Escherichia coli 562 -11532594 5000690037 (de:(ecoli_3321) (pn:phosphoenolpyruvate carboxykinase) (gn:pcka) (gtcfc:1.2:1.8:2.4) (ec:4.1.1.49) (ppck_ecoli) (keggfc:1.2:1.8:2.3) (rileyfc:1.3.2) (db:gtc-escherichia coli)) ECOLI_3321 ECOLI_3321 Escherichia coli 562 10032856				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820499	7090	29246	1179	392
<u>Description</u>				
6500728737 ilvi:b0077 acetolactate synthase isozyme iii large subunit (gtcfc:1.11:1.12:5.7:9.5) (ec:4.1.3.18) (keggfc:1.11:1.12:5.7:9.5) (rileyfc:1.4.7) (db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-c5-branched dibasic acid metabolism:l-amino acid metabolism-valine-... b0077 b0077 Escherichia coli 562 -11532595 7000688885 ilvi acetolactate synthase:iii large chain:acetohydroxy-acid synthase iii large chain (cl:acetolactate synthase large chain:thiamine pyrophosphate-binding domain homology) (ec:4.1.3.18) (db:pir1.dat) (mp:2 min) YCEC3I E64729 Escherichia coli 562 -11532595 7500953329 ilvi acetolactate synthase iii:valine sensitive (fn:enzyme; amino acid biosynthesis: isoleucine,) (db:genpept-bct2) (ec:4.1.3.18) (de:escherichia coli k-12 mg1655 section 8 of 400 of the completegenome.) (nt:o604; 98 pct identical (1 gap) to 522 residues) (le:1995) (re:3809) (di:direct) AE000118 AE000118 g1786265 Escherichia coli 562 -11532595 5000690001 (de:(ecoli_77) (pn:acetolactate synthase iii, valine sensitive, large subunit) (gn:ilvi) (gtcfc:1.11:1.12:5.7:9.5) (ec:4.1.3.18) (ilvi_ecoli) (keggfc:1.11:1.12:5.7:9.5) (rileyfc:1.4.7) (db:gtc-escherichia coli)) ECOLI_77 ECOLI_77 Escherichia coli 562 10122649				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820517	7091	29247	639	212

Description

6500728738 ilvh:brnp:b0078 acetolactate synthase isozyme iii small subunit:ahas-iii:acetohydroxy-acid synthase iii small subunit:als-iii (gtcfc:1.11:1.12:5.7:9.5) (ec:4.1.3.18) (keggfc:1.11:1.12:5.7:9.5) (rileyfc:1.4.7) (db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-c5-branched dibasic acid metabolism:l-amino acid metabolism-valine-... b0078 b0078 Escherichia coli 562 -11532596 7000688886 ilvh acetolactate synthase:iii small chain:acetohydroxy-acid synthase iii small chain (cl:acetolactate synthase small chain) (ec:4.1.3.18) (db:pir1.dat) (mp:2 min) YCEC3H F64729 Escherichia coli 562 -11532596 7500953331 ilvh acetolactate synthase iii:valine sensitive (fn:enzyme; amino acid biosynthesis: isoleucine,) (db:genpept-bct2) (ec:4.1.3.18) (de:escherichia coli k-12 mg1655 section 8 of 400 of the completegenome.) (nt:o163; 99 pct identical to ilvh\_ecoli sw: p00894) (le:3812) (re:4303) (di:direct) AE000118 AE000118 g1786266 Escherichia coli 562 -11532596 5000690002 (de:(ecoli\_78) (pn:acetolactate synthase iii, valine sensitive, small subunit) (gn:ilvh) (gtcfc:1.11:1.12:5.7:9.5) (ec:4.1.3.18) (ilvh\_ecoli) (keggfc:1.11:1.12:5.7:9.5) (rileyfc:1.4.7) (db:gtc-escherichia coli)) ECOLI\_78 ECOLI\_78 Escherichia coli 562 10122650

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820531	7092	29248	351	116

Description

6500728739 lpxd:fira:omsa:b0179 udp-3-o-3-hydroxymyristoyl glucosamine n-acyltransferase:fira protein:rifampicin resistance protein (gtcfc:13.3:11.2:8.1:1.11:5.8:6.14:7.1) (ec:2.3.1.-) (keggfc:1.11:4.4:5.6:5.8:5.12:5.13:6.7) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0179 b0179 Escherichia coli 562 -11532597 163054 lpxd:fira udp-3-o-3-hydroxymyristoyl glucosamine n-acyltransferase,) (cl:udp-3-o-(3-hydroxymyristoyl) glucosamine n-acyltransferase) (ec:2.3.1.-) (db:pir2.dat) (mp:4 min) S13729 S13729 Escherichia coli 562 -11532597 304566 fira fira (db:genpept-bct1) (de:e.coli fira gene, fira(200) and fira(201) allele, and skp gene (3'end).) (le:277) (re:1302) (di:direct) ECFIRA X54797 g41470 Escherichia coli 562 -11532597 239807 fira unknown (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (le:10529) (re:11554) (di:direct) ECOTSF D83536 g1208950 Escherichia coli 562 -11532597 303245 fira udp-3-o-3-hydroxymyristoyl glucosamine) (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:32046) (re:33071) (di:direct) ECU70214 U70214 g1552756 Escherichia coli 562 -11532597 232887 lpxd udp-3-o-3-hydroxymyristoyl -glucosamine (fn:enzyme; surface polysaccharides and antigens) (db:genpept-bct2) (ec:2.3.1.-) (de:escherichia coli k-12 mg1655 section 17 of 400 of the completegenome.) (nt:o341; 100 pct identical to lpxd\_ecoli sw: p21645) (le:6191) (re:7216) (di:direct) AE000127 AE000127 g1786376 Escherichia coli 562 -11532597 236168 fira fira (db:genpept-bct1) (de:e.coli fira gene, fira(200) and fira(201) allele, and skp gene (3'end).) (le:277) (re:1302) (di:direct) ECFIRA X54797 g41470 Escherichia coli 562 -11532597 5000690003 (de:(ecoli\_179) (pn:udp-3-o-:3-hydroxymyristoyl-glucosamine n-acyltransferase; third step of endotoxin:lipida synthesis) (gn:lpxd) (gtcfc:1.11:5.12:5.13:5.6:5.8:6.14:6.16:6.8:7.1:8.1) (ec:2.3.1.-) (lpxd\_ecoli) (keggfc:1.11:4.4:5.) ECOLI\_179 ECOLI\_179 Escherichia coli 562 10086744

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820535	7093	29249	330	109

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820542	7094	29250	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820546	7095	29251	579	192

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820547	7096	29252	825	274

Description

6500728740 fabz:sefa:b0180 3r-hydroxymyristol acyl carrier protein dehydrase (gtcfc:8.1:1.11:1.5:3.5) (ec:4.2.1.-) (keggfc:1.5:1.11:3.5:5.12:5.13:5.15:6.5) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0180 b0180 Escherichia coli 562 -11532598 71028 fabz:sefa (ec:4.2.1.-) (de:(17 kd actomyosin component)) (db:swissprot) FABZ\_ECOLI P21774 ESCHERICHIA COLI 562 -11532598 7000685216 fabz 3r -hydroxymyristoyl-acyl carrier protein dehydratase,) (cl:(3r)-hydroxymyristoyl-(acyl carrier protein) dehydratase) (ec:4.2.1.-) (db:pir2.dat) D64742 D64742 Escherichia coli 562 -11532598 236169 fabz 17 kd protein (fn:possible involved in lipid biosynthesis) (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (le:11659) (re:12114) (di:direct) ECOTSF D83536 g1208951 Escherichia coli 562 -11532598 239808 fabz 3r -hydroxymyristol acyl carrier protein (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:33176) (re:33631) (di:direct) ECU70214 U70214 g1552757 Escherichia coli 562 -11532598 235014 fabz 3r -hydroxymyristol acyl carrier protein (fn:enzyme; fatty acid and phosphatidic acid) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 17 of 400 of the completegenome.) (nt:o151; 100 pct identical to fabz\_ecoli sw:) (le:7321) (re:7776) (di:direct) AE000127 AE000127 g1786377 Escherichia coli 562 -11532598 303246 fabz 3r -hydroxymyristol acyl carrier protein (sr:escherichia coli k12 dna, clone plc26-43) (db:genpept-bct2) (de:escherichia coli lipid a biosynthesis (lpxa) gene, lipid adisaccharide synthase (lpxb) gene, (3r)-hydroxymyristol acylcarrier protein dehydrase (fabz) gene, and alpha subunit of dnapol... ECOLPXA M19334 g450761 Escherichia coli 562 -11532598 5000690004 (de:(ecoli\_180) (pn:3r-hydroxymyristoyl-acyl carrier protein dehydratase::3r-hydroxymyristoyl-) (gn:fabz) (gtcfc:1.11:1.5:3.5:5.12:5.13:5.15:6.5) (ec:4.2.1.-) (fabz\_ecoli) (keggfc:1.5:1.11:3.5:5.12:5.13:5.15:6.5) (rileyfc:5.7.0) ECOLI\_180 ECOLI\_180 Escherichia coli 562 10013603

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820551	7097	29253	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820555	7098	29254	678	226

Description

6500728741 mhpf:mhpe:b0351 4-hydroxy-2-oxovalerate aldolase:acetaldehyde dehydrogenase:acetylating (gtcfc:1.4:1.8) (ec:1.2.1.10) (keggfc:1.8:1.11) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0351 b0351 Escherichia coli 562 -11532599 239968 mhpf:mhpe (ec:1.2.1.10) (de:(acetylating))) (db:swissprot) MHPF\_ECOLI P77580 ESCHERICHIA COLI 562 -11532599 7000685845 mhpe acetaldehyde dehydrogenase acetylating (ec:1.2.1.10) (db:pir2.dat) G64762 G64762 Escherichia coli 562 -11532599 222961 mhpe mhpe (sr:escherichia coli (strain:k-12, sub\_strain:w3110) dna) (db:genpept-bct1) (de:escherichia coli genes for mhpr, mhpa, mhp b, mhpc, mhp d, mhpe and mhp f, complete sequence of the mhp operon.) (le:5334) (re:6284) (di:direct) D86239 D86239 g1665750 Escherichia coli 562 -11532599 5000690100 mhp f (fn:acetaldehyde dehydrogenase (acylating)) (db:genpept-bct1) (de:e.coli mhp cluster for 3-hydroxy-phenylpropionic acid degradation.) (nt:putative) (le:5353) (re:6303) (di:direct) ECMHP Y09555 g1702885 Escherichia coli 562 -11532599 7500885613 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:similar to p. putida acetaldehyde dehydrogenase) (le:80716) (re:81666) (di:direct) ECU73857 U73857 g1657547 Escherichia coli 562 -11532599 233388 mhp f acetaldehyde dehydrogenase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:1.2.1.10) (de:escherichia coli k-12 mg1655 section 32 of 400 of the complete genome.) (nt:o316; also called mhpe) (le:4379) (re:5329) (di:direct) AE000142 AE000142 g1786547 Escherichia coli 562 -11532599 120053 mhp f:mhpe (ec:1.2.1.10) (de:(acetylating))) (db:swissprot) MHPF\_ECOLI P77580 ESCHERICHIA COLI 562 -11532599

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820556	7099	29255	339	112

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820559	7100	29256	516	171

Description

6500728742 lnt:cute:b0657 apolipoprotein n-acyltransferase:alp  
n-acyltransferase:copper homeostasis protein cute  
(gtcfc:1.11:5.12:5.13:5.6:5.8:6.14:6.8:7.1) (ec:2.3.1.-)  
(keggfc:1.11:4.4:5.6:5.8:5.12:5.13:6.7) (rileyfc:5.8.0) (db:gtc-escherichia  
coli) b0657 b0657 Escherichia coli 562 -11532600 240172 lnt:cute  
(ec:2.3.1.-) (de:(copper homeostasis protein cute)) (db:swissprot) LNT\_ECOLI  
P23930 ESCHERICHIA COLI 562 -11532600 162880 lnt:cute apolipoprotein  
n-acyltransferase::copper homeostasis protein cute (cl:apolipoprotein  
n-acyltransferase) (ec:2.3.1.-) (db:pir2.dat) S18194 S18194 Escherichia coli  
562 -11532600 5000690005 cute (db:genpept-bct1) (de:e.coli cute gene.)  
(le:394) (re:1932) (di:direct) ECCUTE X58070 g41173 Escherichia coli 562  
-11532600 7500885091 cute apolipoprotein n-acyltransferase  
(db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.)  
(le:129973) (re:131511) (di:complement) ECU82598 U82598 g1778576 Escherichia  
coli 562 -11532600 232602 lnt apolipoprotein n-acyltransferase:copper  
(fn:enzyme; transport of small molecules: cations) (db:genpept-bct2)  
(ec:2.3.1.-) (de:escherichia coli k-12 mg1655 section 60 of 400 of the  
completegenome.) (nt:f512; 100 pct identical to lnt\_ecoli sw: p23930;)  
(le:2619) (re:4157) (di:complement) AE000170 AE000170 g1786878 Escherichia  
coli 562 -11532600 82303 lnt:cute (ec:2.3.1.-) (de:(copper homeostasis  
protein cute)) (db:swissprot) LNT\_ECOLI P23930 ESCHERICHIA COLI 562  
-11532600

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820569	7101	29257	465	154

Description

6500728743 sdhc:cyba:b0721 succinate dehydrogenase cytochrome b-556 subunit (gtcfc:2.8:11.1:1.2:2.1) (ec:1.3.99.1) (keggfc:1.2:1.11:2.1:2.4) (rileyfc:1.2.3) (db:gtc-escherichia coli) (keggfc:carbohydrate metabolism-citrate cycle (tca cycle):carbohydrate metabolism-butanoate metabolism:energy metabolism-oxidative phosphorylation... b0721 b0721 Escherichia coli 562 -11532601 7500880299 sdhc:cyba (de:succinate dehydrogenase cytochrome b-556 subunit) (db:swissprot) DHSC\_ECOLI P10446 ESCHERICHIA COLI 562 -11532601 122709 sdhc:cyba succinate dehydrogenase:cytochrome b556 (cl:succinate dehydrogenase 14k hydrophobic protein) (ec:1.3.99.1) (db:pir1.dat) (mp:17 min) DEECS4 A28836 Escherichia coli 562 -11532601 223169 sdhc succinate dehydrogenase cytochrome b-556 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #176) (db:genpept-bct1) (de:escherichia coli genomic dna. (16.1 - 16.4 min).) (le:4401) (re:4790) (di:direct) D90711 D90711 g1651317 Escherichia coli 562 -11532601 235956 sdhc succinate dehydrogenase (sr:escherichia coli k12 dna) (db:genpept-bct1) (ec:1.3.99.1) (de:e.coli glta gene, sdhcdab operon and sucabcd operon encoding ninecomplete proteins.) (le:3081) (re:3470) (di:direct) ECOGLTA J01619 g146197 Escherichia coli 562 -11532601 238219 sdhc succinate dehydrogenase (sr:escherichia coli (sub\_strain ed8641, strain k-12) (library: plasmid) (db:genpept-bct1) (de:escherichia coli succinate dehydrogenase (sdhc and sdhd) genes, complete cds and 5' region.) (le:441) (re:830) (di:direct) ECOSDHCD M28989 g495784 Escherichia coli 562 -11532601 5000690006 (db:genpept-bct1) (de:e. coli sdha, sdhc, sdhd gene for flavoprotein and two hydrophobic subunits of the succinate dehydrogenase (sdh; ec1.3.99.1).) (nt:succinate dehydrogenase (sdhc) hydrophobic subunit) (le:1091) (re:1480) (di:direct) ECSDHACD X00980 g42923 Escherichia coli 562 -11532601 234529 sdhc succinate dehydrogenase:cytochrome b556 (fn:enzyme; energy metabolism, carbon: tca cycle) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 65 of 400 of the completegenome.) (nt:o129; 100 pct identical to dhsc\_ecoli sw: p10446;) (le:7340) (re:7729) (di:direct) AE000175 AE000175 g1786940 Escherichia coli 562 -11532601 7502851782 cyba succinate dehydrogenase cytochrome b-556 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #176) (db:genpept) (de:escherichia coli genomic dna. (16.2 - 16.5 min).) (nt:orf\_id:o176#3; similar to swissprot accession) (le:4401) (re:4790) (di:direct) D90711 D90711 g1651317 Escherichia coli 562 -11532601 68616 sdhc:cyba (de:succinate dehydrogenase cytochrome b-556 subunit) (db:swissprot) DHSC\_ECOLI P10446 ESCHERICHIA COLI 562 -11532601

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820582	7102	29258	213	70

Description

6500728744 sdhd:b0722 succinate dehydrogenase 13 kd hydrophobic protein:succinate dehydrogenase hydrophobic membrane anchor protein (gtcfc:2.8:11.1:1.2:2.1) (ec:1.3.99.1) (keggfc:1.2:1.11:2.1:2.4) (rileyfc:1.2.3) (db:gtc-escherichia coli) (keggfc:carbohydrate metabolism-citrate cycle (tca cycle):carbohydrate metabolism-butanoate metabolism:energy metabolism-oxidative phosphorylation... b0722 b0722 Escherichia coli 562 -11532602 7500880300 sdhd (de:succinate dehydrogenase hydrophobic membrane anchor protein) (db:swissprot) DHSD\_ECOLI P10445 ESCHERICHIA COLI 562 -11532602 122690 sdhd succinate dehydrogenase:13k protein (cl:succinate dehydrogenase 13k hydrophobic protein) (ec:1.3.99.1) (db:pir1.dat) (mp:17 min) DEECS2 B28836 Escherichia coli 562 -11532602 223170 sdhd succinate dehydrogenase:13k hydrophobic (sr:escherichia coli(strain:k12) dna, clone:kohara clone #176) (db:genpept-bct1) (de:escherichia coli genomic dna. (16.1 - 16.4 min).) (le:4784) (re:5131) (di:direct) D90711 D90711 g1651318 Escherichia coli 562 -11532602 238220 sdhd succinate dehydrogenase (sr:escherichia coli k12 dna) (db:genpept-bct1) (de:e.coli glta gene, sdhcdab operon and sucabcd operon encoding ninecomplete proteins.) (le:3464) (re:3811) (di:direct) ECOGLTA J01619 g146198 Escherichia coli 562 -11532602 5000690007 (db:genpept-bct1) (de:e.coli sdha, sdhc, sdhd gene for flavoprotein and two hydrophobic subunits of the succinate dehydrogenase (sdh; ec1.3.99.1).) (nt:succinate dehydrogenase hydrophobic subunit (sdhd)) (le:1474) (re:1821) (di:direct) ECSDHACD X00980 g42924 Escherichia coli 562 -11532602 234530 sdhd succinate dehydrogenase:hydrophobic subunit (fn:enzyme; energy metabolism, carbon: tca cycle) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 65 of 400 of the completegenome.) (nt:o115; 100 pct identical to dhds\_ecoli sw: p10445) (le:7723) (re:8070) (di:direct) AE000175 AE000175 g1786941 Escherichia coli 562 -11532602 7502851783 sdhd succinate dehydrogenase ec 1.3.99.1 13k (sr:escherichia coli(strain:k12) dna, clone:kohara clone #176) (db:genpept) (de:escherichia coli genomic dna. (16.2 - 16.5 min).) (nt:orf\_id:o176#4; similar to pir accession number) (le:4784) (re:5131) (di:direct) D90711 D90711 g1651318 Escherichia coli 562 -11532602 68620 sdhd (de:succinate dehydrogenase hydrophobic membrane anchor protein) (db:swissprot) DHSD\_ECOLI P10445 ESCHERICHIA COLI 562 -11532602

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820583	7103	29259	474	158

Description

6500728745 sdha:b0723 succinate dehydrogenase flavoprotein subunit  
 (gtcfc:1.11:1.2:2.1:2.5) (ec:1.3.99.1) (keggfc:1.2:1.11:2.1:2.4)  
 (rileyfc:1.2.3) (db:gtc-escherichia coli) (gtcfc:carbohydrate  
 metabolism-butanoate metabolism:carbohydrate metabolism-citrate cycle (tca  
 cycle):energy metabolism-oxidative phosphorylation... b0723 b0723  
 Escherichia coli 562 -11532603 68595 sdha (ec:1.3.99.1) (de:succinate  
 dehydrogenase flavoprotein subunit,) (db:swissprot) DHSA\_ECOLI P10444  
 ESCHERICHIA COLI 562 -11532603 7000685047 sdha succinate  
 dehydrogenase:flavoprotein (cl:fumarate reductase flavoprotein:3-oxosteroid  
 1-dehydrogenase homology:fumarate reductase flavoprotein homology)  
 (ec:1.3.99.1) (db:pir1.dat) (mp:17 min) DEECSE B64808 Escherichia coli 562  
 -11532603 223171 sdha succinate dehydrogenase:flavoprotein (sr:escherichia  
 coli(strain:k12) dna, clone:kohara clone #176) (db:genpept-bct1)  
 (de:escherichia coli genomic dna. (16.1 - 16.4 min).) (le:5131) (re:6897)  
 (di:direct) D90711 D90711 g1651319 Escherichia coli 562 -11532603  
 7500880289 sdha succinate dehydrogenase:flavoprotein subunit (fn:enzyme;  
 energy metabolism, carbon: tca cycle) (db:genpept-bct2) (ec:1.3.99.1)  
 (de:escherichia coli k-12 mg1655 section 65 of 400 of the completegenome.)  
 (nt:o592; 99 pct identical to dhase\_coli sw: p10444) (le:8070) (re:9836)  
 (di:direct) AE000175 AE000175 g1786942 Escherichia coli 562 -11532603  
 5000690008 sdha succinate dehydrogenase ec 1.3.99.1 (sr:escherichia  
 coli(strain:k12) dna, clone:kohara clone #176) (db:genpept) (de:escherichia  
 coli genomic dna. (16.2 - 16.5 min).) (nt:orf\_id:o176#5; similar to pir  
 accession number) (le:5131) (re:6897) (di:direct) D90711 D90711 g1651319  
 Escherichia coli 562 -11532603

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820593	7104	29260	459	152

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820609	7105	29261	477	158

Description

6500728746 sdhb:b0724 succinate dehydrogenase iron-sulfur protein (gtcfc:1.11:1.2:2.1:2.5) (ec:1.3.99.1) (keggfc:1.2:1.11:2.1:2.4) (rileyfc:1.2.3) (db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-citrate cycle (tca cycle):energy metabolism-oxidative phosphorylation... b0724 b0724 Escherichia coli 562 -11532604 7500880291 sdhb (ec:1.3.99.1) (de:succinate dehydrogenase iron-sulfur protein,) (db:swissprot) DHSB\_ECOLI P07014 ESCHERICHIA COLI 562 -11532604 122706 sdhb succinate dehydrogenase:iron-sulfur protein (cl:fumarate reductase iron-sulfur protein:ferredoxin 2(4fe-4s) homology:ferredoxin (2fe-2s) homology) (ec:1.3.99.1) (db:pir1.dat) (mp:17 min) DEECSE A28837 Escherichia coli 562 -11532604 223172 sdhb succinate dehydrogenase:iron-sulfur protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #176) (db:genpept-bct1) (de:escherichia coli genomic dna. (16.1 - 16.4 min).) (le:6913) (re:7629) (di:direct) D90711 D90711 g1651320 Escherichia coli 562 -11532604 238223 sdhb succinate dehydrogenase small subunit (sr:escherichia coli k12 dna) (db:genpept-bct1) (de:e.coli glta gene, sdhcdab operon and sucabcd operon encoding ninecomplete proteins.) (le:5593) (re:6309) (di:direct) ECOGLTA J01619 g146200 Escherichia coli 562 -11532604 5000690009 (db:genpept-bct1) (de:e. coli sdhb gene for iron-sulphur protein subunit of succinatedehydrogenase (ec 1.3.99.1).) (nt:suc. dehydrogenase iron- sulphur protein subunit) (le:52) (re:768) (di:direct) ECSDHB X01070 g42928 Escherichia coli 562 -11532604 234532 sdhb succinate dehydrogenase:iron sulfur protein (fn:enzyme; energy metabolism, carbon: tca cycle) (db:genpept-bct2) (ec:1.3.99.1) (de:escherichia coli k-12 mg1655 section 65 of 400 of the completegenome.) (nt:o238; 100 pct identical to dhsb\_ecoli sw: p07014) (le:9852) (re:10568) (di:direct) AE000175 AE000175 g1786943 Escherichia coli 562 -11532604 7502851784 sdhb succinate dehydrogenase ec 1.3.99.1 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #176) (db:genpept) (de:escherichia coli genomic dna. (16.2 - 16.5 min).) (nt:orf\_id:o176#6; similar to pir accession number) (le:6913) (re:7629) (di:direct) D90711 D90711 g1651320 Escherichia coli 562 -11532604 68606 sdhb (ec:1.3.99.1) (de:succinate dehydrogenase iron-sulfur protein,) (db:swissprot) DHSB\_ECOLI P07014 ESCHERICHIA COLI 562 -11532604

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820613	7106	29262	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820617	7107	29263	861	287

Description

6500728747 pflb:pfl:b0903 formate acetyltransferase 1:pyruvate formate-lyase 1 (gtcfc:1.11:1.8:2.2) (ec:2.3.1.54) (keggfc:1.8:1.11) (rileyfc:1.2.7) (db:gtc-escherichia coli) b0903 b0903 Escherichia coli 562 -11532605 163078 pflb:pfl formate c-acetyltransferase:1:pyruvate formate-lyase i (cl:formate c-acetyltransferase 1:glycyl radical homology) (ec:2.3.1.54) (db:pir1.dat) (mp:20.5) S01788 S01788 Escherichia coli 562 -11532605 223264 pfl formate c-acetyltransferase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #216) (db:genpept-bct1) (de:escherichia coli genomic dna. (20.3 - 20.7 min).) (le:6965) (re:9247) (di:complement) D90728 D90728 g1651427 Escherichia coli 562 -11532605 7500959742 (db:genpept-bct1) (de:e. coli pfl gene for pyruvate formate-lyase (ec 2.3.1.54).) (nt:pyruvate formate-lyase (aa 1-760)) (le:101) (re:2383) (di:direct) ECPFL X08035 g42370 Escherichia coli 562 -11532605 237793 pflb formate acetyltransferase 1 (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (ec:2.3.1.54) (de:escherichia coli k-12 mg1655 section 82 of 400 of the completegenome.) (nt:f760; 100 pct identical to pflb\_ecoli sw: p09373) (le:5588) (re:7870) (di:complement) AE000192 AE000192 g1787131 Escherichia coli 562 -11532605 5000690010 pfl formate c-acetyltransferase ec 2.3.1.54 . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #216) (db:genpept) (de:escherichia coli genomic dna. (20.4 - 20.8 min).) (nt:orf\_id:o216#7; similar to pir accession number) (le:6965) (re:9247) (di:complement) D90728 D90728 g1651427 Escherichia coli 562 -11532605

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820628	7108	29264	609	202

#### Description

6500728748 htrb:b1054 membrane protein affecting cell division:growth and high temperature survival:lipid a biosynthesis lauroyl acyltransferase:heat shock protein b (gtcfc:11.1:12.8:8.4:12.7) (ec:2.3.1.-) (keggfc:1.11:4.4:5.6:5.8:5.12:5.13:6.7) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1054 b1054 Escherichia coli 562 -11532606 7500883606 htrb (ec:2.3.1.-) (de:protein b)) (db:swissprot) HTRB\_ECOLI P24187 ESCHERICHIA COLI 562 -11532606 163213 htrb lipid a biosynthesis lauroyl acyltransferase::htrb protein (ec:2.3.1.-) (db:pir2.dat) S16888 S16888 Escherichia coli 562 -11532606 223345 htrb heat shock protein b (sr:escherichia coli(strain:k12) dna, clone:kohara clone #233) (db:genpept-bct1) (de:escherichia coli genomic dna. (24.0 - 24.4 min).) (le:2028) (re:2948) (di:complement) D90743 D90743 g1651522 Escherichia coli 562 -11532606 5000691972 htrb htrb protein (db:genpept-bct1) (de:e. coli k12 htrb gene.) (le:1960) (re:2880) (di:direct) ECHTRB X61000 g48957 Escherichia coli 562 -11532606 233165 htrb heat shock protein (fn:factor; adaptations, atypical conditions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 96 of 400 of the completegenome.) (nt:f306; 96 pct identical to htrb\_ecoli sw: p24187) (le:9920) (re:10840) (di:complement) AE000206 AE000206 g1787292 Escherichia coli 562 -11532606 7502851785 htrb htrb protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #232) (db:genpept) (de:escherichia coli genomic dna. (23.8 - 24.2 min).) (nt:orf\_id:o233#3; similar to pir accession number) (le:12282) (re:13202) (di:complement) D90742 D90742 g4062628 Escherichia coli 562 -11532606 7502851786 htrb htrb protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #233) (db:genpept) (de:escherichia coli genomic dna. (24.1 - 24.5 min).) (nt:orf\_id:o233#3; similar to pir accession number) (le:2028) (re:2948) (di:complement) D90743 D90743 g1651522 Escherichia coli 562 -11532606 78033 htrb (ec:2.3.1.-) (de:protein b)) (db:swissprot) HTRB\_ECOLI P24187 ESCHERICHIA COLI 562 -11532606

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820631	7109	29265	186	61

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820633	7110	29266	783	260

Description

6500728749 ydbu:b1395 hypothetical protein:putative 3-hydroxybutyryl-coa dehydrogenase:bhbd (gtcfc:1.11) (ec:1.1.1.157) (keggfc:1.11) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1395 b1395 Escherichia coli 562 -11532607 4000707887 paah (ec:1.1.1.157) (de:hydroxybutyryl-coa dehydrogenase) (bhbd)) (db:swissprot) HBDH\_ECOLI P76083 ESCHERICHIA COLI 562 -11532607 7000685500 probable 3-hydroxybutyryl-coa dehydrogenase:ydbu (cl:3-hydroxyacyl-coa dehydrogenase homology) (ec:1.1.1.157) (db:pir2.dat) F64890 F64890 Escherichia coli 562 -11532607 7500883044 ydbu putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 126 of 400 of the completegenome.) (nt:o475; 38 pct identical (1 gap) to 283 residues) (le:7611) (re:9038) (di:direct) AE000236 AE000236 g1787661 Escherichia coli 562 -11532607 5000692199 (de:(ecoli\_1355) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_1355 ECOLI\_1355 Escherichia coli 562 10123301

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820634	7111	29267	390	129

Description

6500728750 riml:b1427 ribosomal-protein-serine acetyltransferase:acetylating enzyme for n-terminal of ribosomal protein 17/112 (gtcfc:10.5) (ec:2.3.1.-) (keggfc:1.11:4.4:5.6:5.8:5.12:5.13:6.7) (rileyfc:3.1.3) (db:gtc-escherichia coli) b1427 b1427 Escherichia coli 562 -11532608 300488 riml (ec:2.3.1.-) (de:enzyme for n-terminal of ribosomal protein 17/112)) (db:swissprot) RIML\_ECOLI P13857 ESCHERICHIA COLI 562 -11532608 123327 riml ribosomal-protein-serine acetyltransferase::peptide n-acetyltransferase riml (cl:peptide n-acetyltransferase riml) (ec:2.3.1.-) (db:pir1.dat) (mp:33 min) XXECPL S04776 Escherichia coli 562 -11532608 223723 riml ribosomal-protein-serine acetyltransferase ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #270(32.0-32.3 min.)) (nt:orf\_id:o270#17; similar to (swissprot accession) (le:14609) (re:15148) (di:direct) D90781 D90781 g1742324 Escherichia coli 562 -11532608 300498 riml ribosomal-protein-serine acetyltransferase ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #271(32.1-32.5 min.)) (nt:orf\_id:o270#17; similar to (swissprot accession) (le:7348) (re:7887) (di:direct) D90782 D90782 g1742335 Escherichia coli 562 -11532608 5000690011 (db:genpept-bct1) (de:e.coli riml gene for ribosomal protein 112.) (nt:ribosomal protein 112 (aa 1-179)) (le:603) (re:1142) (di:direct) ECRIML X15860 g42749 Escherichia coli 562 -11532608 238090 riml acetylation of n-terminal serine of 30s (fn:enzyme; ribosomes - maturation and) (db:genpept-bct2) (ec:2.3.1.-) (de:escherichia coli k-12 mg1655 section 130 of 400 of the completegenome.) (nt:o179; 100 pct identical to riml\_ecoli sw: p13857;) (le:297) (re:836) (di:direct) AE000240 AE000240 g1787697 Escherichia coli 562 -11532608 94363 riml (ec:2.3.1.-) (de:enzyme for n-terminal of ribosomal protein 17/112)) (db:swissprot) RIML\_ECOLI P13857 ESCHERICHIA COLI 562 -11532608 223733 riml ribosomal-protein-serine acetyltransferase ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #271(32.1-32.5 min.)) (nt:orf\_id:o270#17; similar to (swissprot accession) (le:7348) (re:7887) (di:direct) D90782 D90782 g1742335 Escherichia coli 562 -11532608

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820644	7112	29268	321	106

Description

6500728751 gadb:b1493 glutamate decarboxylase-beta:glutamate decarboxylase  
beta:gad-beta (gtcfc:1.11:2.3:5.1:5.2:6.1) (ec:4.1.1.15)  
(keggfc:1.11:5.1:5.2:6.1:6.2) (rileyfc:1.3.1) (db:gtc-escherichia coli)  
b1493 b1493 Escherichia coli 562 -11532609 67997 gadb (ec:4.1.1.15)  
(de:glutamate decarboxylase beta, (gad-beta)) (db:swissprot) DCEB\_ECOLI  
P28302 ESCHERICHIA COLI 562 -11532609 125296 gadb glutamate  
decarboxylase:beta:l-glutamate 1-carboxy-lyase (cl:escherichia coli  
glutamate decarboxylase) (ec:4.1.1.15) (db:pir1.dat) (mp:78 min) B43332  
B43332 Escherichia coli 562 -11532609 223839 gadb glutamate decarboxylase  
ec 4.1.1.15 beta (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara  
lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#280(33.7-34.1 min.)) (nt:orf\_id:o280#1; similar to (pir accession number)  
(le:8282) (re:9682) (di:complement) D90791 D90791 g1742450 Escherichia coli  
562 -11532609 300576 gadb glutamate decarboxylase-beta (sr:escherichia coli  
dna) (db:genpept-bct1) (ec:4.1.1.15) (de:e. coli glutamate  
decarboxylase-beta (gadb) gene, complete cds.) (le:18) (re:1418) (di:direct)  
ECOGADB M84025 g146060 Escherichia coli 562 -11532609 234425 gadb glutamate  
decarboxylase isozyme (fn:enzyme; central intermediary metabolism: pool,)  
(db:genpept-bct2) (ec:4.1.1.15) (de:escherichia coli k-12 mg1655 section 136  
of 400 of the completengenome.) (nt:f466; 100 pct identical to dceb\_ecoli sw:  
p28302;) (le:7502) (re:8902) (di:complement) AE000246 AE000246 g1787769  
Escherichia coli 562 -11532609 5000690012 (de:(ecoli\_1453) (pn:glutamate  
decarboxylase isozyme) (gn:gadb) (gtcfc:1.11:5.1:5.2:6.1:6.2) (ec:4.1.1.15)  
(dceb\_ecoli) (keggfc:1.11:5.1:5.2:6.1:6.2) (rileyfc:1.3.1)  
(db:gtc-escherichia coli)) ECOLI\_1453 ECOLI\_1453 Escherichia coli 562  
10010590

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820645	7113	29269	228	75

# Description

6500728752 rspb:b1580 starvation sensing protein rspb (gtcfc:12.13:13.2) (ec:1.1.1.-) (keggfc:1.5:1.6:1.7:1.11:3.5:4.3:5.3:5.9:5.13:9.3) (rileyfc:5.8.0) (db:gtc-escherichia coli) (keggfc:carbohydrate metabolism-fructose and mannose metabolism:carbohydrate metabolism-galactose metabolism:carbohydrate metab... b1580 b1580 Escherichia coli 562 -11532610 97491 rspb (ec:1.1.1.-) (de:starvation sensing protein rspb,) (db:swissprot) RSPB\_ECOLI P38105 ESCHERICHIA COLI 562 -11532610 164585 rspb starvation sensing protein rspb::l-iditol 2-dehydrogenase homolog:sorbitol dehydrogenase homolog (cl:alcohol dehydrogenase:long-chain alcohol dehydrogenase homology) (ec:1.1.1.-) (db:pir1.dat) (mp:36.5 min) I81185 I81185 Escherichia coli 562 -11532610 223962 rspb starvation sensing protein rspb ec 1.1.1.-. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #308(35.3-35.7 min.)) (nt:orf\_id:o309#12; similar to (swissprot accession) (le:14863) (re:15882) (di:complement) D90799 D90799 g1742581 Escherichia coli 562 -11532610 300703 rspb starvation sensing protein rspb ec 1.1.1.-. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #309(35.4-35.7 min.)) (nt:orf\_id:o309#12; similar to (swissprot accession) (le:11639) (re:12658) (di:complement) D90800 D90800 g1742604 Escherichia coli 562 -11532610 300681 rspb (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli rspa and rspb genes, complete cds.) (nt:putative) (le:1530) (re:2549) (di:direct) ECORSPAB L31628 g495783 Escherichia coli 562 -11532610 235941 rspb starvation sensing protein (fn:enzyme; global regulatory functions) (db:genpept-bct2) (ec:1.1.1.-) (de:escherichia coli k-12 mg1655 section 144 of 400 of the completegenome.) (nt:f339; 100 pct identical to rspb\_ecoli sw: p38105;) (le:124) (re:1143) (di:complement) AE000254 AE000254 g1787863 Escherichia coli 562 -11532610 223984 rspb starvation sensing protein rspb ec 1.1.1.-. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #309(35.4-35.7 min.)) (nt:orf\_id:o309#12; similar to (swissprot accession) (le:11639) (re:12658) (di:complement) D90800 D90800 g1742604 Escherichia coli 562 -11532610 5000690013 (de:(ecoli\_1539) (pn:starvation sensing protein rspb) (gn:rspb) (gtcfc:1.11:1.5:1.6:1.7:3.5:4.3:5.13:5.3:5.9:9.3) (ec:1.1.1.-) (rspb\_ecoli) (keggfc:1.5:1.6:1.7:1.11:3.5:4.3:5.3:5.9:5.13:9.3) (rileyfc:5.7.0) (db:gtc-escherichia c) ECOLI\_1539 ECOLI\_1539 Escherichia coli 562 10039381

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820649	7114	29270	282	93

Description

6500728753 msbb:b1855 msbb protein:lipid a biosynthesis:kdo2-:lauroyl-lipid  
iva acyltransferase (gtcfc:1.11:5.12:5.13:5.6:5.8:6.14:6.8:7.1) (ec:2.3.1.-)  
(keggfc:1.11:4.4:5.6:5.8:5.12:5.13:6.7) (rileyfc:5.8.0) (db:gtc-escherichia  
coli) b1855 b1855 Escherichia coli 562 -11532611 84289 msbb (ec:2.3.1.-)  
(de:(ec 2.3.1.-)) (db:swissprot) MSBB\_ECOLI P24205 ESCHERICHIA COLI 562  
-11532611 164057 msbb:mlt kdo 2-lauroyl -lipid iv4  
acyltransferase::membrane-bound lytic transglycosylase (ec:2.3.1.-)  
(db:pir2.dat) A42608 A42608 Escherichia coli 562 -11532611 224346 msbb  
membrane-bound lytic transglycosylase (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #336gap(41.6-41.9 min.)) (nt:orf\_id:o336gap#8; similar to (pir  
accession number) (le:8748) (re:9719) (di:complement) D90828 D90828 g1736498  
Escherichia coli 562 -11532611 235186 msbb (sr:escherichia coli (strain  
k-12) dna) (db:genpept-bct1) (de:escherichia coli multicopy suppressor  
(msbb) gene, complete cds;orf gene, 3'end.) (nt:originally thought to be a  
lytic transglycosylase) (le:168) (re:1139) (di:direct) ECOMSBB M87660  
g146877 Escherichia coli 562 -11532611 300986 msbb (sr:escherichia coli  
(strain k-12) dna) (db:genpept-bct1) (de:e.coli msbb protein gene, complete  
cds.) (le:999) (re:1970) (di:direct) ECOMSBBA M77039 g146891 Escherichia  
coli 562 -11532611 235183 msbb suppressor of htrb:heat shock protein  
(fn:putative factor; adaptations, atypical) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 169 of 400 of the completegenome.)  
(nt:f323; 100 pct identical to msbb\_ecoli sw: p24205;) (le:8438) (re:9409)  
(di:complement) AE000279 AE000279 g1788161 Escherichia coli 562 -11532611  
5000692551 (de:(ecoli\_1812) (pn:msbb protein:multicopy suppressor of htrb)  
(gn:msbb) (gtcfc:13.7:14.1) (ec:) (msbb\_ecoli) (keggfc:11.2) (rileyfc:5.7.0)  
(db:gtc-escherichia coli)) ECOLI\_1812 ECOLI\_1812 Escherichia coli 562  
10026490

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820652	7115	29271	297	98

Description

6500728754 wcac:b2054 hypothetical protein:putative colanic acid biosynthesis acetyltransferase wcac  
(gtcfc:1.11:5.12:5.13:5.6:5.8:6.14:6.8:7.1) (ec:2.3.1.-)  
(keggfc:1.11:4.4:5.6:5.8:5.12:5.13:6.7) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2054 b2054 Escherichia coli 562 -11532612 1500686871 wcac  
(ec:2.3.1.-) (de:(ec 2.3.1.-)) (db:swissprot) WCAF\_ECOLI P71240 ESCHERICHIA COLI 562 -11532612 7000687010 hypothetical protein b2054 (db:pir2.dat) E64971 E64971 Escherichia coli 562 -11532612 224593 galactoside acetyltransferase ec 2.3.1.18 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #353(45.6-46.0 min.)) (nt:orf\_id:o353#7; similar to (swissprot accession) (le:10108) (re:10656) (di:complement) D90843 D90843 g1736760 Escherichia coli 562 -11532612 301233 wcac putative transferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 185 of 400 of the completegenome.) (nt:f182; this 182 aa orf is 31 pct identical (3 gaps)) (le:15123) (re:15671) (di:complement) AE000295 AE000295 g1788367 Escherichia coli 562 -11532612 5000692664 (de:(ecoli\_2002) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2002 ECOLI\_2002 Escherichia coli 562 10062879

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820653	7116	29272	375	124

Description

6500728755 wcab:b2058 putative acetyl transferase:putative colanic acid biosynthesis acetyltransferase wcab  
(gtcfc:1.11:5.12:5.13:5.6:5.8:6.14:6.8:7.1) (ec:2.3.1.-)  
(keggfc:1.11:4.4:5.6:5.8:5.12:5.13:6.7) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2058 b2058 Escherichia coli 562 -11532613 1500686867 wcab  
(ec:2.3.1.-) (de:(ec 2.3.1.-)) (db:swissprot) WCAB\_ECOLI P77558 ESCHERICHIA COLI 562 -11532613 7000687005 wcab probable acetyl transferase  
(db:pir2.dat) A64972 A64972 Escherichia coli 562 -11532613 301234 serine acetyltransferase ec 2.3.1.30 sat . (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #353(45.6-46.0 min.)) (nt:orf\_id:o353#11; similar to (swissprot accession) (le:13835) (re:14323) (di:complement) D90843 D90843 g1736761 Escherichia coli 562 -11532613 239536 wcab putative transferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 185 of 400 of the completegenome.) (nt:f162; 100 pct identical to gb: ecu38473\_5 accession) (le:18850) (re:19338) (di:complement) AE000295 AE000295 g1788371 Escherichia coli 562 -11532613 296195 wcab putative acetyl transferase (db:genpept-bct2) (de:escherichia coli k-12 wca gene cluster.) (le:4418) (re:4906) (di:direct) ECU38473 U38473 g1407607 Escherichia coli 562 -11532613 224594 serine acetyltransferase ec 2.3.1.30 sat . (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #353(45.6-46.0 min.)) (nt:orf\_id:o353#11; similar to (swissprot accession) (le:13835) (re:14323) (di:complement) D90843 D90843 g1736761 Escherichia coli 562 -11532613 5000692668 (de:(ecoli\_2006) (pn:putative acetyl transferase) (gn:wcab) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2006 ECOLI\_2006 Escherichia coli 562 10062875

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820671	7117	29273	546	181

Description

6500728756 gatd:b2091 galactitol-1-phosphate dehydrogenase  
 (gtcfc:1.11:1.4:1.5:1.6:1.7:3.5:4.3:5.13:5.3:5.9:9.3) (ec:1.1.1.-)  
 (keggfc:1.5:1.6:1.7:1.11:3.5:4.3:5.3:5.9:5.13:9.3) (rileyfc:1.1.1)  
 (db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-butanoate  
 metabolism:carbohydrate metabolism-pentose and gluc... b2091 b2091  
 Escherichia coli 562 -11532614 73169 gatd (ec:1.1.1.251)  
 (de:galactitol-1-phosphate 5-dehydrogenase,) (db:swissprot) GATD\_ECOLI  
 P37190 ESCHERICHIA COLI 562 -11532614 7000685367 gatd  
 galactitol-1-phosphate dehydrogenase (cl:alcohol dehydrogenase:long-chain  
 alcohol dehydrogenase homology) (ec:1.1.1.-) (db:pir1.dat) B64976 B64976  
 Escherichia coli 562 -11532614 224637 gatd galactitol-1-phosphate  
 dehydrogenase ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara  
 lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
 #358(46.6-46.9 min.)) (nt:orf\_id:o358#1; similar to (swissprot accession)  
 (le:9230) (re:10270) (di:complement) D90847 D90847 g1736808 Escherichia coli  
 562 -11532614 301277 gatd galactitol-1-phosphate dehydrogenase (fn:enzyme;  
 degradation of small molecules: carbon) (db:genpept-bct2) (ec:1.1.1.-)  
 (de:escherichia coli k-12 mg1655 section 188 of 400 of the completegenome.)  
 (nt:f346; 97 pct identical to gatd\_ecoli sw: p37190) (le:6789) (re:7829)  
 (di:complement) AE000298 AE000298 g1788407 Escherichia coli 562 -11532614  
 5000690014 (de:(ecoli\_2039) (pn:galactitol-1-phosphate dehydrogenase)  
 (gn:gatd) (gtcfc:1.11:1.5:1.6:1.7:3.5:4.3:5.13:5.3:5.9:9.3) (ec:1.1.1.-)  
 (gatd\_ecoli) (keggfc:1.5:1.6:1.7:1.11:3.5:4.3:5.3:5.9:5.13:9.3)  
 (rileyfc:1.1.1) (db:gtc-escheric) ECOLI\_2039 ECOLI\_2039 Escherichia coli 562  
 10120001

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820673	7118	29274	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820678	7119	29275	273	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820689	7120	29276	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820694	7121	29277	582	193

# Description

6500728757 pdxb:b2320 erythronate-4-phosphate dehydrogenase  
 (gtcfc:1.11:1.5:1.6:1.7:3.5:4.3:5.13:5.3:5.9:9.3) (ec:1.1.1.-)  
 (keggfc:1.5:1.6:1.7:1.11:3.5:4.3:5.3:5.9:5.13:9.3) (rileyfc:1.7.6)  
 (db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-butanoate  
 metabolism:carbohydrate metabolism-fructose and mannose... b2320 b2320  
 Escherichia coli 562 -11532615 88902 pdxb (ec:1.1.1.-)  
 (de:erythronate-4-phosphate dehydrogenase,) (db:swissprot) PDXB\_ECOLI P05459  
 ESCHERICHIA COLI 562 -11532615 122571 pdxb probable erythronate-4-phosphate  
 dehydrogenase (cl:phosphoglycerate dehydrogenase) (ec:1.1.1.-) (db:pir1.dat)  
 (mp:50 min) DEECPP JV0051 Escherichia coli 562 -11532615 224864 pdxb  
 probable erythronate-4-phosphate dehydrogenase (sr:escherichia coli  
 (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
 (de:e.coli genomic dna, kohara clone #407(52.4-52.8 min.)) (nt:similar to  
 (pir accession number jv0051)) (le:7357) (re:8493) (di:complement) D90863  
 D90863 g1799713 Escherichia coli 562 -11532615 240031 (sr:e.coli (strain  
 k-12, isolate w3110) dna) (db:genpept-bct1) (de:e.coli  
 erythronate-4-phosphate dehydrogenase (pdx) gene, completecds., usg1 and  
 div protein genes, 5' end.) (nt:erythronate-4-phosphate dehydrogenase)  
 (le:218) (re:1354) (di:direct) ECOPDXB M29962 g147124 Escherichia coli 562  
 -11532615 7500887774 pdxb 4-phosphoerythronate dehydrogenase  
 (db:genpept-bct1) (de:escherichia coli beta-ketoacyl-acyl synthase i (fabb)  
 gene, partialcds, div (div) and 4-phosphoerythronate dehydrogenase (pdx)  
 genes,complete cds.) (nt:d-isomer specific, 2-hydroxyacid dehydrogenase)  
 (le:2555) (re:3691) (di:direct) ECU76961 U76961 g1684788 Escherichia coli  
 562 -11532615 235376 pdxb erythronate-4-phosphate dehydrogenase (fn:enzyme;  
 biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:1.1.1.-)  
 (de:escherichia coli k-12 mg1655 section 211 of 400 of the completegenome.)  
 (nt:f378; 100 pct identical to pdxb\_ecoli sw: p05459) (le:63) (re:1199)  
 (di:complement) AE000321 AE000321 g1788660 Escherichia coli 562 -11532615  
 5000690015 (de:(ecoli\_2269) (pn:erythronate-4-phosphate dehydrogenase)  
 (gn:pdx) (gtcfc:1.11:1.5:1.6:1.7:3.5:4.3:5.13:5.3:5.9:9.3) (ec:1.1.1.-)  
 (pdx\_ecoli) (keggfc:1.5:1.6:1.7:1.11:3.5:4.3:5.3:5.9:5.13:9.3)  
 (rileyfc:1.7.6) (db:gtc-escheric) ECOLI\_2269 ECOLI\_2269 Escherichia coli 562  
 10031029

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820696	7122	29278	228	76

Description

6500728758 gabd:b2661 succinate-semialdehyde dehydrogenase:nadp+:ssdh  
 (gtcfc:1.4:1.8) (ec:1.2.1.16) (keggfc:1.11:5.1:5.12) (rileyfc:1.3.1)  
 (db:gtc-escherichia coli) b2661 b2661 Escherichia coli 562 -11532616 72876  
 gabd (ec:1.2.1.16) (de:succinate-semialdehyde dehydrogenase (nadp+), (ssdh))  
 (db:swissprot) GABD\_ECOLI P25526 ESCHERICHIA COLI 562 -11532616 7000685342  
 gabd succinate-semialdehyde dehydrogenase nad p + (cl:aldehyde dehydrogenase  
 (nad+):aldehyde dehydrogenase homology) (ec:1.2.1.16) (db:pir2.dat) F65045  
 F65045 Escherichia coli 562 -11532616 236054 gabd succinate-semialdehyde  
 dehydrogenase (fn:enzyme; central intermediary metabolism: pool,)  
 (db:genpept-bct2) (ec:1.2.1.16) (de:escherichia coli k-12 mg1655 section 241  
 of 400 of the completegenome.) (nt:o482; 100 pct identical to gabd\_ecoli sw:  
 p25526) (le:2996) (re:4444) (di:direct) AE000351 AE000351 g1789015  
 Escherichia coli 562 -11532616 7500882056 gabd succinic semialdehyde  
 dehydrogenase (sr:escherichia coli (strain k-12) dna) (db:genpept-bct2)  
 (ec:1.2.1.16) (de:e.coli succinic semialdehyde dehydrogenase (gabd) gene,  
 completecds; gaba transaminase (gabt) gene, complete cds; gaba  
 permease(gabp) gene, complete cds.) (le:638) (re:2086) (d... ECOSUSEDEH  
 M88334 g147901 Escherichia coli 562 -11532616 5000690016 (de:(ecoli\_2594)  
 (pn:succinate-semialdehyde dehydrogenase, nadp-dependent activity) (gn:gabd)  
 (gtcfc:1.11:5.1:5.12) (ec:1.2.1.16) (gabd\_ecoli) (keggfc:1.11:5.1:5.12)  
 (rileyfc:1.3.1) (db:gtc-escherichia coli)) ECOLI\_2594 ECOLI\_2594 Escherichia  
 coli 562 10015422

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820699	7123	29279	456	151

Description

6500728759 yhas:b3114 probable formate acetyltransferase 3:pyruvate  
formate-lyase 3 (gtcfc:1.8) (ec:2.3.1.54) (keggfc:1.8:1.11) (rileyfc:5.8.0)  
(db:gtc-escherichia coli) b3114 b3114 Escherichia coli 562 -11532617 89193  
tdce (ec:2.3.1.-) (de:lyase)) (db:swissprot) TDCE\_ECOLI P42632 ESCHERICHIA  
COLI 562 -11532617 7000686121 yhas:tdce formate  
c-acetyltransferase:3:keto-acid formate lyase (cl:formate  
c-acetyltransferase 1:glycyl radical homology) (ec:2.3.1.54) (db:pir2.dat)  
G65100 G65100 Escherichia coli 562 -11532617 7500892862 (db:genpept-bct1)  
(de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.)  
(nt:orf\_f746) (le:40932) (re:43172) (di:complement) ECOUW67 U18997 g606055  
Escherichia coli 562 -11532617 236354 tdce probable formate  
acetyltransferase 3 (fn:putative enzyme; energy metabolism, carbon:)  
(db:genpept-bct2) (ec:2.3.1.54) (de:escherichia coli k-12 mg1655 section 283  
of 400 of the completegenome.) (nt:f746; 100 pct identical amino acid  
sequence and) (le:1034) (re:3274) (di:complement) AE000393 AE000393 g1789502  
Escherichia coli 562 -11532617 5000690017 (de:(ecoli\_3039) (pn:probable  
formate acetyltransferase 3:pyruvate formate- lyase 3) (gn:yhas)  
(gtcfc:1.11:1.8) (ec:2.3.1.54) (pfl3\_ecoli) (keggfc:1.8:1.11)  
(rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_3039 ECOLI\_3039 Escherichia  
coli 562 10031316

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820712	7124	29280	1515	505

Description

6500728760 gada:gads:b3517 gad alpha protein:glutamate decarboxylase  
alpha:gad-alpha (gtcfc:1.11:2.3:5.1:5.2:6.1) (ec:4.1.1.15)  
(keggfc:1.11:5.1:5.2:6.1:6.2) (rileyfc:1.3.1) (db:gtc-escherichia coli)  
b3517 b3517 Escherichia coli 562 -11532618 67996 gada:gads (ec:4.1.1.15)  
(de:glutamate decarboxylase alpha, (gad-alpha)) (db:swissprot) DCEA\_ECOLI  
P80063 ESCHERICHIA COLI 562 -11532618 141461 gada glutamate  
decarboxylase:alpha:gad alpha protein:l-glutamate 1-carboxy-lyase  
(cl:escherichia coli glutamate decarboxylase) (ec:4.1.1.15) (db:pir1.dat)  
(mp:78 min) S24234 S47737 Escherichia coli 562 -11532618 236753 gada gad  
alpha protein (sr:escherichia coli dna) (db:genpept-bct1) (ec:4.1.1.15)  
(de:e. coli glutamate decarboxylase-alpha (gada) gene, complete cds.)  
(le:18) (re:1418) (di:direct) ECOGADA M84024 g146058 Escherichia coli 562  
-11532618 7500880052 gada gad alpha protein (sr:escherichia coli  
(sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e.  
coli chromosomal region from 76.0 to 81.5 minutes.) (le:80439) (re:81839)  
(di:complement) ECOUW76 U00039 g466654 Escherichia coli 562 -11532618  
234424 gada glutamate decarboxylase isozyme (fn:enzyme; central  
intermediary metabolism: pool,) (db:genpept-bct2) (ec:4.1.1.15)  
(de:escherichia coli k-12 mg1655 section 318 of 400 of the completegenome.)  
(nt:f466; 100 pct identical amino acid sequence and) (le:2502) (re:3902)  
(di:complement) AE000428 AE000428 g1789934 Escherichia coli 562 -11532618  
5000690018 (de:(ecoli\_3436) (pn:glutamate decarboxylase isozyme) (gn:gada)  
(gtcfc:1.11:5.1:5.2:6.1:6.2) (ec:4.1.1.15) (dcea\_ecoli)  
(keggfc:1.11:5.1:5.2:6.1:6.2) (rileyfc:1.3.1) (db:gtc-escherichia coli))  
ECOLI\_3436 ECOLI\_3436 Escherichia coli 562 10010589

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820727	7125	29281	504	167

Description

6500728761 ilvn:b3670 acetohydroxy acid synthase i:small  
subunit:acetolactate synthase isozyme i small  
subunit:ahas-i:acetohydroxy-acid synthase i small subunit:als-i  
(gtcfc:1.11:1.12:5.7:9.5) (ec:4.1.3.18) (keggfc:1.11:1.12:5.7:9.5)  
(rileyfc:1.4.7) (db:gtc-escherichia coli) (gtcfc:carbohydrate  
metabolism-butanoate metabolism:carbohydrate metabolism-c5-branched dibasic  
acid metabolism:l-amino acid metabolism-valine-... b3670 b3670 Escherichia  
coli 562 -11532619 7000688887 ilvn acetolactate synthase:i small chain  
(cl:acetolactate synthase small chain) (ec:4.1.3.18) (db:pir1.dat) (mp:82  
min) YCEC1S G65168 Escherichia coli 562 -11532619 7500953332 ilvn::cg site  
no. 1... acetohydroxy acid synthase i:small subunit (sr:escherichia coli k12  
strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the  
region from 81.5 to 84.5 minutes.) (le:40196) (re:40486) (di:complement)  
ECOUW82 L10328 g290519 Escherichia coli 562 -11532619 236907 ilvn  
acetolactate synthase i:valine sensitive:small (fn:enzyme; amino acid  
biosynthesis: isoleucine,) (db:genpept-bct2) (ec:4.1.3.18) (de:escherichia  
coli k-12 mg1655 section 334 of 400 of the completegenome.) (nt:f96; 98 pct  
identical amino acid sequence and equal) (le:10616) (re:10906)  
(di:complement) AE000444 AE000444 g1790103 Escherichia coli 562 -11532619  
5000690019 (de:(ecoli\_3589) (pn:acetolactate synthase i, valine sensitive,  
small subunit) (gn:ilvn) (gtcfc:1.11:1.12:5.7:9.5) (ec:4.1.3.18)  
(ilvn\_ecoli) (keggfc:1.11:1.12:5.7:9.5) (rileyfc:1.4.7) (db:gtc-escherichia  
coli)) ECOLI\_3589 ECOLI\_3589 Escherichia coli 562 10124064



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820742	7126	29282	309	102

Description

6500728762 ilvb:b3671 acetohydroxy acid synthase i:small  
subunit:acetolactate synthase isozyme i large  
subunit:ahas-i:acetohydroxy-acid synthase i large subunit:als-i  
(gtcfc:1.11:1.12:5.7:9.5) (ec:4.1.3.18) (keggfc:1.11:1.12:5.7:9.5)  
(rileyfc:1.4.7) (db:gtc-escherichia coli) (gtcfc:carbohydrate  
metabolism-butanoate metabolism:carbohydrate metabolism-c5-branched dibasic  
acid metabolism:l-amino acid metabolism-valine-... b3671 b3671 Escherichia  
coli 562 -11532620 234848 ilvb (ec:4.1.3.18) (de:(acetohydroxy-acid  
synthase i large subunit) (als-i)) (db:swissprot) ILVB\_ECOLI P08142  
ESCHERICHIA COLI 562 -11532620 125552 ilvb acetolactate synthase:i large  
chain (cl:acetolactate synthase large chain:thiamine pyrophosphate-binding  
domain homology) (ec:4.1.3.18) (db:pir1.dat) (mp:82 min) YCEC1L A93569  
Escherichia coli 562 -11532620 236908 (db:genpept-bct1) (de:e. coli ilvbn  
operon for ahas-i (acetohydroxy acid synthase).) (nt:ilvb gene product (aa  
1-562)) (le:345) (re:2033) (di:direct) ECILVBN X02541 g41785 Escherichia  
coli 562 -11532620 5000690020 ilvb acetohydroxy acid synthase ahas i  
(sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli acetohydroxy acid  
synthase (ahas) i (ilvb) and acetolactatesynthase small subunit (ilvn) genes  
(from the ilv-leu operon),complete cds.) (le:353) (re:2041) (di:direct)  
ECOILVBP J01633 g146455 Escherichia coli 562 -11532620 7500884037 ilvb::cg  
site no. 608 acetohydroxy acid synthase i:small subunit (sr:escherichia coli  
k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the  
region from 81.5 to 84.5 minutes.) (le:40490) (re:42178) (di:complement)  
ECOUW82 L10328 g290520 Escherichia coli 562 -11532620 233191 ilvb  
acetolactate synthase i:valine-sensitive:large (fn:enzyme; amino acid  
biosynthesis: isoleucine,) (db:genpept-bct2) (ec:4.1.3.18) (de:escherichia  
coli k-12 mg1655 section 334 of 400 of the completegenome.) (nt:f562; 100  
pct identical to ilvb\_ecoli sw: p08142;) (le:10910) (re:12598)  
(di:complement) AE000444 AE000444 g1790104 Escherichia coli 562 -11532620  
79236 ilvb (ec:4.1.3.18) (de:(acetohydroxy-acid synthase i large subunit)  
(als-i)) (db:swissprot) ILVB\_ECOLI P08142 ESCHERICHIA COLI 562 -11532620

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501820743	7127	29283	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820746	7128	29284	327	108

Description

GTC ORF with score 215 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820747	7129	29285	210	69

Description

6500728763 ilvg\_1:b3767 acetohydroxy acid synthase ii:large subunit (gtcfc:1.11:1.12:5.7:9.5) (ec:4.1.3.18) (keggfc:1.11:1.12:5.7:9.5) (rileyfc:1.4.7) (db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-c5-branched dibasic acid metabolism:l-amino acid metabolism-valine-... b3767 b3767 Escherichia coli 562 -11532621 7000690843 ilvg\_1 acetohydroxy acid synthase ii:large subunit (cl:acetolactate synthase large chain:thiamine pyrophosphate-binding domain homology) (db:pir2.dat) B65180 B65180 Escherichia coli 562 -11532621 7500954399 ilvg\_1 acetolactate synthase ii:large subunit (fn:enzyme; amino acid biosynthesis: isoleucine,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 343 of 400 of the completegenome.) (nt:o327; cgsc no. 603; inactive in wild-type e. coli) (le:6920) (re:7903) (di:direct) AE000453 AE000453 gl790203 Escherichia coli 562 -11532621 5000690021 (de:(ecoli\_3680) (pn:acetolactate synthase ii, valine insensitive, large subunit, silent in k-12) (gn:ilvg) (gtcfc:1.11:1.12:5.7:9.5) (ec:4.1.3.18) (ilvg\_ecoli) (keggfc:1.11:1.12:5.7:9.5) (rileyfc:1.4.7) (db:gtc-escherichia coli) ECOLI\_3680 ECOLI\_3680 Escherichia coli 562 10124089

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820759	7130	29286	1128	375

#### Description

6500728764 ilvm:b3769 acetohydroxy acid synthase ii:small  
subunit:acetolactate synthase isozyme ii small  
subunit:ahas-ii:acetohydroxy-acid synthase ii small subunit:als-ii  
(gtcfc:1.11:1.12:5.7:9.5) (ec:4.1.3.18) (keggfc:1.11:1.12:5.7:9.5)  
(rileyfc:1.4.7) (db:gtc-escherichia coli) (gtcfc:carbohydrate  
metabolism-butanoate metabolism:carbohydrate metabolism-c5-branched dibasic  
acid metabolism:l-amino acid metabolism-valine-... b3769 b3769 Escherichia  
coli 562 -11532622 162655 ilvm acetolactate synthase:ii small  
chain:acetohydroxy-acid synthase ii (ec:4.1.3.18) (db:pir2.dat) B26570  
B26570 Escherichia coli 562 -11532622 237000 ilvm (db:genpept-bct1)  
(de:e.coli ilvgmeda operon.) (nt:ahasii small subunit) (le:2374) (re:2637)  
(di:direct) ECILVGMED X04890 g288530 Escherichia coli 562 -11532622  
7500959669 ilvm::cgsc no. 18214 acetohydroxy acid synthase ii:small subunit  
(db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to  
86.5 minutes.) (le:5337) (re:5600) (di:direct) ECOUW85 M87049 g148176  
Escherichia coli 562 -11532622 233200 ilvm acetolactate synthase ii:valine  
insensitive (fn:enzyme; amino acid biosynthesis: isoleucine,)  
(db:genpept-bct2) (ec:4.1.3.18) (de:escherichia coli k-12 mg1655 section 343  
of 400 of the completegenome.) (nt:o87; 100 pct identical to ilvm\_ecoli sw:  
p13048) (le:8561) (re:8824) (di:direct) AE000453 AE000453 g1790204  
Escherichia coli 562 -11532622 5000690022 (de:(ecoli\_3681) (pn:acetolactate  
synthase ii, valine insensitive, small subunit) (gn:ilvm)  
(gtcfc:1.11:1.12:5.7:9.5) (ec:4.1.3.18) (ilvm\_ecoli)  
(keggfc:1.11:1.12:5.7:9.5) (rileyfc:1.4.7) (db:gtc-escherichia coli))  
ECOLI\_3681 ECOLI\_3681 Escherichia coli 562 10086569

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820761	7131	29287	576	191

#### Description

GTC ORF with score 290 to: (sr:saccharomyces carlbergensis y379-5d)  
(db:genpept-pln1) (de:yeast (s. carlbergensis) gal7-gal10 region with gal7  
mrna start,gall7 coding sequence 5' end and gall10 coding sequence 3'end.)  
(nt:gall10) (le:1280) (re:2477) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820764	7132	29288	645	214

Description

6500728765 rffd:b3787 udp-mannac  
 dehydrogenase:udp-n-acetyl-d-mannosaminuronic acid dehydrogenase:udp-mannaca  
 dehydrogenase (gtcfc:11.3:11.4:1.5) (ec:1.1.1.-)  
 (keggfc:1.5:1.6:1.7:1.11:3.5:4.3:5.3:5.9:5.13:9.3) (rileyfc:3.3.2)  
 (db:gtc-escherichia coli) (keggfc:carbohydrate metabolism-fructose and  
 mannose metabolism:carbohydrate metabolism-galactose metabolism:carbohydrate  
 me... b3787 b3787 Escherichia coli 562 -11532623 7500894378 wecc:rffd  
 (ec:1.1.1.-) (de:(udp-mannaca dehydrogenase)) (db:swissprot) WECC\_ECOLI  
 P27829 ESCHERICHIA COLI 562 -11532623 7000691928 rffd udp-mannac  
 dehydrogenase:hypothetical protein 379 nfrc 3 region  
 (cl:udp-n-acetyl-d-mannosaminuronic acid dehydrogenase) (db:pir2.dat) F65182  
 F65182 Escherichia coli 562 -11532623 7500894380 wecc  
 udp-n-acetyl-d-mannosaminuronic acid (fn:enzyme; central intermediary  
 metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 345  
 of 400 of the completegenome.) (nt:o420; formerly designated rffd) (le:1177)  
 (re:2439) (di:direct) AE000455 AE000455 g2367284 Escherichia coli 562  
 -11532623

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820776	7133	29289	342	114

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820777	7134	29290	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820788	7135	29291	678	225

Description

6500728766 pfld:b3951 formate acetyltransferase 2:pyruvate formate-lyase 2 (gtcfc:1.11:1.8:2.2) (ec:2.3.1.54) (keggfc:1.8:1.11) (rileyfc:1.2.7) (db:gtc-escherichia coli) b3951 b3951 Escherichia coli 562 -11532624 89199 pfld (ec:2.3.1.54) (de:formate acetyltransferase 2, (pyruvate formate-lyase 2)) (db:swissprot) PFLD\_ECOLI P32674 ESCHERICHIA COLI 562 -11532624 7000686123 pfld formate c-acetyltransferase:2:pyruvate formate-lyase ii (cl:formate c-acetyltransferase 2:glycyl radical homology) (ec:2.3.1.54) (db:pir2.dat) (mp:89.3) B65202 B65202 Escherichia coli 562 -11532624 237169 pfld formate acetyltransferase 2 (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (ec:2.3.1.54) (de:escherichia coli k-12 mg1655 section 359 of 400 of the completegenome.) (nt:o765; 100 pct identical amino acid sequence and) (le:1763) (re:4060) (di:direct) AE000469 AE000469 g1790388 Escherichia coli 562 -11532624 7500887894 (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:similar to e. coli pyruvate formate-lyase) (le:9236) (re:11533) (di:direct) ECOUW89 U00006 g396298 Escherichia coli 562 -11532624 5000690024 (de:(ecoli\_3849) (pn:formate acetyltransferase 2) (gn:pfld) (gtcfc:1.11:1.8) (ec:2.3.1.54) (pfld\_ecoli) (keggfc:1.8:1.11) (rileyfc:1.2.7) (db:gtc-escherichia coli)) ECOLI\_3849 ECOLI\_3849 Escherichia coli 562 10031322

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820790	7136	29292	657	218

Description

GTC ORF with score 373 to: (fn:converts p-cumic aldehyde + h2o + nad to) (db:genpept-bct1) (de:pseudomonas putida p-cymene catabolism (cym) and p-cumatecatabolism (cmt) operons and enol-coenzyme a hydratase gene,complete cds.) (nt:cymc) (le:4105) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820803	7137	29293	1401	466

Description

6500728767 frdd:b4151 fumarate reductase:membrane anchor polypeptide:fumarate reductase 13 kd hydrophobic protein (gtcfc:1.11:1.2:2.1:2.5:2.8:11.1:12.13) (ec:1.3.99.1) (keggfc:1.2:1.11:2.1:2.4:12.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-citrate cycle (tca cycle):energy metabolism-oxida... b4151 b4151 Escherichia coli 562 -11532625 233782 frdd (de:fumarate reductase 13 kd hydrophobic protein) (db:swissprot) FRDD\_ECOLI P03806 ESCHERICHIA COLI 562 -11532625 122710 frdd fumarate reductase:13k membrane anchor protein (cl:fumarate reductase 13k protein) (ec:1.3.99.1) (db:pir1.dat) (mp:94 min) WMEC13 A04431 Escherichia coli 562 -11532625 5000690025 (db:genpept-bct1) (de:fragments of the e. coli genes frdb and ampc. frd is the gene forfumarate reductase and ampc codes for a beta-lactamase (e.colik-12). two unknown reading frames are also found.) (nt:unknown gene) (le:448) (re:807) (di:direct) ECFRDB V00277 g41484 Escherichia coli 562 -11532625 237359 (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli frd operon, fumarate reductase (flavoprotein subunit frdaand iron/sulfur subunit frdb), and beta-lactamase (ampc) genes,complete cds.) (nt:g13 protein) (le:3734) (re:4093) (di:direct) ECOAMPCFR J01611 g145266 Escherichia coli 562 -11532625 7500881746 frdd fumarate reductase:membrane anchor polypeptide (db:genpept-bct1) (ec:1.3.99.1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 739) (le:69835) (re:70194) (di:complement) ECOUW93 U14003 g536995 Escherichia coli 562 -11532625 232913 frdd fumarate reductase:anaerobic:membrane anchor (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (ec:1.3.99.1) (de:escherichia coli k-12 mg1655 section 377 of 400 of the completegenome.) (nt:f119; 100 pct identical to frdd\_ecoli sw: p03806;) (le:10497) (re:10856) (di:complement) AE000487 AE000487 g1790594 Escherichia coli 562 -11532625 72316 frdd (de:fumarate reductase 13 kd hydrophobic protein) (db:swissprot) FRDD\_ECOLI P03806 ESCHERICHIA COLI 562 -11532625

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820814	7138	29294	726	241

Description

GTC ORF with score 100 to: (sr:african clawed frog) (db:genpept-vrt) (de:xenopus laevis middle molecular weight neurofilament proteinnf-m(1) mrna, complete cds.) (nt:neuronal intermediate filament protein; duplicated) (le:11) (re:2704) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820829	7139	29295	957	319

Description

6500728768 frdc:b4152 fumarate reductase:membrane anchor polypeptide:fumarate reductase 15 kd hydrophobic protein (gtcfc:1.11:1.2:2.1:2.5:2.8:11.1:12.13) (ec:1.3.99.1) (keggfc:1.2:1.11:2.1:2.4:12.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-citrate cycle (tca cycle):energy metabolism-oxida... b4152 b4152 Escherichia coli 562 -11532626 233781 frdc (de:fumarate reductase 15 kd hydrophobic protein) (db:swissprot) FRDC\_ECOLI P03805 ESCHERICHIA COLI 562 -11532626 136583 frdc succinate dehydrogenase:frdc:fumarate reductase:membrane anchor polypeptide (cl:fumarate reductase 15k protein) (ec:1.3.99.1) (db:pir2.dat) S56380 S56380 Escherichia coli 562 -11532626 5000690026 (db:genpept-bct1) (de:fragments of the e. coli genes frdb and ampc. frd is the gene for fumarate reductase and ampc codes for a beta-lactamase (e.colik-12). two unknown reading frames are also found.) (nt:unknown gene) (le:42) (re:437) (di:direct) ECFRDB V00277 g41483 Escherichia coli 562 -11532626 237360 (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli frd operon, fumarate reductase (flavoprotein subunit frdaand iron/sulfur subunit frdb), and beta-lactamase (ampc) genes, complete cds.) (nt:g15 protein) (le:3328) (re:3723) (di:direct) ECOAMPCFR J01611 g145265 Escherichia coli 562 -11532626 7500881743 frdc fumarate reductase:membrane anchor polypeptide (db:genpept-bct1) (ec:1.3.99.1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 740) (le:70205) (re:70600) (di:complement) ECOUW93 U14003 g536996 Escherichia coli 562 -11532626 232912 frdc fumarate reductase:anaerobic:membrane anchor (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (ec:1.3.99.1) (de:escherichia coli k-12 mg1655 section 377 of 400 of the complete genome.) (nt:f131; 100 pct identical to frdc\_ecoli sw: p03805;) (le:10867) (re:11262) (di:complement) AE000487 AE000487 g1790595 Escherichia coli 562 -11532626 72311 frdc (de:fumarate reductase 15 kd hydrophobic protein) (db:swissprot) FRDC\_ECOLI P03805 ESCHERICHIA COLI 562 -11532626

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820831	7140	29296	528	175

Description

6500728769 frdb:b4153 fumarate reductase iron-sulfur protein  
 (gtcfc:1.2:2.1:2.5:2.8:11.1:12.13) (ec:1.3.99.1)  
 (keggfc:1.2:1.11:2.1:2.4:12.1) (rileyfc:1.2.6) (db:gtc-escherichia coli)  
 (gtcfc:carbohydrate metabolism-citrate cycle (tca cycle):energy  
 metabolism-oxidative phosphorylation:energy metabolism-reductive c... b4153  
 b4153 Escherichia coli 562 -11532627 122702 frdb fumarate  
 reductase:iron-sulfur protein (cl:fumarate reductase iron-sulfur  
 protein:ferredoxin 2(4fe-4s) homology:ferredoxin (2fe-2s) homology)  
 (ec:1.3.99.1) (db:pir1.dat) (mp:94 min) RDECFS A00377 Escherichia coli 562  
 -11532627 237361 frdb fumarate reductase iron-sulfur subunit  
 (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli frd  
 operon, fumarate reductase (flavoprotein subunit frdaand iron/sulfur subunit  
 frdb), and beta-lactamase (ampc) genes,complete cds.) (le:2583) (re:3317)  
 (di:direct) ECOAMPCFR J01611 g145264 Escherichia coli 562 -11532627  
 7500953197 frdb fumarate reductase:iron-sulfur protein (db:genpept-bct1)  
 (ec:1.3.99.1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1  
 minutes.) (nt:cg site no. 741) (le:70611) (re:71345) (di:complement) ECOUW93  
 U14003 g536997 Escherichia coli 562 -11532627 233780 frdb fumarate  
 reductase:anaerobic:iron-sulfur (fn:enzyme; energy metabolism, carbon:  
 anaerobic) (db:genpept-bct2) (ec:1.3.99.1) (de:escherichia coli k-12 mg1655  
 section 377 of 400 of the completegenome.) (nt:f244; 100 pct identical to  
 frdb\_ecoli sw: p00364;) (le:11273) (re:12007) (di:complement) AE000487  
 AE000487 g1790596 Escherichia coli 562 -11532627 5000690027  
 (de:(ecoli\_4039) (pn:fumarate reductase, anaerobic, iron-sulfur protein  
 subunit) (gn:frdb) (gtcfc:1.11:1.2:2.1:2.5) (ec:1.3.99.1) (frdb\_ecoli)  
 (keggfc:1.2:1.11:2.1:2.4) (rileyfc:1.2.6) (db:gtc-escherichia coli))  
 ECOLI\_4039 ECOLI\_4039 Escherichia coli 562 10065595

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820844	7141	29297	252	83

Description

Hypothetical protein



ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820845	7142	29298	1164	387

#### Description

6500728770 frda:b4154 fumarate reductase flavoprotein subunit  
 (gtcfc:1.11:1.2:2.1:2.5:2.8:12.13) (ec:1.3.99.1)  
 (keggfc:1.2:1.11:2.1:2.4:12.1) (rileyfc:1.2.6) (db:gtc-escherichia coli)  
 (gtcfc:carbohydrate metabolism-butanoate metabolism:carbohydrate  
 metabolism-citrate cycle (tca cycle):energy metabolism-oxidative ... b4154  
 b4154 Escherichia coli 562 -11532628 122695 frda fumarate  
 reductase:flavoprotein (cl:fumarate reductase flavoprotein:3-oxosteroid  
 1-dehydrogenase homology:fumarate reductase flavoprotein homology)  
 (ec:1.3.99.1) (db:pir1.dat) (mp:94 min) RDECFF A00376 Escherichia coli 562  
 -11532628 7500953195 frda fumarate reductase:flavoprotein subunit  
 (db:genpept-bct1) (ec:1.3.99.1) (de:escherichia coli k-12 chromosomal region  
 from 92.8 to 00.1 minutes.) (nt:cg site no. 742) (le:71338) (re:73146)  
 (di:complement) ECOUW93 U14003 g536998 Escherichia coli 562 -11532628  
 237362 frda fumarate reductase:anaerobic:flavoprotein (fn:enzyme; energy  
 metabolism, carbon: anaerobic) (db:genpept-bct2) (ec:1.3.99.1)  
 (de:escherichia coli k-12 mg1655 section 377 of 400 of the completegenome.)  
 (nt:f602; 100 pct identical to frda\_ecoli sw: p00363;) (le:12000) (re:13808)  
 (di:complement) AE000487 AE000487 g1790597 Escherichia coli 562 -11532628  
 5000690028 (de:(ecoli\_4040) (pn:fumarate reductase, anaerobic, flavoprotein  
 subunit) (gn:frda) (gtcfc:1.11:1.2:2.1:2.5) (ec:1.3.99.1) (frda\_ecoli)  
 (keggfc:1.2:1.11:2.1:2.4) (rileyfc:1.2.6) (db:gtc-escherichia coli))  
 ECOLI\_4040 ECOLI\_4040 Escherichia coli 562 10065593

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501820855	7143	29299	330	109

#### Description

6500728771 acnb:b0118 aconitate hydratase 2:citrate hydro-lyase 2:aconitase  
 2 (gtcfc:1.2:1.9:2.5) (ec:4.2.1.3) (keggfc:1.2:1.9:2.4) (rileyfc:5.8.0)  
 (db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-citrate cycle (tca  
 cycle):carbohydrate metabolism-glyoxylate and dicarboxylate  
 metabolism:energy metabolism-reductive carboxy... b0118 b0118 Escherichia  
 coli 562 -11532629 109606 acnb (ec:4.2.1.3) (de:(aconitase 2))  
 (db:swissprot) ACO2\_ECOLI P36683 ESCHERICHIA COLI 562 -11532629 7000684502  
 acnb aconitate hydratase:2 (ec:4.2.1.3) (db:pir2.dat) F64734 F64734  
 Escherichia coli 562 -11532629 7500876327 acnb aconitate hydrase b  
 (fn:enzyme; energy metabolism, carbon: tca cycle) (db:genpept-bct2)  
 (ec:4.2.1.3) (de:escherichia coli k-12 mg1655 section 11 of 400 of the  
 completegenome.) (nt:o865; 100 pct identical to aco2\_ecoli sw: p36683)  
 (le:3896) (re:6493) (di:direct) AE000121 AE000121 g2367097 Escherichia coli  
 562 -11532629

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820856	7144	29300	282	93

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820866	7145	29301	291	96

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820873	7146	29302	780	259

Description

GTC ORF with score 124 to: (sr:african clawed frog) (db:genpept-vrt)  
(de:xenopus laevis middle molecular weight neurofilament proteinnf-m(2)  
mrna, complete cds.) (nt:neuronal intermediate filament protein; duplicated)  
(le:31) (re:2772) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820883	7147	29303	525	174

Description

6500728772 prpc:b0333 hypothetical protein:possible citrate synthase 2  
(gtcfc:1.2:1.9) (ec:4.1.3.7) (keggfc:1.2:1.9) (rileyfc:5.7.0)  
(db:gtc-escherichia coli) b0333 b0333 Escherichia coli 562 -11532630 64690  
prpc (ec:4.1.3.7) (de:possible citrate synthase 2,) (db:swissprot)  
CISZ\_ECOLI P31660 ESCHERICHIA COLI 562 -11532630 7000684825 prbc citrate si  
-synthase::citrate synthase ii:citrate-condensing  
enzyme:citrogenase:oxaloacetate transacetase (cl:citrate (si)-synthase)  
(ec:4.1.3.7) (db:pir2.dat) E64760 E64760 Escherichia coli 562 -11532630  
7500878771 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.)  
(nt:similar to e. coli glta citrate synthase) (le:57807) (re:58976)  
(di:direct) ECU73857 U73857 g1657529 Escherichia coli 562 -11532630 239950  
prpc putative citrate synthase:propionate (fn:putative enzyme; not  
classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 30 of  
400 of the completegenome.) (nt:o389; 37 pct identical (2 gaps) to 377  
residues of) (le:4860) (re:6029) (di:direct) AE000140 AE000140 g1786527  
Escherichia coli 562 -11532630 5000691521 (de:(ecoli\_317) (pn:function not  
assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0)  
(db:gtc-escherichia coli)) ECOLI\_317 ECOLI\_317 Escherichia coli 562 10122782

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820884	7148	29304	555	184

Description

6500728773 citf:b0615 hypothetical protein:citrate lyase alpha chain:citrace (gtcfc:1.2:2.5) (ec:4.1.3.6) (keggfc:1.2:2.4) (rileyfc:5.7.0) (db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-citrate cycle (tca cycle):energy metabolism-reductive carboxylate cycle (co2 fixation)) (keggfc:carbohydrate metabolism-citrate cycle... b0615 b0615 Escherichia coli 562 -11532631 1500686908 citf (ec:4.1.3.6:2.8.3.10) (de:transferase subunit),) (db:swissprot) CILA\_ECOLI P75726 ESCHERICHIA COLI 562 -11532631 7000684814 citf citrate pro-3s -lyase:alpha chain (ec:4.1.3.6) (db:pir2.dat) E64795 E64795 Escherichia coli 562 -11532631 7500878744 citf citrate lyase alpha chain (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 56 of 400 of the completegenome.) (nt:f510 was f195; this 195 aa orf is 74 pct identical) (le:11427) (re:12959) (di:complement) AE000166 AE000166 g1786832 Escherichia coli 562 -11532631 5000691698 (de:(ecoli\_596) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_596 ECOLI\_596 Escherichia coli 562 10062983

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820899	7149	29305	1023	340

Description

6500728774 cite:b0616 hypothetical protein:citrate lyase beta chain:acyl lyase subunit:citrace (gtcfc:1.2:2.5) (ec:4.1.3.6) (keggfc:1.2:2.4) (rileyfc:5.7.0) (db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-citrate cycle (tca cycle):energy metabolism-reductive carboxylate cycle (co2 fixation)) (keggfc:carbohydrate metabolism-citrate cycle... b0616 b0616 Escherichia coli 562 -11532632 7000684815 cite citrate pro-3s -lyase:beta chain (ec:4.1.3.6) (db:pir2.dat) F64795 F64795 Escherichia coli 562 -11532632 240129 putative citrate lyase beta chain (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to h. influenzae hi0023) (le:90212) (re:91135) (di:complement) ECU82598 U82598 g1778533 Escherichia coli 562 -11532632 7500959890 cite citrate lyase beta chain acyl lyase subunit (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 56 of 400 of the completegenome.) (nt:f307; this 307 aa orf is 76 pct identical (1 gap)) (le:12970) (re:13893) (di:complement) AE000166 AE000166 g1786833 Escherichia coli 562 -11532632 1500686909 cilb\_ecoli (de:citrate lyase beta chain, \ (acyl lyase subunit\ \ (citrace\),) P77770 P77770 Escherichia coli 562 -11532632 5000691699 (de:(ecoli\_597) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_597 ECOLI\_597 Escherichia coli 562 10062984

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820902	7150	29306	534	177

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820904	7151	29307	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820919	7152	29308	1530	509

Description

6500728775 glta:glut:icdb:b0720 glta:citrate synthase (gtcfc:1.2:1.9)  
(ec:4.1.3.7) (keggfc:1.2:1.9) (rileyfc:1.2.3) (db:gtc-escherichia coli)  
b0720 b0720 Escherichia coli 562 -11532633 7000688884 glta:glut:icdb  
citrate si -synthase (cl:citrate (si)-synthase) (ec:4.1.3.7) (db:pirl.dat)  
(mp:17 min) YKEC G64807 Escherichia coli 562 -11532633 223168 glta citrate  
synthase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #176)  
(db:genpept-bct1) (de:escherichia coli genomic dna. (16.1 - 16.4 min).)  
(le:2409) (re:3692) (di:complement) D90711 D90711 g1651316 Escherichia coli  
562 -11532633 7500953327 glta citrate synthase (fn:enzyme; energy  
metabolism, carbon: tca cycle) (db:genpept-bct2) (de:escherichia coli k-12  
mg1655 section 65 of 400 of the completegenome.) (nt:f427; 97 pct identical  
to cisy\_ecoli sw: p00891;) (le:5348) (re:6631) (di:complement) AE000175  
AE000175 g1786939 Escherichia coli 562 -11532633 5000690029 glta citrate  
synthase ec 4.1.3.7 . (sr:escherichia coli(strain:k12) dna, clone:kohara  
clone #176) (db:genpept) (de:escherichia coli genomic dna. (16.2 - 16.5  
min).) (nt:orf\_id:o176#2; similar to swissprot accession) (le:2409)  
(re:3692) (di:complement) D90711 D90711 g1651316 Escherichia coli 562  
-11532633

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820941	7153	29309	1029	342
<u>Description</u>				
6500728776 suca:b0726 2-oxoglutarate dehydrogenase e1 component:alpha-ketoglutarate dehydrogenase (gtcfc:1.2:5.14:5.9) (ec:1.2.4.2) (keggfc:1.2:5.9:5.14) (rileyfc:1.2.3) (db:gtc-escherichia coli) b0726 b0726 Escherichia coli 562 -11532634 87460 suca (ec:1.2.4.2) (de:ketoglutarate dehydrogenase)) (db:swissprot) ODO1_ECOLI P07015 ESCHERICHIA COLI 562 -11532634 7000686034 suca oxoglutarate dehydrogenase lipoamide::2-oxoglutarate dehydrogenase complex e1 component:alpha-ketoglutaric dehydrogenase:oxoglutarate decarboxylase (cl:oxoglutarate dehydrogenase (lipoamide):thiamine pyrophosphate-binding domain homology) (ec:1.2.4.2) (db:pir1.dat) (mp:17 min) DEECOG E64808 Escherichia coli 562 -11532634 223173 suca oxoglutarate dehydrogenase lipoamide (sr:escherichia coli(strain:k12) dna, clone:kohara clone #176) (db:genpept-bct1) (de:escherichia coli genomic dna. (16.1 - 16.4 min).) (le:7930) (re:10731) (di:direct) D90711 D90711 g1651321 Escherichia coli 562 -11532634 7500887096 suca 2-oxoglutarate dehydrogenase decarboxylase (fn:enzyme; energy metabolism, carbon: tca cycle) (db:genpept-bct2) (ec:1.2.4.2) (de:escherichia coli k-12 mgl655 section 65 of 400 of the completegenome.) (nt:o933; 99 pct identical to odo1_ecoli sw: p07015) (le:10869) (re:13670) (di:direct) AE000175 AE000175 g1786945 Escherichia coli 562 -11532634 5000690030 suca oxoglutarate dehydrogenase lipoamide ec (sr:escherichia coli(strain:k12) dna, clone:kohara clone #176) (db:genpept) (de:escherichia coli genomic dna. (16.2 - 16.5 min).) (nt:orf_id:o176#7; similar to pir accession number) (le:7930) (re:10731) (di:direct) D90711 D90711 g1651321 Escherichia coli 562 -11532634				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820955	7154	29310	762	253

Description

6500728777 suchb:b0727 e2:dihydrolipoamide succinyltransferase component:e2 of 2-oxoglutarate dehydrogenase complex (gtcfc:1.2) (ec:2.3.1.61) (keggfc:1.2) (rileyfc:1.2.3) (db:gtc-escherichia coli) b0727 b0727 Escherichia coli 562 -11532635 7000686036 suchb dihydrolipoamide s-succinyltransferase::2-oxoglutarate dehydrogenase complex e2 component (cl:dihydrolipoamide acetyltransferase:lipoyl/biotin-binding homology) (ec:2.3.1.61) (db:pir1.dat) (mp:17 min) XUECSD F64808 Escherichia coli 562 -11532635 223174 suchb dihydrolipoamide succinyltransferase component (sr:escherichia coli(strain:k12) dna, clone:kohara clone #176) (db:genpept-bct1) (de:escherichia coli genomic dna. (16.1 - 16.4 min).) (le:10746) (re:11963) (di:direct) D90711 D90711 g1651322 Escherichia coli 562 -11532635 238315 suchb dihydrolipoamide succinyltransferase (sr:escherichia coli k12 dna) (db:genpept-bct1) (ec:2.3.1.61) (de:e.coli glta gene, sdhcdab operon and sucabcd operon encoding ninecomplete proteins.) (le:9425) (re:10642) (di:direct) ECOGLTA J01619 g146202 Escherichia coli 562 -11532635 7500887099 (db:genpept-bct1) (de:e.coli suchb gene for dihydrolipoamide succinyltransferase.) (nt:e20 component) (le:23) (re:1240) (di:direct) ECSUCB X00664 g43022 Escherichia coli 562 -11532635 234534 suchb 2-oxoglutarate dehydrogenase (fn:enzyme; energy metabolism, carbon: tca cycle) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 65 of 400 of the completegenome.) (nt:o405; 100 pct identical to odo2\_ecoli sw: p07016) (le:13685) (re:14902) (di:direct) AE000175 AE000175 g1786946 Escherichia coli 562 -11532635 5000690031 suchb dihydrolipoamide succinyltransferase component (sr:escherichia coli(strain:k12) dna, clone:kohara clone #176) (db:genpept) (de:escherichia coli genomic dna. (16.2 - 16.5 min).) (nt:orf\_id:o177#1; similar to swissprot accession) (le:10746) (re:11963) (di:direct) D90711 D90711 g1651322 Escherichia coli 562 -11532635 87468 suchb (ec:2.3.1.61) (de:dehydrogenase complex,) (db:swissprot) ODO2\_ECOLI P07016 ESCHERICHIA COLI 562 -11532635

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820969	7155	29311	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501820973	7156	29312	285	94

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821004	7157	29313	2826	941
<u>Description</u>				
6500728778 icd:icda:icde:b1136 isocitrate dehydrogenase:nadp:oxalosuccinate decarboxylase:ldh:nadp+-specific icdh:ldh (gtcfc:1.2:2.5:6.16) (ec:1.1.1.42) (keggfc:1.2:2.4:6.9) (rileyfc:5.8.0) (db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-citrate cycle (tca cycle):energy metabolism-reductive carboxylate cycle (co2 fixation):metabolism of other amino acids-glut... b1136 b1136 Escherichia coli 562 -11532636 78804 icd:icda:icde (ec:1.1.1.42) (de:decarboxylase) (ldh) (nadp+-specific icdh) (ldh)) (db:swissprot) IDH_ECOLI P08200 ESCHERICHIA COLI 562 -11532636 122554 icda:icd:icde isocitrate dehydrogenase nadp+:oxalosuccinate decarboxylase (cl:isocitrate dehydrogenase (nadp)) (ec:1.1.1.42) (db:pir1.dat) (mp:25 min) DCECIS A28482 Escherichia coli 562 -11532636 223379 icda isocitrate dehydrogenase nadp (sr:escherichia coli(strain:k12) dna, clone:kohara clone #239) (db:genpept-bct1) (de:escherichia coli genomic dna.(25.6 - 26.0 min).) (le:11357) (re:12607) (di:direct) D90748 D90748 g1651560 Escherichia coli 562 -11532636 223384 icda isocitrate dehydrogenase nadp (sr:escherichia coli(strain:k12) dna, clone:kohara clone #240) (db:genpept-bct1) (de:escherichia coli genomic dna.(25.6 - 26.0 min).) (le:5674) (re:6924) (di:direct) D90749 D90749 g1651566 Escherichia coli 562 -11532636 7500883825 (sr:e.coli dna, clone ptk512) (db:genpept-bct1) (de:e.coli icd gene encoding isocitrate dehydrogenase, complete cds.) (nt:isocitrate dehydrogenase (icd; ec 1.1.1.42)) (le:291) (re:1541) (di:direct) ECOICD J02799 g146432 Escherichia coli 562 -11532636 234834 icda isocitrate dehydrogenase:specific for nadp+ (fn:enzyme; energy metabolism, carbon: tca cycle) (db:genpept-bct2) (ec:1.1.1.42) (de:escherichia coli k-12 mg1655 section 103 of 400 of the completegenome.) (nt:o416; 100 pct identical to ldh_ecoli sw: p08200) (le:9434) (re:10684) (di:direct) AE000213 AE000213 g1787381 Escherichia coli 562 -11532636 5000690032 icd isocitrate dehydrogenase nadp ec 1.1.1.42 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #239) (db:genpept) (de:escherichia coli genomic dna. (25.6 - 25.9 min).) (nt:orf_id:o240#7; similar to swissprot accession) (le:11357) (re:12607) (di:direct) D90748 D90748 g1651560 Escherichia coli 562 -11532636 7502851787 icd isocitrate dehydrogenase nadp ec 1.1.1.42 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #240) (db:genpept) (de:escherichia coli genomic dna. (25.7 - 26.1 min).) (nt:orf_id:o240#7; similar to swissprot accession) (le:5674) (re:6924) (di:direct) D90749 D90749 g1651566 Escherichia coli 562 -11532636				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821008	7158	29314	264	87

Description

6500728779 acna:acn:b1276 aconitate hydratase 1:citrate hydro-lyase  
1:aconitase 1 (gtcfc:1.2:1.9:2.5) (ec:4.2.1.3) (keggfc:1.2:1.9:2.4)  
(rileyfc:1.2.3) (db:gtc-escherichia coli) (gtcfc:carbohydrate  
metabolism-citrate cycle (tca cycle):carbohydrate metabolism-glyoxylate and  
dicarboxylate metabolism:energy metabolism-reductive carboxy... b1276 b1276  
Escherichia coli 562 -11532637 7000690847 acna:acn aconitate hydratase  
(cl:iron-responsive element-binding protein) (ec:4.2.1.3) (db:pir2.dat)  
G64875 G64875 Escherichia coli 562 -11532637 7500959671 acna aconitate  
hydratase 1 (fn:enzyme; energy metabolism, carbon: tca cycle)  
(db:genpept-bct2) (ec:4.2.1.3) (de:escherichia coli k-12 mg1655 section 115  
of 400 of the completegenome.) (nt:o891; 99 pct identical to acol\_ecoli sw:  
p25516; cg) (le:9115) (re:11790) (di:direct) AE000225 AE000225 g1787531  
Escherichia coli 562 -11532637 5000690033 (de:(ecoli\_1236) (pn:aconitate  
hydratase a) (gn:acna) (gtcfc:1.2:1.9:2.5) (ec:4.2.1.3) (acol\_ecoli)  
(keggfc:1.2:1.9:2.4) (rileyfc:1.2.3) (db:gtc-escherichia coli)) ECOLI\_1236  
ECOLI\_1236 Escherichia coli 562 10123249

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821012	7159	29315	294	97

Description

6500728780 fumc:b1611 fumarate hydratase class ii:fumarase (gtcfc:1.2:2.5) (ec:4.2.1.2) (keggfc:1.2:2.4) (rileyfc:1.2.3) (db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-citrate cycle (tca cycle):energy metabolism-reductive carboxylate cycle (co2 fixation)) (keggfc:carbohydrate metabolism-citrate cycle... b1611 b1611 Escherichia coli 562 -11532638  
300732 fumc (ec:4.2.1.2) (de:fumarate hydratase class ii, (fumarase)) (db:swissprot) FUMC\_ECOLI P05042 ESCHERICHIA COLI 562 -11532638 125624 fumc fumarate hydratase:fumc:fumarase c:fumarate hydratase class ii:protein g48 (cl:fumarate hydratase) (ec:4.2.1.2) (db:pir1.dat) (mp:35.5 min) UFEC S07138 Escherichia coli 562 -11532638 224027 fumc fumarate hydratase ec 4.2.1.2 fumc (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #312(36.0-36.3 min.)) (nt:orf\_id:o312#11; similar to (pir accession number) (le:12891) (re:14294) (di:complement) D90803 D90803 g1742650 Escherichia coli 562 -11532638 224037 fumc fumarate hydratase ec 4.2.1.2 fumc (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #313(36.1-36.4 min.)) (nt:orf\_id:o312#11; similar to (pir accession number) (le:9005) (re:10408) (di:complement) D90804 D90804 g1742661 Escherichia coli 562 -11532638  
5000690034 fumarase fumc:aa 1-467 (db:genpept-bct1) (de:e. coli fumc gene for fumarase (ec 4.2.1.2).) (le:163) (re:1566) (di:direct) ECFUMC X04065 g41513 Escherichia coli 562 -11532638 232939 fumc fumarase c= fumarate hydratase class ii (fn:enzyme; energy metabolism, carbon: tca cycle) (db:genpept-bct2) (ec:4.2.1.2) (de:escherichia coli k-12 mg1655 section 146 of 400 of the completegenome.) (nt:f467; 100 pct identical to fumc\_ecoli sw: p05042;) (le:7127) (re:8530) (di:complement) AE000256 AE000256 g1787896 Escherichia coli 562 -11532638 72523 fumc (ec:4.2.1.2) (de:fumarate hydratase class ii, (fumarase)) (db:swissprot) FUMC\_ECOLI P05042 ESCHERICHIA COLI 562 -11532638

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821018	7160	29316	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821023	7161	29317	438	145

Description

6500728781 fuma:b1612 fumarate hydratase class i:fumarate hydratase class i:aerobic:fumarase (gtcfc:1.2:2.5) (ec:4.2.1.2) (keggfc:1.2:2.4) (rileyfc:1.2.3) (db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-citrate cycle (tca cycle):energy metabolism-reductive carboxylate cycle (co2 fixation)) (keggfc:carbohydrate metabolism-citrate cycle... b1612 b1612 Escherichia coli 562 -11532639 125616 fuma fumarate hydratase:fuma:iron-dependent:fumarase:fumarate hydratase class i (cl:iron-dependent fumarate hydratase:iron-dependent tartrate dehydratase alpha chain homology:iron-dependent tartrate dehydratase beta chain homology) (ec:4.2.1.2) (db:pir1.dat) (mp:35.5 min) UFECAQ A03531 Escherichia coli 562 -11532639 224038 fuma fumarate hydratase ec 4.2.1.2 fuma (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #313(36.1-36.4 min.)) (nt:orf\_id:o312#12; similar to (pir accession number) (le:10551) (re:12197) (di:complement) D90804 D90804 g1742662 Escherichia coli 562 -11532639 300737 fuma fumarate hydratase ec 4.2.1.2 fuma (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #314(36.3-36.7 min.)) (nt:orf\_id:o312#12; similar to (pir accession number) (le:1415) (re:3061) (di:complement) D90805 D90805 g1742667 Escherichia coli 562 -11532639 300733 (db:genpept-bct1) (de:fumarase gene fuma from escherichia coli.) (nt:fumarase) (le:357) (re:2003) (di:direct) ECFUMA X00522 g41511 Escherichia coli 562 -11532639 232937 fuma fumarase a = fumarate hydratase class i:aerobic (fn:enzyme; energy metabolism, carbon: tca cycle) (db:genpept-bct2) (ec:4.2.1.2) (de:escherichia coli k-12 mg1655 section 146 of 400 of the completegenome.) (nt:f548; 100 pct identical to fuma\_ecoli sw: p00923;) (le:8673) (re:10319) (di:complement) AE000256 AE000256 g1787897 Escherichia coli 562 -11532639 224042 fuma fumarate hydratase ec 4.2.1.2 fuma (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #314(36.3-36.7 min.)) (nt:orf\_id:o312#12; similar to (pir accession number) (le:1415) (re:3061) (di:complement) D90805 D90805 g1742667 Escherichia coli 562 -11532639 5000690035 (de:(ecoli\_1571) (pn:fumarase a , fumarate hydratase class i; aerobic isozyme:fumarase a ) (gn:fuma) (gtcfc:1.2:2.5) (ec:4.2.1.2) (fuma\_ecoli) (keggfc:1.2:2.4) (rileyfc:1.2.3) (db:gtc-escherichia coli)) ECOLI\_1571 ECOLI\_1571 Escherichia coli 562 10066374

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821028	7162	29318	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821040	7163	29319	378	125

Description

6500728782 mdh:b3236 malate dehydrogenase (gtcfc:1.2:1.8:1.9:2.4:2.5)  
(ec:1.1.1.37) (keggfc:1.2:1.8:1.9:2.3:2.4) (rileyfc:1.2.3)  
(db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-citrate cycle (tca  
cycle):carbohydrate metabolism-pyruvate and acetyl-coa  
metabolism:carbohydrate metabolism... b3236 b3236 Escherichia coli 562  
-11532640 83312 mdh (ec:1.1.1.37) (de:malate dehydrogenase,) (db:swissprot)  
MDH\_ECOLI P06994 ESCHERICHIA COLI 562 -11532640 7000685808 mdh malate  
dehydrogenase (cl:l-lactate dehydrogenase) (ec:1.1.1.37) (db:pir1.dat)  
(mp:70 min) DEECM F65115 Escherichia coli 562 -11532640 7500885426 mdh  
malate dehydrogenase (db:genpept-bct1) (ec:1.1.1.37) (de:escherichia coli  
k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 523;  
different end due to fs in) (le:164075) (re:165013) (di:complement) ECOUW67  
U18997 g606175 Escherichia coli 562 -11532640 236474 mdh malate  
dehydrogenase (fn:enzyme; energy metabolism, carbon: tca cycle)  
(db:genpept-bct2) (ec:1.1.1.37) (de:escherichia coli k-12 mg1655 section 293  
of 400 of the completegenome.) (nt:f312; cg site no. 523; different end due  
to fs in) (le:62) (re:1000) (di:complement) AE000403 AE000403 g1789632  
Escherichia coli 562 -11532640 5000690036 (de:(ecoli\_3159) (pn:malate  
dehydrogenase) (gn:mdh) (gtcfc:1.2:1.8:1.9:2.4:2.5) (ec:1.1.1.37)  
(mdh\_ecoli) (keggfc:1.2:1.8:1.9:2.3:2.4) (rileyfc:1.2.3) (db:gtc-escherichia  
coli)) ECOLI\_3159 ECOLI\_3159 Escherichia coli 562 10025530

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821053	7164	29320	273	90

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821056	7165	29321	234	77

Description

6500728783 fumb:b4122 fumarate hydratase class i:anaerobic:fumarase  
 (gtcfc:1.2:2.5) (ec:4.2.1.2) (keggfc:1.2:2.4) (rileyfc:1.2.3)  
 (db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-citrate cycle (tca  
 cycle):energy metabolism-reductive carboxylate cycle (co2 fixation))  
 (keggfc:carbohydrate metabolism-citrate cycle... b4122 b4122 Escherichia  
 coli 562 -11532641 7000688891 fumb fumarate  
 hydratase:fumb:iron-dependent:fumarase b (cl:iron-dependent fumarate  
 hydratase:iron-dependent tartrate dehydratase alpha chain  
 homology:iron-dependent tartrate dehydratase beta chain homology)  
 (ec:4.2.1.2) (db:pir1.dat) (mp:93.5 min) B44511 A65222 Escherichia coli 562  
 -11532641 7500953336 fumb fumarase b= fumarate hydratase class i  
 (fn:enzyme; energy metabolism, carbon: tca cycle) (db:genpept-bct2)  
 (ec:4.2.1.2) (de:escherichia coli k-12 mg1655 section 375 of 400 of the  
 completegenome.) (nt:f548; 99 pct identical amino acid sequence and) (le:91)  
 (re:1737) (di:complement) AE000485 AE000485 g1790564 Escherichia coli 562  
 -11532641 5000690038 (de:(ecoli\_4009) (pn:fumarase b, fumarate hydratase  
 class i; anaerobic isozyme:fumarase b) (gn:fumb) (gtcfc:1.2:2.5)  
 (ec:4.2.1.2) (fumb\_ecoli) (keggfc:1.2:2.4) (rileyfc:1.2.3)  
 (db:gtc-escherichia coli)) ECOLI\_4009 ECOLI\_4009 Escherichia coli 562  
 10124150

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821058	7166	29322	213	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821104	7167	29323	594	197

Description

6500728784 talb:b0008 transaldolase b (gtcfc:1.3) (ec:2.2.1.2) (keggfc:1.3) (rileyfc:1.2.4) (db:gtc-escherichia coli) b0008 b0008 Escherichia coli 562 -11532642 163371 talb transaldolase:b (ec:2.2.1.2) (db:pir2.dat) S40535 S40535 Escherichia coli 562 -11532642 233549 talb transaldolase (sr:escherichia coli (strain:k-12, sub\_strain:w3110) dna) (db:genpept-bct1) (ec:2.2.1.2) (de:escherichia coli talb gene for transaldolase, complete cds.) (le:1) (re:954) (di:direct) D13161 D13161 g2337776 Escherichia coli 562 -11532642 5500686819 orf (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (nt:transaldolase homolog(swiss:p15019)) (le:7899) (re:8852) (di:direct) ECO110K D10483 g216439 Escherichia coli 562 -11532642 7500960468 talb transaldolase b (sr:escherichia coli k-12) (db:genpept-bct1) (de:talb=transaldolase b (escherichia coli, k-12, genomic, 1139 nt).) (nt:this sequence comes from fig. 1;) (le:103) (re:1056) (di:direct) S80045 S80045 g1839303 Escherichia coli 562 -11532642 293851 talb transaldolase b (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:2.2.1.2) (de:escherichia coli k-12 mg1655 section 1 of 400 of the completegenome.) (nt:o317; 100 pct identical to talb\_ecoli sw: p30148) (le:8238) (re:9191) (di:direct) AE000111 AE000111 g1786189 Escherichia coli 562 -11532642 5000690039 (de:(ecoli\_8) (pn:transaldolase b) (gn:talb) (gtcfc:1.3) (ec:2.2.1.2) (talb\_ecoli) (keggfc:1.3) (rileyfc:1.2.4) (db:gtc-escherichia coli)) ECO110K ECO110K Escherichia coli 562 10086895

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821106	7168	29324	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821113	7169	29325	669	222

Description

GTC ORF with score 310 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821115	71170	29326	360	119

Description

GTC ORF with score 391 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821116	71171	29327	399	133

Description

GTC ORF with score 262 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821117	71172	29328	564	187

Description

GTC ORF with score 559 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821122	71173	29329	417	138

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821125	71174	29330	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821128	71175	29331	219	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821146	7176	29332	471	156

Description

6500728785 gcd:b0124 glucose dehydrogenase:pyrroloquinoline-quinone (gtcfc:9.12:1.4) (ec:1.1.99.17) (keggfc:1.3) (rileyfc:1.1.1) (db:gtc-escherichia coli) b0124 b0124 Escherichia coli 562 -11532643 68515 gcd (ec:1.1.99.17) (de:glucose dehydrogenase (pyrroloquinoline-quinone),) (db:swissprot) DHG\_ECOLI P15877 ESCHERICHIA COLI 562 -11532643 7000685042 gcd glucose dehydrogenase pyrroloquinoline-quinone (cl:glucose dehydrogenase (pyrroloquinoline-quinone)) (ec:1.1.99.17) (db:pir1.dat) (mp:3 min) JV0107 D64735 Escherichia coli 562 -11532643 301602 gcd glucose dehydrogenase (sr:escherichia coli (sub\_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (ec:1.1.99.17) (de:escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0 min).) (le:27444) (re:29834) (di:complement) EC082K D26562 g473791 Escherichia coli 562 -11532643 233664 gcd glucose dehydrogenase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:1.1.99.17) (de:escherichia coli k-12 mg1655 section 12 of 400 of the completegenome.) (nt:f796; 98 pct identical to dhg\_ecoli sw: p15877) (le:131) (re:2521) (di:complement) AE000122 AE000122 g1786316 Escherichia coli 562 -11532643 5000690040 (de:(ecoli\_124) (pn:glucose dehydrogenase) (gn:gcd) (gtcfc:1.3) (ec:1.1.99.17) (dhg\_ecoli) (keggfc:1.3) (rileyfc:1.1.1) (db:gtc-escherichia coli)) ECOLI\_124 ECOLI\_124 Escherichia coli 562 10122671

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821147	7177	29333	1437	479

Description

6500728786 prsa:b1207 ribose-phosphate pyrophosphokinase (gtcfc:1.3:4.1) (ec:2.7.6.1) (keggfc:1.3:4.1) (rileyfc:1.6.1) (db:gtc-escherichia coli) b1207 b1207 Escherichia coli 562 -11532644 7000688868 prsa:prs ribose-phosphate pyrophosphokinase::phosphoribosylpyrophosphate synthetase (cl:ribose-phosphate pyrophosphokinase catalytic chain) (ec:2.7.6.1) (db:pir1.dat) (mp:26 min) KIECRY D64867 Escherichia coli 562 -11532644 7500953269 prsa phosphoribosylpyrophosphate synthetase (fn:enzyme; purine ribonucleotide biosynthesis) (db:genpept-bct2) (ec:2.7.6.1) (de:escherichia coli k-12 mg1655 section 109 of 400 of the completegenome.) (nt:f315; 99 pct identical to kprs\_ecoli sw: p08330 but) (le:4622) (re:5569) (di:complement) AE000219 AE000219 g1787458 Escherichia coli 562 -11532644 5000690041 prs ribose-phosphate pyrophosphokinase ec 2.7.6.1 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #247) (db:genpept) (de:escherichia coli genomic dna. (27.1 - 27.5 min).) (nt:orf\_id:o247#5; similar to swissprot accession) (le:5190) (re:6137) (di:complement) D90756 D90756 g4062790 Escherichia coli 562 -11532644

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821149	7178	29334	474	157
<u>Description</u>				
6500728787 edd:b1851 phosphogluconate dehydratase:6-phosphogluconate dehydratase (gtcfc:1.3:2.1) (ec:4.2.1.12) (keggfc:1.3) (rileyfc:1.2.5) (db:gtc-escherichia coli) b1851 b1851 Escherichia coli 562 -11532645 240392 edd (ec:4.2.1.12) (de:dehydratase)) (db:swissprot) EDD_ECOLI P25530 ESCHERICHIA COLI 562 -11532645 300982 edd phosphogluconate dehydratase ec 4.2.1.12 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #336gap(41.6-41.9 min.)) (nt:orf_id:o336gap#3; similar to (pir accession number) (le:2319) (re:4130) (di:complement) D90828 D90828 g1736494 Escherichia coli 562 -11532645 5000690042 edd phosphogluconate dehydratase (db:genpept-bct1) (ec:4.2.1.12) (de:e.coli genes zwf, edd and eda for glucose-6-phosphate dehydrogenase(partial), 6-phosphogluconate dehydratase andphospho-2-keto-3-deoxygluconate aldolase.) (le:751) (re:2562) (di:direct) ECZWFEDDA X63694 g395403 Escherichia coli 562 -11532645 224342 edd 6-phosphogluconate dehydratase (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:4.2.1.12) (de:escherichia coli k-12 mg1655 section 169 of 400 of the completegenome.) (nt:f603; 100 pct identical to edd_ecoli sw: p25530; cg) (le:2009) (re:3820) (di:complement) AE000279 AE000279 g1788157 Escherichia coli 562 -11532645 69721 edd (ec:4.2.1.12) (de:dehydratase)) (db:swissprot) EDD_ECOLI P25530 ESCHERICHIA COLI 562 -11532645 164303 (de:phosphogluconate dehydratase (ec 4.2.1.12) - escherichia coli) S35911 S35911 Escherichia coli 562 -11532645				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821167	7179	29335	366	121
<u>Description</u>				
6500728788 zwf:b1852 glucose 6-phosphate 1 dehydrogenase:glucose-6-phosphate 1-dehydrogenase:g6pd (gtcfc:1.3:6.16) (ec:1.1.1.49) (keggfc:1.3:6.9) (rileyfc:1.2.4) (db:gtc-escherichia coli) b1852 b1852 Escherichia coli 562 -11532646 72780 zwf (ec:1.1.1.49) (de:glucose-6-phosphate 1-dehydrogenase, (g6pd)) (db:swissprot) G6PD_ECOLI P22992 ESCHERICHIA COLI 562 -11532646 7000685338 zwf glucose-6-phosphate 1-dehydrogenase (cl:glucose-6-phosphate dehydrogenase) (ec:1.1.1.49) (db:pir2.dat) (mp:41 min) D64947 D64947 Escherichia coli 562 -11532646 224343 zwf glucose-6-phosphate 1-dehydrogenase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #336gap(41.6-41.9 min.)) (nt:orf_id:o336gap#4; similar to (swissprot accession) (le:4365) (re:5840) (di:complement) D90828 D90828 g1736495 Escherichia coli 562 -11532646 300983 zwf glucose-6-phosphate dehydrogenase (fn:enzyme; energy metabolism, carbon: oxidative) (db:genpept-bct2) (ec:1.1.1.49) (de:escherichia coli k-12 mg1655 section 169 of 400 of the completegenome.) (nt:f491; residues 1-425 are 94 pct identical (1 gap)) (le:4055) (re:5530) (di:complement) AE000279 AE000279 g1788158 Escherichia coli 562 -11532646 5000690043 (de:(ecoli_1809) (pn:glucose-6-phosphate dehydrogenase) (gn:zwf) (gtcfc:1.3:6.16) (ec:1.1.1.49) (g6pd_ecoli) (keggfc:1.3:6.9) (rileyfc:1.2.4) (db:gtc-escherichia coli)) ECOLI_1809 ECOLI_1809 Escherichia coli 562 10119873				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821171	7180	29336	312	103
<u>Description</u>				
6500728789 gnd:b2029 6-phosphogluconate dehydrogenase:decarboxylating (gtcfc:1.3) (ec:1.1.1.44) (keggfc:1.3) (rileyfc:1.2.4) (db:gtc-escherichia coli) b2029 b2029 Escherichia coli 562 -11532647 57633 gnd (ec:1.1.1.44) (de:6-phosphogluconate dehydrogenase, decarboxylating,) (db:swissprot) 6PGD_ECOLI P00350 ESCHERICHIA COLI 562 -11532647 7000684471 gnd phosphogluconate dehydrogenase decarboxylating::gluconate-6-phosphate dehydrogenase (cl:phosphogluconate dehydrogenase (decarboxylating):3-hydroxyisobutyrate dehydrogenase homology) (ec:1.1.1.44) (db:pir1.dat) (mp:44 min) DEECGC D64968 Escherichia coli 562 -11532647 224552 gnd phosphogluconate dehydrogenase decarboxylating (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #351(45.1-45.5 min..)) (nt:orf_id:o351#2; similar to (pir accession number) (le:6162) (re:7568) (di:complement) D90841 D90841 g1736717 Escherichia coli 562 -11532647 301192 gnd gluconate-6-phosphate dehydrogenase (fn:enzyme; energy metabolism, carbon: oxidative) (db:genpept-bct2) (ec:1.1.1.44) (de:escherichia coli k-12 mg1655 section 184 of 400 of the completegenome.) (nt:f468; 99 pct identical to 6pgd_ecoli sw: p00350; cg) (le:2619) (re:4025) (di:complement) AE000294 AE000294 g1788341 Escherichia coli 562 -11532647 5000690044 (de:(ecoli_1977) (pn:gluconate-6-phosphate dehydrogenase, decarboxylating) (gn:gnd) (gtcfc:1.3) (ec:1.1.1.44) (6pgd_ecoli) (keggfc:1.3) (rileyfc:1.2.4) (db:gtc-escherichia coli)) ECOLI_1977 ECOLI_1977 Escherichia coli 562 10119964				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821172	7181	29337	1044	347
<u>Description</u>				
6500728790 tala:b2464 hypothetical protein:transaldolase a (gtcfc:1.3) (ec:2.2.1.2) (keggfc:1.3) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2464 b2464 Escherichia coli 562 -11532648 7000686751 tala (ec:2.2.1.2) (de:transaldolase a,) (db:swissprot) TALA_ECOLI P78258 ESCHERICHIA COLI 562 -11532648 7000686752 transaldolase:b2464 (ec:2.2.1.2) (db:pir2.dat) G65021 G65021 Escherichia coli 562 -11532648 225027 tala transaldolase (sr:escherichia coli (strain:k-12, sub_strain:w3110) dna, clone:pai235) (db:genpept-bct1) (ec:2.2.1.2) (de:escherichia coli tala gene for transaldolase, complete cds.) (le:150) (re:1100) (di:direct) D13159 D13159 g2337774 Escherichia coli 562 -11532648 5500687862 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #422(55.5-55.8 min.)) (nt:similar to (pir accession number s40535)) (le:1759) (re:2709) (di:direct) D90875 D90875 g1799888 Escherichia coli 562 -11532648 7500892741 tala transaldolase a (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 223 of 400 of the completegenome.) (nt:o316; residues 11-309 are 66 pct identical to) (le:2709) (re:3659) (di:direct) AE000333 AE000333 g1788807 Escherichia coli 562 -11532648 5000692953 (de:(ecoli_2404) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2404 ECOLI_2404 Escherichia coli 562 10120210				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821186	7182	29338	786	261

Description

6500728791 tktb:b2465 transketolase 2:tk 2 (gtcfc:1.3:2.4) (ec:2.2.1.1) (keggfc:1.3:2.3) (rileyfc:1.2.4) (db:gtc-escherichia coli) b2465 b2465 Escherichia coli 562 -11532649 101616 tktb (ec:2.2.1.1) (de:transketolase 2, (tk 2)) (db:swissprot) TKT2\_ECOLI P33570 ESCHERICHIA COLI 562 -11532649 123322 tktb transketolase:b:glycolaldehydetransferase b:transketolase:2 (cl:transketolase:thiamine pyrophosphate-binding domain homology) (ec:2.2.1.1:2.2.1.1) (db:pir1.dat) (mp:53 min) A48660 A48660 Escherichia coli 562 -11532649 225028 transketolase ec 2.2.1.1 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #422(55.5-55.8 min.)) (nt:similar to (pir accession number a48660)) (le:2729) (re:4732) (di:direct) D90875 D90875 g1799889 Escherichia coli 562 -11532649 7500893206 tktb transketolase (sr:escherichia coli (strain k-12) dna, clone pai198) (db:genpept-bct1) (ec:2.2.1.1) (de:e. coli tktb gene for transketolase, complete cds.) (le:221) (re:2224) (di:direct) ECOTKTB D12473 g460975 Escherichia coli 562 -11532649 236103 tktb transketolase 2 isozyme (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:2.2.1.1) (de:escherichia coli k-12 mgl655 section 223 of 400 of the completegenome.) (nt:o667; 100 pct identical to tkt2\_ecoli sw: p33570) (le:3679) (re:5682) (di:direct) AE000333 AE000333 g1788808 Escherichia coli 562 -11532649 5000690045 tktb transketolase (sr:escherichia coli (strain:k-12) dna, clone:pai198) (db:genpept) (ec:2.2.1.1) (de:escherichia coli gene for transketolase, complete cds.) (le:221) (re:2224) (di:direct) ECOTKTB D12473 g460975 Escherichia coli 562 -11532649

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821194	7183	29339	270	89

Description

6500728792 rpia:b2914 ribose 5-phosphate isomerase:ribose 5-phosphate isomerase a:phosphoriboisomerase a (gtcfc:1.3:2.4) (ec:5.3.1.6) (keggfc:1.3:2.3) (rileyfc:1.2.4) (db:gtc-escherichia coli) b2914 b2914 Escherichia coli 562 -11532650 239127 rpia (ec:5.3.1.6) (de:ribose 5-phosphate isomerase a, (phosphoriboisomerase a)) (db:swissprot) RPIA\_ECOLI P27252 ESCHERICHIA COLI 562 -11532650 7000686452 rpia ribose-5-phosphate isomerase::constitutive (cl:haemophilus influenzae ribose-5-phosphate isomerase) (ec:5.3.1.6) (db:pir2.dat) (mp:63 min) A65076 A65076 Escherichia coli 562 -11532650 5000690046 rpia ribose 5-phosphate isomerase (db:genpept-bct1) (ec:5.3.1.6) (de:e.coli genes icia and rpia.) (le:957) (re:1616) (di:direct) ECRPIAA X73026 g405640 Escherichia coli 562 -11532650 7500890586 rpia ribose 5-phosphate isomerase (db:genpept-bct1) (ec:5.3.1.6) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:cg site no. 264) (le:13057) (re:13716) (di:complement) ECU28377 U28377 g882443 Escherichia coli 562 -11532650 238124 rpia ribosephosphate isomerase:constitutive (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:5.3.1.6) (de:escherichia coli k-12 mg1655 section 264 of 400 of the completengenome.) (nt:f219; 100 pct identical to rpia\_ecoli sw: p27252;) (le:9596) (re:10255) (di:complement) AE000374 AE000374 g1789280 Escherichia coli 562 -11532650 96131 rpia (ec:5.3.1.6) (de:ribose 5-phosphate isomerase a, (phosphoriboisomerase a)) (db:swissprot) RPIA\_ECOLI P27252 ESCHERICHIA COLI 562 -11532650

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821195	7184	29340	426	141

Description

6500728793 tkta:tkt:b2935 transketolase:transketolase 1:tk 1 (gtcfc:1.3:2.4) (ec:2.2.1.1) (keggfc:1.3:2.3) (rileyfc:1.2.4) (db:gtc-escherichia coli) b2935 b2935 Escherichia coli 562 -11532651 101614 tkta:tkt (ec:2.2.1.1) (de:transketolase 1, (tk 1)) (db:swissprot) TKT1\_ECOLI P27302 ESCHERICHIA COLI 562 -11532651 7000686800 tkta:tkt transketolase:a:glycolaldehydetransferase a (cl:transketolase:thiamine pyrophosphate-binding domain homology) (ec:2.2.1.1) (db:pir1.dat) (mp:62 min) XJECTK F65078 Escherichia coli 562 -11532651 7500893203 tkta transketolase 1 isozyme (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:2.2.1.1) (de:escherichia coli k-12 mg1655 section 266 of 400 of the completengenome.) (nt:f663; differs from earlier version (tkt1\_ecoli) (le:9687) (re:11678) (di:complement) AE000376 AE000376 g2367177 Escherichia coli 562 -11532651

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821198	7185	29341	456	152
<u>Description</u>				
6500728794 rpe:dod:b3386 dod protein:ribulose-phosphate 3-epimerase:pentose-5-phosphate 3-epimerase:ppe (gtcfc:1.3:1.4:2.4) (ec:5.1.3.1) (keggfc:1.3:1.4:2.3) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3386 b3386 Escherichia coli 562 -11532652 96122 rpe:dod (ec:5.1.3.1) (de:epimerase) (ppe) (r5p3e)) (db:swissprot) RPE_ECOLI P32661 ESCHERICHIA COLI 562 -11532652 7000686450 rpe ribulose-phosphate 3-epimerase (cl:yeast ribulose-5-phosphate-epimerase) (ec:5.1.3.1) (db:pir2.dat) E65133 E65133 Escherichia coli 562 -11532652 7500890580 ybfd (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:24 kd protein) (le:295130) (re:295807) (di:complement) ECOUW67 U18997 g606320 Escherichia coli 562 -11532652 236619 rpe d-ribulose-5-phosphate 3-epimerase (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 304 of 400 of the completegenome.) (nt:f225; 24 kd protein; 100 pct identical amino) (le:3394) (re:4071) (di:complement) AE000414 AE000414 g1789788 Escherichia coli 562 -11532652 5000690048 (de:(ecoli_3304) (pn:ribulose-phosphate 3-epimerase:pentose-5-phosphate 3- epimerase:ppe) (gn:rpe) (gtcfc:1.3:1.4:2.4) (ec:5.1.3.1) (rpe_ecoli) (keggfc:1.3:1.4:2.3) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3304 ECOLI_3304 Escherichia coli 562 10038066				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821212	7186	29342	747	248
<u>Description</u>				
6500728795 gntk:b3437 thermoresistant glucokinase (gtcfc:1.3) (ec:2.7.1.12) (keggfc:1.3) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3437 b3437 Escherichia coli 562 -11532653 7000690891 gntk gluconokinase::thermoresistant (cl:conserved hypothetical protein ydr248c) (ec:2.7.1.12) (db:pir2.dat) H65139 H65139 Escherichia coli 562 -11532653 7500959747 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f162) (le:357803) (re:358291) (di:complement) ECOUW67 U18997 g606372 Escherichia coli 562 -11532653 236671 gntk gluconokinase 2:thermoresistant (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:2.7.1.12) (de:escherichia coli k-12 mg1655 section 310 of 400 of the completegenome.) (nt:f162; 100 pct identical to gntk_ecoli sw: p46859) (le:3456) (re:3944) (di:complement) AE000420 AE000420 g1789845 Escherichia coli 562 -11532653 5000690049 (de:(ecoli_3355) (pn:gluconokinase 2, thermoresistant) (gn:gntk) (gtcfc:1.3) (ec:2.7.1.12) (gntk_ecoli) (keggfc:1.3) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3355 ECOLI_3355 Escherichia coli 562 10124035				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821223	7187	29343	243	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821229	7188	29344	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821254	7189	29345	411	136

Description

6500728796 kdgk:b3526 2-dehydro-3-deoxygluconokinase (gtcfc:1.3:1.4) (ec:2.7.1.45) (keggfc:1.3:1.4) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3526 b3526 Escherichia coli 562 -11532654 163829 kdgk 2-dehydro-3-deoxygluconokinase::hypothetical protein o382 (ec:2.7.1.45) (db:pir2.dat) S47747 S47747 Escherichia coli 562 -11532654 7500959662 (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:93456) (re:94604) (di:direct) ECOUW76 U00039 g912468 Escherichia coli 562 -11532654 236763 kdgk ketodeoxygluconokinase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:2.7.1.45) (de:escherichia coli k-12 mg1655 section 319 of 400 of the completegenome.) (nt:o382; 100 pct identical to 309 amino acids) (le:4686) (re:5834) (di:direct) AE000429 AE000429 g1789945 Escherichia coli 562 -11532654 5000690050 (de:(ecoli\_3446) (pn:ketodeoxygluconokinase) (gn:kdgk) (gtcfc:1.3:1.4) (ec:2.7.1.45) (kdgk\_ecoli) (keggfc:1.3:1.4) (rileyfc:1.1.1) (db:gtc-escherichia coli)) ECOLI\_3446 ECOLI\_3446 Escherichia coli 562 10087058

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821263	7190	29346	1077	358

Description

GTC ORF with score 956 to: (or:Homo sapiens) (sr:homo sapiens male myeloblast cell-line kg-1 cDNA to mRNA) (db:genpept-pri2) (de:human mRNA for kiaa0073 gene, partial cds.) (nt:the ha1539 protein is related to cyclophilin.) (le:<1) (re:1939) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821273	7191	29347	1260	419
<u>Description</u>				
6500728797 rbsk:b3752 ribokinase (gtcfc:1.3:1.4) (ec:2.7.1.15) (keggfc:1.3) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3752 b3752 Escherichia coli 562 -11532655 93579 rbsk (ec:2.7.1.15) (de:ribokinase,) (db:swissprot) RBSK_ECOLI P05054 ESCHERICHIA COLI 562 -11532655 123531 rbsk ribokinase (cl:ribokinase) (ec:2.7.1.15) (db:pir1.dat) (mp:84 min) KIECRB A26305 Escherichia coli 562 -11532655 236990 rbsk ribokinase (sr:e.coli k12 dna) (db:genpept-bct1) (ec:2.7.1.15) (de:e.coli k12 rbsd, rbsa, rbsc, rbsb, rbsk, and rbsr genes encodingthe high affinity ribose transport system, complete cds.) (le:4128) (re:5057) (di:direct) ECORBS M13169 g147516 Escherichia coli 562 -11532655 7500889477 rbsk::cg site no. 315 ribokinase (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e.coli; the region from 81.5 to 84.5 minutes.) (le:126682) (re:127611) (di:direct) ECOUW82 L10328 g290602 Escherichia coli 562 -11532655 235697 rbsk ribokinase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 342 of 400 of the completegenome.) (nt:o309; cg site no. 315) (le:4299) (re:5228) (di:direct) AE000452 AE000452 g1790193 Escherichia coli 562 -11532655 5000690051 (de:(ecoli_3671) (pn:ribokinase) (gn:rbsk) (gtcfc:1.3) (ec:2.7.1.15) (rbsk_ecoli) (keggfc:1.3) (rileyfc:1.1.1) (db:gtc-escherichia coli)) ECOLI_3671 ECOLI_3671 Escherichia coli 562 10035572				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821274	7192	29348	195	65

Description

6500728798 rpib:b4090 hypothetical 16.1 kd protein in fdhf-phnp intergenic region:ribose 5-phosphate isomerase b:phosphoriboisomerase b (gtcfc:1.3:2.4) (ec:5.3.1.6) (keggfc:1.3:2.3) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4090 b4090 Escherichia coli 562 -11532656 96135 rpib (ec:5.3.1.6) (de:ribose 5-phosphate isomerase b, (phosphoriboisomerase b)) (db:swissprot) RPIB\_ECOLI P37351 ESCHERICHIA COLI 562 -11532656 164552 rpib:yjca ribose-5-phosphate isomerase:b:hypothetical 16.1k protein fdhf-phnp intergenic region:ribose phosphate isomerase b (cl:galactoside o-acetyltransferase) (ec:5.3.1.6) (db:pir2.dat) JC6054 JC6054 Escherichia coli 562 -11532656 238127 yjca (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:4279) (re:4728) (di:direct) ECOUW93 U14003 g536934 Escherichia coli 562 -11532656 7500890590 rpib ribose phosphate isomerase b (db:genpept-bct1) (de:e.coli rpir and rpib genes.) (le:1700) (re:2149) (di:direct) ECRPIRB X82203 g1197467 Escherichia coli 562 -11532656 237298 rpib ribose 5-phosphate isomerase b (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 372 of 400 of the completegenome.) (nt:ol49; 100 pct identical amino acid sequence and) (le:8998) (re:9447) (di:direct) AE000482 AE000482 g1790528 Escherichia coli 562 -11532656 5000690052 (de:(ecoli\_3976) (pn:ribose 5-phosphate isomerase b:phosphoriboisomerase b) (gn:rpib) (gtcfc:1.3:2.4) (ec:5.3.1.6) (rpib\_ecoli) (keggfc:1.3:2.3) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_3976 ECOLI\_3976 Escherichia coli 562 10038079

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821288	7193	29349	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821299	7194	29350	405	134
<u>Description</u>				
6500728799 gntv:b4268 gluconate kinase:thermosensitive gluconokinase:gluconate kinase 1 (gtcfc:1.3:1.4) (ec:2.7.1.12) (keggfc:1.3) (rileyfc:1.1.1) (db:gtc-escherichia coli) b4268 b4268 Escherichia coli 562 -11532657 74259 gntv (ec:2.7.1.12) (de:thermosensitive gluconokinase, (gluconate kinase 1)) (db:swissprot) GNTV_ECOLI P39208 ESCHERICHIA COLI 562 -11532657 163111 gntv gluconokinase:gntv (cl:conserved hypothetical protein ydr248c) (ec:2.7.1.12) (db:pir2.dat) S56494 S56494 Escherichia coli 562 -11532657 7500882622 gntv gluconate kinase (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 17686) (le:185458) (re:186021) (di:direct) ECOUW93 U14003 g537110 Escherichia coli 562 -11532657 237474 idnk gluconate kinase:thermosensitive glucokinase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:2.7.1.12) (de:escherichia coli k-12 mg1655 section 387 of 400 of the completegenome.) (nt:ol87; formerly designated gntv; cg site no. 17686) (le:8601) (re:9164) (di:direct) AE000497 AE000497 g1790719 Escherichia coli 562 -11532657 5000690053 (de:(ecoli_4152) (pn:gluconokinase 1, thermosensitive) (gn:gntv) (gtcfc:1.3) (ec:2.7.1.12) (gntv_ecoli) (keggfc:1.3) (rileyfc:1.1.1) (db:gtc-escherichia coli)) ECOLI_4152 ECOLI_4152 Escherichia coli 562 10016781				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821300	7195	29351	228	75
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821310	7196	29352	189	62
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821311	7197	29353	396	131
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821331	7198	29354	198	65
<u>Description</u>				
6500728800 deoc:dra:thyr:b4381 deoxyribose-phosphate aldolase:phosphodeoxyriboaldolase:deoxyriboaldolase (gtcfc:1.3:4.4) (ec:4.1.2.4) (keggfc:1.3) (rileyfc:1.6.4) (db:gtc-escherichia coli) b4381 b4381 Escherichia coli 562 -11532658 68252 deoc:dra:thyr (ec:4.1.2.4) (de:(deoxyriboaldolase)) (db:swissprot) DEOC_ECOLI P00882 ESCHERICHIA COLI 562 -11532658 125490 deoc deoxyribose-phosphate aldolase (cl:deoxyribose-phosphate aldolase) (ec:4.1.2.4) (db:pir1.dat) (mp:100 min) ADECD A01102 Escherichia coli 562 -11532658 7500880164 deoc deoxyribose-phosphate aldolase (db:genpept-bct1) (ec:4.1.2.4) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 866; alternate gene names dra, thyr) (le:308154) (re:308933) (di:direct) ECOUW93 U14003 g537221 Escherichia coli 562 -11532658 237586 deoc 2-deoxyribose-5-phosphate aldolase (fn:enzyme; salvage of nucleosides and nucleotides) (db:genpept-bct2) (ec:4.1.2.4) (de:escherichia coli k-12 mg1655 section 398 of 400 of the completegenome.) (nt:o259b; 100 pct identical to deoc_ecoli sw:) (le:7971) (re:8750) (di:direct) AE000508 AE000508 g1790841 Escherichia coli 562 -11532658 5000690054 (de:(ecoli_4263) (pn:2-deoxyribose-5-phosphate aldolase) (gn:deoc) (gtcfc:1.3) (ec:4.1.2.4) (deoc_ecoli) (keggfc:1.3) (rileyfc:1.6.4) (db:gtc-escherichia coli)) ECOLI_4263 ECOLI_4263 Escherichia coli 562 10010845				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501821343	7199	29355	1593	531

Description

6500728801 deob:drm:thyr:b4383 phosphopentomutase:phosphodeoxyribomutase (gtcfc:1.3:4.4) (ec:5.4.2.7) (keggfc:1.3) (rileyfc:1.6.4) (db:gtc-escherichia coli) b4383 b4383 Escherichia coli 562 -11532659 68250 deob:drm:thyr (ec:5.4.2.7) (de:phosphopentomutase, (phosphodeoxyribomutase)) (db:swissprot) DEOB\_ECOLI P07651 ESCHERICHIA COLI 562 -11532659 164314 deob phosphopentomutase (cl:phosphopentomutase) (ec:5.4.2.7) (db:pir2.dat) (mp:100 min) S56607 S56607 Escherichia coli 562 -11532659 7500880159 deob phosphopentomutase (db:genpept-bct1) (ec:2.7.5.6) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 867; alternate gene names drm, thyr) (le:310434) (re:311657) (di:direct) ECOUW93 U14003 g537223 Escherichia coli 562 -11532659 237588 deob phosphopentomutase (fn:enzyme; salvage of nucleosides and nucleotides) (db:genpept-bct2) (ec:5.4.2.7) (de:escherichia coli k-12 mg1655 section 398 of 400 of the completegenome.) (nt:o407; 100 pct identical to deob\_ecoli sw: p07651;) (le:10251) (re:11474) (di:direct) AE000508 AE000508 g1790843 Escherichia coli 562 -11532659 5000690055 (de:(ecoli\_4265) (pn:phosphopentomutase) (gn:deob) (gtcfc:1.3) (ec:5.4.2.7) (deob\_ecoli) (keggfc:1.3) (rileyfc:1.6.4) (db:gtc-escherichia coli)) ECOLI\_4265 ECOLI\_4265 Escherichia coli 562 10010843

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501821347	7200	29356	1236	411

Description

GTC ORF with score 143 to: (sr:fowlpox virus isolate hp-438(munich) gifted from a. mayr, passed i) (db:genpept-vrl) (de:fowlpox virus, 11.2 kilobase,near-terminal,bamhi fragment withtwenty open reading frames.) (nt:orf 7) (le:6674) (re:7906) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501821360	7201	29357	549	182
Description				
<p>6500728802 arad:b0061 l-ribulose-5-phosphate 4-epimerase (gtcfc:1.4) (ec:5.1.3.4) (keggfc:1.4) (rileyfc:1.1.1) (db:gtc-escherichia coli) b0061 b0061 Escherichia coli 562 -11532660 233591 arad (ec:5.1.3.4) (de:l-ribulose-5-phosphate 4-epimerase,) (db:swissprot) ARAD_ECOLI P08203 ESCHERICHIA COLI 562 -11532660 7000684602 arad l-ribulose-phosphate 4-epimerase (cl:l-ribulose-phosphate 4-epimerase) (ec:5.1.3.4) (db:pir1.dat) (mp:1 min) ISECP4 E64727 Escherichia coli 562 -11532660 5000690056 arad l-ribulose-phosphate 4-epimerase (db:genpept-bct1) (de:e. coli arad gene for l-ribulose-phosphate 4-epimerase (ec5.1.3.4).) (le:466) (re:1161) (di:direct) ECARADG X56048 g40939 Escherichia coli 562 -11532660 235516 arad l-ribulose-phosphate 4-epimerase (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (ec:5.1.3.4) (de:e.coli k12 genome, 0-2.4min. region.) (le:65515) (re:66210) (di:complement) ECO110K D10483 g216481 Escherichia coli 562 -11532660 7500877065 arad l-ribulose-5-phosphate 4-epimerase (sr:e.coli dna) (db:genpept-bct1) (ec:5.1.3.4) (de:e.coli dna polymerase ii (polb) and l-ribulose-5-phosphate4-epimerase (arad) genes, complete cds.) (le:463) (re:1158) (di:direct) ECOPOLB M62646 g147317 Escherichia coli 562 -11532660 232373 arad l-ribulose-5-phosphate 4-epimerase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:5.1.3.4) (de:escherichia coli k-12 mg1655 section 6 of 400 of the completegenome.) (nt:f231; 100 pct identical to arad_ecoli sw: p08203) (le:8649) (re:9344) (di:complement) AE000116 AE000116 g1786247 Escherichia coli 562 -11532660 59963 arad (ec:5.1.3.4) (de:l-ribulose-5-phosphate 4-epimerase,) (db:swissprot) ARAD_ECOLI P08203 ESCHERICHIA COLI 562 -11532660</p>				
ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501821382	7202	29358	375	124
Description				
<p>6500728803 araa:b0062 l-arabinose isomerase (gtcfc:1.4) (ec:5.3.1.4) (keggfc:1.4) (rileyfc:1.1.1) (db:gtc-escherichia coli) b0062 b0062 Escherichia coli 562 -11532661 7000688902 araa l-arabinose isomerase (cl:l-arabinose isomerase) (ec:5.3.1.4) (db:pir1.dat) (mp:1 min) ISECAB F64727 Escherichia coli 562 -11532661 7500953352 araa l-arabinose isomerase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:5.3.1.4) (de:escherichia coli k-12 mg1655 section 6 of 400 of the completegenome.) (nt:f500; 99 pct identical to araa_ecoli sw: p08202) (le:9629) (re:11131) (di:complement) AE000116 AE000116 g1786248 Escherichia coli 562 -11532661 5000690057 (de:(ecoli_62) (pn:l-arabinose isomerase) (gn:araa) (gtcfc:1.4) (ec:5.3.1.4) (araa_ecoli) (keggfc:1.4) (rileyfc:1.1.1) (db:gtc-escherichia coli)) ECOLI_62 ECOLI_62 Escherichia coli 562 10122637</p>				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821395	7203	29359	804	267
<u>Description</u>				
6500728804 arab:b0063 l-ribulokinase (gtcfc:1.4) (ec:2.7.1.16) (keggfc:1.4) (rileyfc:1.1.1) (db:gtc-escherichia coli) b0063 b0063 Escherichia coli 562 -11532662 7000685690 arab ribulokinase::l-ribulokinase (cl:ribulokinase) (ec:2.7.1.16) (db:pir1.dat) (mp:1 min) KIECRU G64727 Escherichia coli 562 -11532662 7500884634 arab l-ribulokinase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:2.7.1.16) (de:escherichia coli k-12 mg1655 section 6 of 400 of the completegenome.) (nt:f566; 98 pct identical to kiri_ecoli sw: p08204) (le:11142) (re:12842) (di:complement) AE000116 AE000116 g1786249 Escherichia coli 562 -11532662 80740 arab (ec:2.7.1.16) (de:l-ribulokinase,) (db:swissprot) KIRI_ECOLI P08204 ESCHERICHIA COLI 562 -11532662 5000690058 (de:(ecoli_63) (pn:l-ribulokinase) (gn:arab) (gtcfc:1.4) (ec:2.7.1.16) (kiri_ecoli) (keggfc:1.4) (rileyfc:1.1.1) (db:gtc-escherichia coli)) ECOLI_63 ECOLI_63 Escherichia coli 562 10122638				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501821397	7204	29360	363	121

# Description

6500728805 galu:b1236 glucose-1-phosphate  
uridylyltransferase:utp--glucose-1-phosphate uridylyltransferase:udp-glucose  
pyrophosphorylase:udpgp:alpha-d-glucosyl-1-phosphate  
uridylyltransferase:uridine diphosphoglucose pyrophosphorylase  
(gtcfc:4.3:1.4:1.6:7.2) (ec:2.7.7.9) (keggfc:1.4:1.6:4.3:7.1)  
(rileyfc:1.1.1) (db:gtc-escherichia coli) b1236 b1236 Escherichia coli 562  
-11532663 139258 galu utp--glucose-1-phosphate  
uridylyltransferase:galu:udp-glucose pyrophosphorylase (cl:escherichia coli  
utp--glucose-1-phosphate uridylyltransferase) (ec:2.7.7.9) (db:pir1.dat)  
(mmp:27 min) JC2265 G64870 Escherichia coli 562 -11532663 7500953272 galu  
utp-glucose-1-phosphate uridylyltransferase (sr:escherichia coli(strain:k12)  
dna, clone:kohara clone #249) (db:genpept-bct1) (de:escherichia coli genomic  
dna(27.5-27.8 min).) (le:12796) (re:13704) (di:direct) D90758 D90758  
g1651627 Escherichia coli 562 -11532663 223437 galu utp-glucose-1-phosphate  
uridylyltransferase (sr:escherichia coli(strain:k12) dna, clone:kohara clone  
#250) (db:genpept-bct1) (de:escherichia coli genomic dna (27.6-28.0 min).)  
(le:8453) (re:9361) (di:direct) D90759 D90759 g1651636 Escherichia coli 562  
-11532663 301354 galu utp--glucose-1-phosphate uridylyltransferase ec  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #251(27.7-28.2  
min.)) (nt:orf\_id:o249#12; similar to (pir accession number) (le:8453)  
(re:9361) (di:direct) D90852 D90852 g1805513 Escherichia coli 562 -11532663  
233412 orf::1 (db:genpept-bct1) (de:e.coli msya gene for histone-like  
protein h-ns.) (le:234) (re:1142) (di:direct) ECMSYA X59940 g42026  
Escherichia coli 562 -11532663 234435 galu glucosephosphate  
uridylyltransferase (fn:synthesizes udpg) (sr:escherichia coli (strain k-12)  
dna) (db:genpept-bct1) (ec:2.7.7.9) (de:escherichia coli  
alpha-d-glucosyl-1-phosphate uridylyltransferase(galu) gene, complete cds.)  
(le:234) (re:1142) (di:direct) ECOGALU M98830 g146073 Escherichia coli 562  
-11532663 260614 galu udp-glucose pyrophosphorylase (db:genpept-bct1)  
(ec:2.7.7.9) (de:shigella flexneri udp-glucose pyrophosphorylase (galu)  
gene,complete cds and virr gene, partial cds.) (le:234) (re:1142)  
(di:direct) SHFGALU L32811 g487881 Shigella flexneri 623 -11532663 224714  
galu glucose-1-phosphate uridylyltransferase (fn:enzyme; degradation of  
small molecules: carbon) (db:genpept-bct2) (ec:2.7.7.9) (de:escherichia coli  
k-12 mg1655 section 112 of 400 of the completegenome.) (nt:o302; 100 pct  
identical to galu\_ecoli sw: p25520) (le:1291) (re:2199) (di:direct) AE000222  
AE000222 g1787488 Escherichia coli 562 -11532663 5000690059 galu  
utp-glucose-1-phosphate uridylyltransferase ec (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #249) (db:genpept) (de:escherichia  
coli genomic dna. (27.6 - 27.9 min).) (nt:orf\_id:o251#2; similar to pir  
accession number) (le:12796) (re:13704) (di:direct) D90758 D90758 g1651627  
Escherichia coli 562 -11532663 7502851788 galu utp-glucose-1-phosphate  
uridylyltransferase ec (sr:escherichia coli(strain:k12) dna, clone:kohara  
clone #250) (db:genpept) (de:escherichia coli genomic dna. (27.7 - 28.1  
min).) (nt:orf\_id:o251#2; similar to pir accession number) (le:8453)

min).) (nt:orf\_id:o251#2; similar to pir accession number) (le:8453)

(re:9361) (di:direct) D90759 D90759 g1651636 Escherichia coli 562 -11532663

ORF Name	NT ID	AA ID	NT	AA
			LENGTH	LENGTH
7501821400	7205	29361	603	200

Description

6500728806 uxab:b1521 altronate oxidoreductase:tagaturonate  
reductase:tagaturonate dehydrogenase (gtcfc:1.4) (ec:1.1.1.58) (keggfc:1.4)  
(rileyfc:1.1.1) (db:gtc-escherichia coli) b1521 b1521 Escherichia coli 562  
-11532664 104074 uxab (ec:1.1.1.58) (de:(tagaturonate dehydrogenase))  
(db:swissprot) UXAB\_ECOLI P24214 ESCHERICHIA COLI 562 -11532664 7000686917  
uxab tagaturonate reductase::d-altronate:nad 3-oxidoreductase:tagaturonate  
dehydrogenase (cl:tagaturonate reductase) (ec:1.1.1.58) (db:pir2.dat) D64906  
D64906 Escherichia coli 562 -11532664 7500893928 uxab altronate  
oxidoreductase (fn:enzyme; degradation of small molecules: carbon)  
(db:genpept-bct2) (ec:1.1.1.58) (de:escherichia coli k-12 mg1655 section 139  
of 400 of the completegenome.) (nt:f483; 99 pct identical to gb: d13327\_1)  
(le:9011) (re:10462) (di:complement) AE000249 AE000249 g1787800 Escherichia  
coli 562 -11532664 5000690060 (de:(ecoli\_1481) (pn:altronate  
oxidoreductase) (gn:uxab) (gtcfc:1.4) (ec:1.1.1.58) (uxab\_ecoli)  
(keggfc:1.4) (rileyfc:1.1.1) (db:gtc-escherichia coli)) ECOLI\_1481  
ECOLI\_1481 Escherichia coli 562 10123367



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821403	7206	29362	579	192

Description

6500728807 eda:hga:kdga:b1850 2-keto-3-deoxygluconate 6-p  
aldolase:2-keto-4-hydroxyglutarate aldolase:4-hydroxy-2-oxoglutarate  
aldolase:2-keto-4-hydroxyglutarate aldolase:khg-aldolase /  
2-dehydro-3-deoxyphosphogluconate  
aldolase:phospho-2-dehydro-3-deoxygluconate  
aldolase:phospho-2-keto-3-deoxygluconate  
aldolase:2-keto-3-deoxy-6-phosphogluconate aldolase:kdpg-aldolase  
(gtcfc:1.4:1.9:2.1:5.10) (keggfc:1.4:1.9:5.10) (rileyfc:1.2.5)  
(db:gtc-escherichia coli) b1850 b1850 Escherichia coli 562 -11532665 300981  
eda:hga:kdga (ec:4.1.3.16:4.1.2.14) (de:(2-keto-3-deoxy-6-phosphogluconate  
aldolase) (kdpg-aldolase)) (db:swissprot) ALKH\_ECOLI P10177 ESCHERICHIA COLI  
562 -11532665 125514 eda:hga:kdga khg-kdpg bifunctional  
aldolase:2-keto-4-hydroxyglutarate aldolase khg  
aldolase:phospho-2-keto-3-deoxygluconate aldolase kdpg aldolase  
(cl:2-dehydro-3-deoxyphosphogluconate aldolase) (db:pir1.dat) (mp:4 min)  
ADEC0G B42986 Escherichia coli 562 -11532665 224341 eda:hga:kdga  
4-hydroxy-2-oxoglutarate aldolase ec 4.1.3.16 (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #336gap(41.6-41.9 min..))  
(nt:orf\_id:o336gap#2; similar to (swissprot accession) (le:1641) (re:2282)  
(di:complement) D90828 D90828 g1736493 Escherichia coli 562 -11532665  
234225 hga 4-hydroxy-2-oxoglutarate aldolase (db:genpept-bct1)  
(ec:4.1.3.16) (de:e.coli hga gene for 4-hydroxy-2-oxoglutarate aldolase.)  
(nt:khg aldolase) (le:1) (re:639) (di:direct) ECHGA X68871 g41689  
Escherichia coli 562 -11532665 234463 eda kdpg aldolase (sr:escherichia  
coli (sub\_strain w3110, strain k-12) dna) (db:genpept-bct1) (de:escherichia  
coli 6-phosphogluconate dehydratase, kdpg aldolase(edd-eda) operon, complete  
cds.) (nt:putative) (le:2003) (re:2644) (di:direct) ECOEDDEDA M87458 g145827  
Escherichia coli 562 -11532665 240393 eda 2-keto-3-deoxy-6-phosphogluconate  
aldolase (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1)  
(de:escherichia coli glycinamide ribonucleotide transformylase (purt)gene,  
2-keto-3-deoxy-6-phosphogluconate aldolase (eda) gene,6-phosphogluconate  
dehydratase (edd) gene, complete cds's.) (le:2... ECOGARA L20897 g304888  
Escherichia coli 562 -11532665 5000690061 eda  
phospho-2-dehydro-3-deoxygluconate aldolase (db:genpept-bct1) (ec:4.1.2.14)  
(de:e.coli genes zwf, edd and eda for glucose-6-phosphate  
dehydrogenase(partial), 6-phosphogluconate dehydratase  
andphospho-2-keto-3-deoxygluconate aldolase.) (le:2599) (re:3240)  
(di:direct) ECZWFEDDA X63694 g395404 Escherichia coli 562 -11532665 233086  
eda 2-keto-3-deoxygluconate 6-phosphate aldolase and (fn:enzyme; central  
intermediary metabolism:) (db:genpept-bct2) (ec:4.1.2.14:4.1.3.16)  
(de:escherichia coli k-12 mg1655 section 169 of 400 of the completegenome.)  
(nt:f213; 100 pct identical to alkh\_ecoli sw: p10177;) (le:1331) (re:1972)  
(di:complement) AE000279 AE000279 g1788156 Escherichia coli 562 -11532665  
59190 eda:hga:kdga (ec:4.1.3.16:4.1.2.14)  
(de:(2-keto-3-deoxy-6-phosphogluconate aldolase) (kdpg-aldolase))

(de:(2-keto-3-deoxy-6-phosphogluconate aldolase) (kdpg-aldolase))

(db:swissprot) ALKH\_ECOLI D10177 ESCHERICHIA COLI 562 -11532665

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501821419	7207	29363	939	312

Description

6500728808 ugd:udg:b2028 hypothetical protein:udp-glucose  
6-dehydrogenase:udp-glc dehydrogenase (gtcfc:4.3:1.1:1.4) (ec:1.1.1.22)  
(keggfc:1.4:4.3:7.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2028 b2028  
Escherichia coli 562 -11532666 1500687086 ugd:udg (ec:1.1.1.22)  
(de:(udp-gldh) (udpgdh)) (db:swissprot) UDG\_ECOLI P76373 ESCHERICHIA COLI  
562 -11532666 7000686854 hypothetical protein b2028 (cl:gdpmannose  
dehydrogenase) (db:pir2.dat) C64968 C64968 Escherichia coli 562 -11532666  
224551 udg protein. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara  
lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#351(45.1-45.5 min.)) (nt:orf\_id:o351#1; similar to (swissprot accession)  
(le:4747) (re:5913) (di:complement) D90841 D90841 g1736716 Escherichia coli  
562 -11532666 301191 ugd udp-glucose 6-dehydrogenase (fn:enzyme; central  
intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655  
section 184 of 400 of the completegenome.) (nt:f388; this 388 aa orf is 93  
pct identical (16 gaps)) (le:1204) (re:2370) (di:complement) AE000294  
AE000294 g1788340 Escherichia coli 562 -11532666 5000692648  
(de:(ecoli\_1976) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)  
(keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_1976  
ECOLI\_1976 Escherichia coli 562 10063573

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501821423	7208	29364	1287	428
Description				
6500728809 galf:b2042 utp-glucose-1-phosphate uridylyltransferase (gtcfc:1.4:1.6:4.3:7.2) (ec:2.7.7.9) (keggfc:1.4:1.6:4.3:7.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2042 b2042 Escherichia coli 562 -11532667 7500882087 galf:wcan (ec:2.7.7.9) (de:uridylyltransferase) (uridine diphosphoglucose pyrophosphorylase)) (db:swissprot) GALF_ECOLI P78083 ESCHERICHIA COLI 562 -11532667 7000688870 galf utp--glucose-1-phosphate uridylyltransferase:galf:udp-glucose pyrophosphorylase:udp-glucose pyrophosphorylase (cl:escherichia coli utp--glucose-1-phosphate uridylyltransferase) (sr:strain k-12, , strain k-12) (sr:strain k-12, ) (ec:2.7.7.9) (db:pir1.dat) A64970 A64970 Escherichia coli 562 -11532667 224579 utp--glucose-1-phosphate uridylyltransferase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #352(45.3-45.7 min.)) (nt:orf_id:o352#1; similar to (swissprot accession) (le:10523) (re:11416) (di:complement) D90842 D90842 g1736745 Escherichia coli 562 -11532667 7000688871 galf homolog of salmonella utp--glucose-1-p (fn:putative enzyme; central intermediary) (db:genpept-bct2) (ec:2.7.7.9) (de:escherichia coli k-12 mg1655 section 185 of 400 of the completegenome.) (nt:f297; 98 pct identical to galf_shif1 sw: p37776) (le:217) (re:1110) (di:complement) AE000295 AE000295 g1788355 Escherichia coli 562 -11532667 7500882089 galf possible glucose-1-p uridylyl transferase (db:genpept-bct2) (de:escherichia coli k-12 wca gene cluster.) (nt:previously referred to as orf2.8) (le:22646) (re:23539) (di:direct) ECU38473 U38473 g3041819 Escherichia coli 562 -11532667 301219 utp--glucose-1-phosphate uridylyltransferase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #352(45.3-45.7 min.)) (nt:orf_id:o352#1; similar to (swissprot accession) (le:10523) (re:11416) (di:complement) D90842 D90842 g1736745 Escherichia coli 562 -11532667 5000690062 (de:(ecoli_1990) (pn:utp-glucose-1-phosphate uridylyltransferase) (gn:galf) (gtcfc:1.4:1.6:4.3:7.2) (ec:2.7.7.9) (keggfc:1.4:1.6:4.3:7.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1990 ECOLI_1990 Escherichia coli 562 10119973				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821426	7209	29365	348	116

Description

6500728810 arae:b2841 l-arabinose isomerase:arabinose-proton  
symport:arabinose transporter (gtcfc:12.2) (ec:5.3.1.4) (keggfc:1.4)  
(rileyfc:4.1.3) (db:gtc-escherichia coli) b2841 b2841 Escherichia coli 562  
-11532668 59966 arae (de:arabinose-proton symport (arabinose transporter))  
(db:swissprot) ARAE\_ECOLI P09830 ESCHERICHIA COLI 562 -11532668 162742 arae  
l-arabinose isomerase (cl:glucose transport protein) (ec:5.3.1.4)  
(db:pir2.dat) (mp:61 min) B26430 B26430 Escherichia coli 562 -11532668  
7500877066 (sr:e.coli (strain jm2433) dna, clone pmm2(3,5))  
(db:genpept-bct1) (de:e.coli arabinose-proton symporter (arae) gene,  
complete cds, andlysa activator protein (lysr) gene, 3' end.)  
(nt:arabinose-proton symporter) (le:434) (re:1852) (di:direct) ECOARAEA  
J03732 g145321 Escherichia coli 562 -11532668 233828 arae low-affinity  
l-arabinose transport system proton (fn:transport; transport of small  
molecules:) (db:genpept-bct2) (ec:5.3.1.4) (de:escherichia coli k-12 mg1655  
section 258 of 400 of the completegenome.) (nt:f472; 99 pct identical to  
arae\_ecoli sw: p09830; cg) (le:95) (re:1513) (di:complement) AE000368  
AE000368 g1789207 Escherichia coli 562 -11532668 5000690063  
(de:(ecoli\_2769) (pn:low-affinity l-arabinose transport system; l-arabinose  
proton symport) (gn:arae) (gtcfc:1.4) (ec:5.3.1.4) (arae\_ecoli) (keggfc:1.4)  
(rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_2769 ECOLI\_2769 Escherichia  
coli 562 10002699

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821428	7210	29366	972	323

Description

6500728811 uxaa:b3091 altronate hydrolase (gtcfc:1.4) (ec:4.2.1.7) (keggfc:1.4) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3091 b3091 Escherichia coli 562 -11532669 104073 uxaa (ec:4.2.1.7) (de:altronate hydrolase,) (db:swissprot) UXAA\_ECOLI P42604 ESCHERICHIA COLI 562 -11532669 7000686916 uxaa altronate dehydratase (ec:4.2.1.7) (db:pir2.dat) H65097 H65097 Escherichia coli 562 -11532669 236329 uxaa altronate dehydratase (sr:escherichia coli (strain:k12) cell\_line:w3110 dna) (db:genpept-bct1) (ec:4.2.1.7) (de:escherichia coli uxaa, uxac, exut and exur genes for altronatedehydratase, uronate isomerase, aldohexuronate transport system andexu regulon repressor, complete c... D13328 D13328 g1906767 Escherichia coli 562 -11532669 7500893927 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf\_f495) (le:22576) (re:24063) (di:complement) ECOUW67 U18997 g606030 Escherichia coli 562 -11532669 303401 uxaa altronate hydrolase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:4.2.1.7) (de:escherichia coli k-12 mg1655 section 281 of 400 of the completengenome.) (nt:f495; 100 pct identical to the first 494 aa of the) (le:3417) (re:4904) (di:complement) AE000391 AE000391 g1789475 Escherichia coli 562 -11532669 5000690064 (de:(ecoli\_3014) (pn:altronate hydrolase) (gn:uxaa) (gtcfc:1.4) (ec:4.2.1.7) (uxaa\_ecoli) (keggfc:1.4) (rileyfc:1.1.1) (db:gtc-escherichia coli)) ECOLI\_3014 ECOLI\_3014 Escherichia coli 562 10118916

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821433	7211	29367	462	153

Description

6500728812 uxac:b3092 uronate isomerase:glucuronate isomerase:uronic isomerase (gtcfc:1.4) (ec:5.3.1.12) (keggfc:1.4) (rileyfc:1.1.1:5.8.0:5.8.0) (db:gtc-escherichia coli) b3092 b3092 Escherichia coli 562 -11532670 104075 uxac (ec:5.3.1.12) (de:isomerase)) (db:swissprot) UXAC\_ECOLI P42607 ESCHERICHIA COLI 562 -11532670 7000686918 uxac glucuronate isomerase (ec:5.3.1.12) (db:pir2.dat) A65098 A65098 Escherichia coli 562 -11532670 237615 uxac uronate isomerase (sr:escherichia coli (strain:k12) cell\_line:w3110 dna) (db:genpept-bct1) (ec:5.3.1.12) (de:escherichia coli uxaa, uxac, exut and exur genes for altronatedehydratase, uronate isomerase, aldohexuronate transport system andexu regulon repressor, complete ... D13328 D13328 g1160318 Escherichia coli 562 -11532670 303402 uxac uronate isomerase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:5.3.1.12) (de:escherichia coli k-12 mg1655 section 281 of 400 of the completengenome.) (nt:f470; sequence changes joined 3 orfs from earlier) (le:4919) (re:6331) (di:complement) AE000391 AE000391 g2367192 Escherichia coli 562 -11532670

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821464	7212	29368	738	245

Description

6500728813 xylb:b3564 xylulose kinase:xylulokinase (gtcfc:1.4) (ec:2.7.1.17) (keggfc:1.4) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3564 b3564  
Escherichia coli 562 -11532671 7500894487 xylb (ec:2.7.1.17) (de:xylulose kinase, (xylulokinase)) (db:swissprot) XYLB\_ECOLI P09099 ESCHERICHIA COLI 562 -11532671 123534 xylb xylulokinase (cl:xylulokinase) (ec:2.7.1.17) (db:pir1.dat) (mp:80 min) KIECXY A30266 Escherichia coli 562 -11532671 237647 xylb xylulokinase (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (ec:2.7.1.17) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 4) (le:142168) (re:143622) (di:complement) ECOUW76 U00039 g466702 Escherichia coli 562 -11532671 240388 xylb (sr:e.coli dna, clone pecx-14 (1); k12 dna, clone px1 (2)) (db:genpept-bct1) (de:e.coli xyla gene coding for xylose isomerase and xylb gene codingfor xylulose kinase, complete cds.) (nt:xylulose kinase) (le:1607) (re:3061) (di:direct) ECOXYLABA K01996 g148280 Escherichia coli 562 -11532671 5000690066 (db:genpept-bct1) (de:e. coli genes for xylose isomerase and xylulose kinase.) (nt:xylulose kinase (aa 1-484)) (le:1607) (re:3061) (di:direct) ECXYLIK X04691 g43315 Escherichia coli 562 -11532671 236801 xylb xylulokinase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:2.7.1.17) (de:escherichia coli k-12 mg1655 section 323 of 400 of the completgenome.) (nt:f484; 100 pct identical to xylb\_ecoli sw: p09099;) (le:8616) (re:10070) (di:complement) AE000433 AE000433 g1789987 Escherichia coli 562 -11532671 108213 xylb (ec:2.7.1.17) (de:xylulose kinase, (xylulokinase)) (db:swissprot) XYLB\_ECOLI P09099 ESCHERICHIA COLI 562 -11532671

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821466	7213	29369	492	163

Description

6500728814 xyla:b3565 d-xylose isomerase:xylose isomerase (gtcfc:1.4:7.1) (ec:5.3.1.5) (keggfc:1.4:1.5) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3565 b3565 Escherichia coli 562 -11532672 108185 xyla (ec:5.3.1.5) (de:xylose isomerase,) (db:swissprot) XYLA\_ECOLI P00944 ESCHERICHIA COLI 562 -11532672 125785 xyla xylose isomerase::xylose ketol-isomerase (cl:xylose isomerase) (ec:5.3.1.5) (db:pir1.dat) (mp:80 min) ISECX1 A30252 Escherichia coli 562 -11532672 237646 xyla d-xylose isomerase (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (ec:5.3.1.5) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 5) (le:143694) (re:145016) (di:complement) ECOUW76 U00039 g466703 Escherichia coli 562 -11532672 7500894484 xyla (sr:e.coli dna, clone pecx-14 (1); k12 dna, clone px1 (2)) (db:genpept-bct1) (de:e.coli xyla gene coding for xylose isomerase and xylb gene codingfor xylulose kinase, complete cds.) (nt:xylose isomerase) (le:213) (re:1535) (di:direct) ECOXYLABA K01996 g148279 Escherichia coli 562 -11532672 236802 xyla d-xylose isomerase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:5.3.1.5) (de:escherichia coli k-12 mg1655 section 323 of 400 of the completegenome.) (nt:f440; 100 pct identical to xyla\_ecoli sw: p00944;) (le:10142) (re:11464) (di:complement) AE000433 AE000433 g1789988 Escherichia coli 562 -11532672 5000690067 (de:(ecoli\_3485) (pn:d-xylose isomerase) (gn:xyla) (gtcfc:1.4:1.5) (ec:5.3.1.5) (xyla\_ecoli) (keggfc:1.4:1.5) (rileyfc:1.1.1) (db:gtc-escherichia coli)) ECOLI\_3485 ECOLI\_3485 Escherichia coli 562 10049917

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821468	7214	29370	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821481	7215	29371	612	203

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821488	7216	29372	642	213

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821495	7217	29373	696	231
<u>Description</u>				
6500728815 lyx:lyxk:xylk:sgbk:b3580 cryptic l-xylulose kinase:l-xylulokinase (gtcfc:1.4:7.1) (ec:2.7.1.53) (keggfc:1.4) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3580 b3580 Escherichia coli 562 -11532673 82780 lyx:lyxk:xylk:sgbk (ec:2.7.1.53) (de:cryptic l-xylulose kinase, (l-xylulokinase)) (db:swissprot) LYXK_ECOLI P37677 ESCHERICHIA COLI 562 -11532673 163852 lyxk l-xylulokinase::cryptic l-xylulose kinase:hypothetical protein o498 (cl:xylulokinase) (ec:2.7.1.53) (db:pir2.dat) S47801 S47801 Escherichia coli 562 -11532673 7500885225 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:161337) (re:162833) (di:direct) ECOUW76 U00039 g466718 Escherichia coli 562 -11532673 236817 lyxk l-xylulose kinase:cryptic (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:2.7.1.53) (de:escherichia coli k-12 mg1655 section 325 of 400 of the completegenome.) (nt:o498; 100 pct identical amino acid sequence and) (le:6122) (re:7618) (di:direct) AE000435 AE000435 gl790005 Escherichia coli 562 -11532673 5000690068 (de:(ecoli_3500) (pn:cryptic xylulose kinase) (gn:lyxk) (gtcfc:1.4) (ec:2.7.1.53) (lyxk_ecoli) (keggfc:1.4) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3500 ECOLI_3500 Escherichia coli 562 10025000				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821507	7218	29374	501	167

Description

6500728816 uxua:b4322 mannonate hydratase:d-mannonate hydrolase (gtcfc:1.4) (ec:4.2.1.8) (keggfc:1.4) (rileyfc:1.1.1) (db:gtc-escherichia coli) b4322 b4322 Escherichia coli 562 -11532674 104078 uxua (ec:4.2.1.8) (de:mannonate dehydratase, (d-mannonate hydrolase)) (db:swissprot) UXUA\_ECOLI P24215 ESCHERICHIA COLI 562 -11532674 164031 uxua mannonate dehydratase::d-mannonate hydrolase (ec:4.2.1.8) (db:pir2.dat) S56547 S56547 Escherichia coli 562 -11532674 237527 uxua mannonate dehydratase (sr:escherichia coli (strain:k12) cell\_line:w3110 dna) (db:genpept-bct1) (ec:4.2.1.8) (de:escherichia coli uxua, uxub and uxur genes for mannonatedehydratase, mannonate oxidoreductase and uxu regulon repressor,complete cds.) (le:580) (re:1764) (di:direct) D13329 D13329 g1841884 Escherichia coli 562 -11532674 7500893929 uxua d-mannonate hydrolase (db:genpept-bct1) (ec:4.2.1.8) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 14) (le:242468) (re:243652) (di:direct) ECOUW93 U14003 g537163 Escherichia coli 562 -11532674 301662 uxua mannonate hydrolase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:4.2.1.8) (de:escherichia coli k-12 mg1655 section 393 of 400 of the completegenome.) (nt:o394; 100 pct identical to uxua\_ecoli sw: p24215;) (le:176) (re:1360) (di:direct) AE000503 AE000503 g1790778 Escherichia coli 562 -11532674 5000690069 (de:(ecoli\_4205) (pn:mannonate hydrolase) (gn:uxua) (gtcfc:1.4) (ec:4.2.1.8) (uxua\_ecoli) (keggfc:1.4) (rileyfc:1.1.1) (db:gtc-escherichia coli)) ECOLI\_4205 ECOLI\_4205 Escherichia coli 562 10045848

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821508	7219	29375	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821511	7220	29376	792	264
<u>Description</u>				
6500728817 uxub:b4323 d-mannonate oxidoreductase:fructuronate reductase (gtcfc:1.4) (ec:1.1.1.57) (keggfc:1.4) (rileyfc:1.1.1) (db:gtc-escherichia coli) b4323 b4323 Escherichia coli 562 -11532675 104081 uxub (ec:1.1.1.57) (de:d-mannonate oxidoreductase, (fructuronate reductase)) (db:swissprot) UXUB_ECOLI P39160 ESCHERICHIA COLI 562 -11532675 205510 uxub fructuronate reductase:uxub:d-mannonate oxidoreductase (cl:conserved hypothetical protein yel070w) (ec:1.1.1.57) (db:pir2.dat) S56548 S56548 Escherichia coli 562 -11532675 237528 uxub mannonate oxidoreductase (sr:escherichia coli (strain:k12) cell_line:w3110 dna) (db:genpept-bct1) (ec:1.1.1.57) (de:escherichia coli uxua, uxub and uxur genes for mannonatedehydratase, mannonate oxidoreductase and uxu regulon repressor,complete cds.) (le:1845) (re:3305) (di:di... D13329 D13329 g1841885 Escherichia coli 562 -11532675 7500893931 uxub d-mannonate oxidoreductase (db:genpept-bct1) (ec:1.1.1.57) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 13) (le:243733) (re:245193) (di:direct) ECOUW93 U14003 g537164 Escherichia coli 562 -11532675 301663 uxub d-mannonate oxidoreductase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:1.1.1.57) (de:escherichia coli k-12 mg1655 section 393 of 400 of the completegenome.) (nt:o486; 100 pct identical to uxub_ecoli sw: p39160;) (le:1441) (re:2901) (di:direct) AE000503 AE000503 g1790779 Escherichia coli 562 -11532675 5000690070 (de:(ecoli_4206) (pn:d-mannonate oxidoreductase) (gn:uxub) (gtcfc:1.4) (ec:1.1.1.57) (uxub_ecoli) (keggfc:1.4) (rileyfc:1.1.1) (db:gtc-escherichia coli)) ECOLI_4206 ECOLI_4206 Escherichia coli 562 10045851				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821527	7221	29377	273	90

#### Description

6500728818 arac:b0064 arabinose operon regulatory protein (gtcfc:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b0064 b0064 Escherichia coli 562 -11532676 233594 arac (de:arabinose operon regulatory protein) (db:swissprot) ARAC\_ECOLI P03021 ESCHERICHIA COLI 562 -11532676 131452 arac arabinose operon transcription regulator:arabinose operon regulatory protein (cl:arabinose operon regulatory protein) (db:pir1.dat) (mp:1 min) RGECA A91473 Escherichia coli 562 -11532676 232378 (db:genpept-bct1) (de:e. coli gene arac.) (nt:reading frame of arac protein) (le:270) (re:1148) (di:direct) ECARAC V00256 g40936 Escherichia coli 562 -11532676 407510 arac (db:genpept-bct1) (de:e. coli gene arac encoding the l-arabinose operon regulator.) (le:165) (re:1043) (di:direct) ECARAX V00259 g808965 Escherichia coli 562 -11532676 233825 arac arabinose operon regulatory protein (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (le:70047) (re:70925) (di:direct) ECO110K D10483 g216484 Escherichia coli 562 -11532676 7500877064 (sr:e.coli) (db:genpept-bct1) (de:e.coli arabad promoter region and arac gene coding for activatorand repressor proteins; l-arabinose operon.) (nt:arac protein) (le:99) (re:977) (di:complement) ECOARABOP J01641 g455167 Escherichia coli 562 -11532676 232372 arac transcriptional regulator for ara operon (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 7 of 400 of the completegenome.) (nt:o292; 100 pct identical to arac\_ecoli sw: p03021) (le:200) (re:1078) (di:direct) AE000117 AE000117 g1786251 Escherichia coli 562 -11532676 7502851789 arac arac protein (db:genpept-syn) (de:cloning vector pbad-gfpuv, complete sequence.) (nt:pid: g455167) (le:96) (re:974) (di:complement) CVU62637 U62637 g1490532 Cloning vector pBAD-GFPuv 50707 -11532676 59960 arac (de:arabinose operon regulatory protein) (db:swissprot) ARAC\_ECOLI P03021 ESCHERICHIA COLI 562 -11532676

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821530	7222	29378	186	61

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821533	7223	29379	483	160

Description

6500728819 sfsa:sfs1:b0146 sugar fermentation stimulation protein  
(gtcf:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b0146  
b0146 Escherichia coli 562 -11532677 98452 sfsa:sfs1 (de:sugar fermentation  
stimulation protein) (db:swissprot) SFSA\_ECOLI P18273 ESCHERICHIA COLI 562  
-11532677 164660 sfsa:sfs1 sugar fermentation stimulation protein:maltose  
metabolism regulatory protein sfs1 (cl:sugar fermentation stimulation  
protein) (db:pir2.dat) (mp:4 min) A43671 A43671 Escherichia coli 562  
-11532677 235972 sfs1 regulatory protein sfs1 involved in maltose  
(sr:escherichia coli (sub\_strain w3110, strain k-12) (library: kohara')  
(db:genpept-bct1) (de:escherichia coli genome, 2.4-4.1 min region  
(110,917-193,643 bpfrom 0 min).) (le:49378) (re:50082) (di:complement)  
ECO82K D26562 g473805 Escherichia coli 562 -11532677 301616 sfs1 sugar  
fermentation stimulation protein 1 (sr:e.coli (strain k-12) dna)  
(db:genpept-bct1) (de:e.coli sfs1 gene, complete cds.) (nt:putative)  
(le:241) (re:945) (di:direct) ECOSFS1A M60726 g147813 Escherichia coli 562  
-11532677 233678 sfsa probable regulator for maltose metabolism  
(fn:putative regulator; degradation of small) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 14 of 400 of the completegenome.)  
(nt:f234; 100 pct identical to sfsa\_ecoli sw: p18273) (le:119) (re:823)  
(di:complement) AE000124 AE000124 g1786340 Escherichia coli 562 -11532677

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821536	7224	29380	198	65

Description

GTC ORF with score 147 to: (sr:thale cress) (db:genpept-pln1)  
(de:arabidopsis thaliana dna chromosome 4, bac clone f28j12  
(essaiiproject).) (nt:similar to hypothetical protein ydl219w - yeast)  
(le:55211:55342:55607) (re:55248:55482:55637) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821542	7225	29381	381	126
<u>Description</u>				
6500728820 hypothetical protein (gtcfc:1.4) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0298 b0298 Escherichia coli 562 -11532678				
7000691144 hypothetical protein b1027:hypothetical protein b0298:hypothetical protein b0373:hypothetical protein b0540:hypothetical protein b2088 (db:pir2.dat) A64845 A64845 Escherichia coli 562 -11532678				
7500959938 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:23080) (re:23388) (di:direct) ECU73857 U73857 g1657498 Escherichia coli 562 -11532678 7500959939 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:100192) (re:100500) (di:complement) ECU73857 U73857 g1657568 Escherichia coli 562 -11532678 7500959940 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:7464) (re:7772) (di:direct) ECU82598 U82598 g1778454 Escherichia coli 562 -11532678 239919 b0298 putative factor (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 27 of 400 of the completegenome.) (nt:o102; 33 pct identical (5 gaps) to 90 residues of) (le:2898) (re:3206) (di:direct) AE000137 AE000137 g1786489 Escherichia coli 562 -11532678 239989 b0373 putative factor (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 34 of 400 of the completegenome.) (nt:f102; this 102 aa orf is 33 pct identical (5 gaps)) (le:2424) (re:2732) (di:complement) AE000144 AE000144 g1786571 Escherichia coli 562 -11532678 240050 b0540 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 50 of 400 of the completegenome.) (nt:o102; this 102 aa orf is 33 pct identical (5 gaps)) (le:181) (re:489) (di:direct) AE000160 AE000160 g1786752 Escherichia coli 562 -11532678 7500959936 b1027 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 94 of 400 of the completegenome.) (nt:f102; this 102 aa orf is 33 pct identical (5 gaps)) (le:10349) (re:10657) (di:complement) AE000204 AE000204 g1787264 Escherichia coli 562 -11532678 7500959937 b2088 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 188 of 400 of the completegenome.) (nt:o102; this 102 aa orf is 33 pct identical (5 gaps)) (le:5183) (re:5491) (di:direct) AE000298 AE000298 g1788404 Escherichia coli 562 -11532678				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821546	7226	29382	330	109

Description

6500728821 cynr:b0338 cyn operon transcriptional activator (gtcfc:10.2:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b0338 b0338  
 Escherichia coli 562 -11532679 67524 cynr (de:cyn operon transcriptional activator) (db:swissprot) CYNR\_ECOLI P27111 ESCHERICHIA COLI 562 -11532679  
 162885 cynr cyn operon regulatory protein cynr (cl:probable transcription regulator lsyr) (db:pir2.dat) A41900 A41900 Escherichia coli 562 -11532679  
 7500879857 cynr (fn:positive regulatory protein for the cyn operon) (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli cynr (cynr) gene, complete cds.) (le:92) (re:991) (di:direct) ECOCYNR M93053 g145646  
 Escherichia coli 562 -11532679 234084 cynr cyn operon positive regulator (fn:regulator; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 31 of 400 of the completegenome.) (nt:f299; 100 pct identical to cynr\_ecoli sw: p27111) (le:199) (re:1098) (di:complement) AE000141 AE000141 g1786533 Escherichia coli 562 -11532679

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821554	7227	29383	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821570	7228	29384	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821571	7229	29385	201	66
<u>Description</u>				
6500728822 laca:b0342 galactoside acetyltransferase:thiogalactoside acetyltransferase (gtcfc:1.4) (ec:2.3.1.18) (keggfc:14.1) (rileyfc:1.1.1) (db:gtc-escherichia coli) b0342 b0342 Escherichia coli 562 -11532680 234949 laca (ec:2.3.1.18) (de:acetyltransferase)) (db:swissprot) THGA_ECOLI P07464 ESCHERICHIA COLI 562 -11532680 123352 laca galactoside o-acetyltransferase::acetyl-coa:beta-d-galactoside 6-acetyltransferase:thiogalactoside acetyltransferase:thiogalactoside transacetylase (cl:galactoside acetyltransferase) (ec:2.3.1.18) (db:pirl.dat) (mp:8 min) XXECTG A94061 Escherichia coli 562 -11532680 1500685580 thiogalactoside transacetylase (db:genpept-bct1) (de:escherichia coli laca gene for thiogalactoside transacetylase.) (le:82) (re:693) (di:direct) ECLACA X51872 g581122 Escherichia coli 562 -11532680 7500893029 laca (sr:escherichia coli dna; mrna; clone lambda-h80dlac dna; clone puk217) (db:genpept-bct1) (de:e.coli lactose operon with laci, lacz, lacy and laca genes.) (nt:thiogalactoside acetyltransferase (ttg start) (le:5727) (re:6338) (di:direct) ECOLAC J01636 g551814 Escherichia coli 562 -11532680 233302 laca thiogalactoside acetyltransferase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:2.3.1.18) (de:escherichia coli k-12 mg1655 section 31 of 400 of the completegenome.) (nt:f203; thiogalactoside acetyltransferase; 100 pct) (le:3657) (re:4268) (di:complement) AE000141 AE000141 g1786537 Escherichia coli 562 -11532680 7502851790 laca thiogalactoside acetyltransferase (db:genpept-syn) (ec:2.3.1.18) (de:synthetic transposon tn5lac, complete sequence.) (le:5444) (re:6055) (di:direct) XXU90436 U90436 g2055400 synthetic construct 32630 -11532680 101296 laca (ec:2.3.1.18) (de:acetyltransferase)) (db:swissprot) THGA_ECOLI P07464 ESCHERICHIA COLI 562 -11532680				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821572	7230	29386	243	81
<u>Description</u>				
6500728823 lacz:b0344 beta-galactosidase:lactase (gtcfc:1.4:1.6:8.1:8.5) (ec:3.2.1.23) (keggfc:1.6:8.1:8.5) (rileyfc:1.1.1) (db:gtc-escherichia coli) b0344 b0344 Escherichia coli 562 -11532681 124682 lacz beta-galactosidase:lacz:beta-d-galactosidase:lactase (cl:beta-galactosidase) (ec:3.2.1.23) (db:pir1.dat) (mp:8 min) GBEC A90981 Escherichia coli 562 -11532681 239961 lacz (sr:escherichia coli dna; mrna; clone lambda-h80dlac dna; clone puk217) (db:genpept-bct1) (de:e.coli lactose operon with laci, lacz, lacy and laca genes.) (nt:beta-d-galactosidase) (le:1284) (re:4358) (di:direct) ECOLAC J01636 g146577 Escherichia coli 562 -11532681 407048 lacz beta-galactosidase (db:genpept-bct1) (ec:3.2.1.23) (de:escherichia coli chromosome minutes 6-8.) (le:71026) (re:74100) (di:complement) ECU73857 U73857 g1657540 Escherichia coli 562 -11532681 234947 lacz beta-d-galactosidase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:3.2.1.23) (de:escherichia coli k-12 mg1655 section 31 of 400 of the completegenome.) (nt:f1024; 100 pct identical to bgal_ecoli sw: p00722) (le:5639) (re:8713) (di:complement) AE000141 AE000141 g1786539 Escherichia coli 562 -11532681 407339 lacz gene fro....:e (db:genpept-syn) (de:artificial dna sequence (pgd57) of pbr322 derived cloning vector.) (le:928) (re:4003) (di:complement) APGD57 X67019 g58035 unidentified 32644 -11532681 408318 lacz beta-galactosidase (db:genpept-syn) (de:cloning vector lambda txf97, lacz transcriptional fusion vector,complete sequence.) (nt:ecori site normally present at the end of lacz has) (le:20812) (re:23886) (di:complement) CVU37692 U37692 g1051183 Cloning vector lambda TXF97 43300 -11532681 408501 (sr:synthetic plasmid ptl61t (natural host e.coli)) (db:genpept-syn) (de:cloning vector ptl61t, complete sequence.) (nt:beta-d-galactosidase) (le:256) (re:3330) (di:direct) SYNPTL61T M29896 g209191 unidentified cloning vector 45196 -11532681 1500689806 lacz beta-galactosidase (db:genpept-syn) (de:cloning vector pz1918 with lacz cassette, complete sequence.) (le:550) (re:3624) (di:direct) U03993 U03993 g434653 Cloning vector pZ1918 31867 -11532681 7500953301 lacz beta-d-galactosidase (db:genpept-syn) (ec:3.2.1.23) (de:synthetic transposon tn5lac, complete sequence.) (le:1001) (re:4075) (di:direct) XXU90436 U90436 g2055398 synthetic construct 32630 -11532681 5000690087 (de:(ecoli_328) (pn:beta-d-galactosidase) (gn:lacz) (gtcfc:1.6:8.4:8.5) (ec:3.2.1.23) (bgal_ecoli) (keggfc:1.6:8.5) (rileyfc:1.1.1) (db:gtc-escherichia coli)) ECOLI_328 ECOLI_328 Escherichia coli 562 10122785				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821576	7231	29387	810	269

Description

6500728824 laci:b0345 lactose operon repressor (gtcfc:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b0345 b0345 Escherichia coli 562 -11532682 130806 laci lactose operon repressor:lac repressor (cl:lac repressor) (db:pir1.dat) (mp:8 min) RPECL A93198 Escherichia coli 562 -11532682 212759 lac repressor (db:pir4.dat) S58116 S58116 synthetic 32630 -11532682 407139 laci transcriptional repressor of the lac operon (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 31 of 400 of the completegenome.) (nt:f360; 99 pct identical to laci\_ecoli sw: p03023) (le:8836) (re:9918) (di:complement) AE000141 AE000141 g1786540 Escherichia coli 562 -11532682 407310 laci lac repressor (db:genpept-syn) (de:shuttle vector pmal-piii, complete sequence.) (nt:transcriptional repressor) (le:81) (re:1163) (di:direct) AF031088 AF031088 g2623822 Shuttle vector pMAL-pIII 69327 -11532682 407822 laci lac repressor (db:genpept-syn) (de:expression vector pmal-x, complete sequence.) (le:81) (re:1163) (di:direct) AF031813 AF031813 g2654022 Expression vector pMal-X 69411 -11532682 408128 laci lac repressor (db:genpept-syn) (de:expression vector ppk121, complete sequence.) (nt:laci) (le:3648) (re:4730) (di:complement) AF055298 AF055298 g3023158 Expression vector pPK121 74939 -11532682 7000688974 laci (db:genpept-syn) (de:artificial dna; cloning vector pniv136.) (le:1835) (re:2917) (di:direct) ASAK3115 AJ223115 g3929621 synthetic construct 32630 -11532682 7502851791 laci (db:genpept-syn) (de:artificial dna; cloning vector pniv143.) (le:1950) (re:3032) (di:direct) ASAK3116 AJ223116 g3929623 synthetic construct 32630 -11532682 7502851792 laci (db:genpept-syn) (de:artificial dna; cloning vector pniv144.) (le:1951) (re:3033) (di:direct) ASAK3117 AJ223117 g3929633 synthetic construct 32630 -11532682 7502851793 laci (db:genpept-syn) (de:artificial dna; cloning vector pin-iii-ompa-hind.) (le:1909) (re:2991) (di:direct) ASAK3118 AJ223118 g3929635 synthetic construct 32630 -11532682 7502851794 laci (db:genpept-syn) (de:artificial dna; cloning vector pniv145.) (le:1946) (re:3028) (di:direct) ASAK3119 AJ223119 g3929637 synthetic construct 32630 -11532682 7502851795 laci (db:genpept-syn) (de:artificial dna; cloning vector pniv212.) (le:1362) (re:2444) (di:direct) ASAK3120 AJ223120 g3929639 synthetic construct 32630 -11532682 7502851796 laci (db:genpept-syn) (de:artificial dna; cloning vector pin-iii-ompa1.) (le:1884) (re:2966) (di:direct) ASAK3121 AJ223121 g3929641 synthetic construct 32630 -11532682 7502851797 laci (db:genpept-syn) (de:artificial dna; cloning vector pin-iii-ompa2.) (le:1885) (re:2967) (di:direct) ASAK3122 AJ223122 g3929643 synthetic construct 32630 -11532682 7502851798 laci (db:genpept-syn) (de:artificial dna; cloning vector pin-iii-ompa3.) (le:1883) (re:2965) (di:direct) ASAK3123 AJ223123 g3929645 synthetic construct 32630 -11532682 408580 lac-repressor (db:genpept-syn) (de:artificial dna for ptnmax5 mini-transposon.) (le:5508) (re:6590) (di:direct) ASTNMAX5 Z50120 g1359488 unidentified 32644 -11532682 408583 lac operon repressor (db:genpept-syn) (de:expression vector pcaln, complete sequence.) (le:940) (re:2022) (di:direct) CVU36454 U36454 g1041778 Cloning vector pCALn 43136 -11532682 408586 repressor protein (sr:cloning vector

vector pCALn 43136 -11532682 408586 repressor protein (sr:cloning vector  
dna) (db:genpept-sym) (de:cloning vector ptugas (derived from a coli jm105))

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501821577	7232	29388	687	228

Description

6500728825 malz:b0403 maltodextrin glucosidase:alpha-glucosidase  
(gtcfc:1.4:1.6:7.2) (ec:3.2.1.20) (keggfc:1.6:7.1) (rileyfc:1.1.1)  
(db:gtc-escherichia coli) b0403 b0403 Escherichia coli 562 -11532683 82920  
malz (ec:3.2.1.20) (de:maltodextrin glucosidase, (alpha-glucosidase))  
(db:swissprot) MALZ\_ECOLI P21517 ESCHERICHIA COLI 562 -11532683 7000685784  
malz alpha-glucosidase::maltodextrin glucosidase  
(cl:neopullulanase:alpha-amylase core homology) (ec:3.2.1.20) (db:pir2.dat)  
(mp:9.3 min) C64769 C64769 Escherichia coli 562 -11532683 7500885283 malz  
maltodextrin glucosidase (db:genpept-bct1) (de:escherichia coli minutes 9 to  
11 genomic sequence.) (le:1965) (re:3782) (di:direct) ECU82664 U82664  
g1773087 Escherichia coli 562 -11532683 240180 malz maltodextrin  
glucosidase (fn:enzyme; degradation of small molecules: carbon)  
(db:genpept-bct2) (ec:3.2.1.20) (de:escherichia coli k-12 mg1655 section 37  
of 400 of the completegenome.) (nt:o605; 99 pct identical to malz\_ecoli sw:  
p21517) (le:108) (re:1925) (di:direct) AE000147 AE000147 g1786604  
Escherichia coli 562 -11532683 5000690088 (de:(ecoli\_387) (pn:maltodextrin  
glucosidase) (gn:malz) (gtcfc:1.6:7.2) (ec:3.2.1.20) (malz\_ecoli)  
(keggfc:1.6:7.1) (rileyfc:1.1.1) (db:gtc-escherichia coli)) ECOLI\_387  
ECOLI\_387 Escherichia coli 562 10122817

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821578	7233	29389	279	92

#### Description

6500728826 galk:gala:b0757 galactokinase (gtcfc:1.4:1.6) (ec:2.7.1.6) (keggfc:1.6) (rileyfc:1.1.1) (db:gtc-escherichia coli) b0757 b0757  
 Escherichia coli 562 -11532684 123515 galk:gala galactokinase (cl:galactokinase) (ec:2.7.1.6) (db:pir1.dat) (mp:17 min) KIECGG B23044  
 Escherichia coli 562 -11532684 223192 galk galactokinase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #179) (db:genpept-bct1) (de:escherichia coli genomic dna. (16.8 - 17.1 min).) (le:8895) (re:10043) (di:complement) D90714 D90714 g1651342 Escherichia coli 562 -11532684 407044 (db:genpept-bct1) (de:e. coli galk gene for galaktokinase and galt carboxy-terminalregion.) (nt:galaktokinase) (le:172) (re:1320) (di:direct) ECGALK X02306 g41532 Escherichia coli 562 -11532684 232963 galk galactokinase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:2.7.1.6) (de:escherichia coli k-12 mg1655 section 68 of 400 of the completegenome.) (nt:f382; 100 pct identical to gall\_ecoli sw: p06976) (le:3981) (re:5129) (di:complement) AE000178 AE000178 g1786972 Escherichia coli 562 -11532684 407049 galk (db:genpept-syn) (de:artificial dna sequence (pgd56) of pbr322 derived cloning vector.) (le:1049) (re:2197) (di:direct) APDG56 X67018 g58030 unidentified 32644 -11532684 408574 galk gene fro...:e (db:genpept-syn) (de:artificial dna sequence (pgd57) of pbr322 derived cloning vector.) (le:4262) (re:5411) (di:direct) APGD57 X67019 g58033 unidentified 32644 -11532684 7500953246 galk galactokinase (db:genpept-syn) (de:pdr540 cloning vector, complete sequence.) (le:282) (re:1430) (di:direct) XXU13847 U13847 g595700 unidentified cloning vector 45196 -11532684 5000690089 galk galactokinase ec 2.7.1.6 . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #179) (db:genpept) (de:escherichia coli genomic dna. (16.8 - 17.1 min).) (nt:orf\_id:ol79#8; similar to pir accession number) (le:8895) (re:10043) (di:complement) D90714 D90714 g1651342 Escherichia coli 562 -11532684

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821579	7234	29390	912	303

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821580	7235	29391	192	63

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821586	7236	29392	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821607	7237	29393	1884	627

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821619	7238	29394	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821629	7239	29395	1674	558

Description

6500728827 galt:galb:b0758 galactose-1-phosphate uridylyltransferase  
(gtcfc:1.4:1.6:4.3) (ec:2.7.7.10) (keggfc:1.6:4.3) (rileyfc:1.1.1)  
(db:gtc-escherichia coli) b0758 b0758 Escherichia coli 562 -11532685 73041  
galt:galb (ec:2.7.7.10) (de:galactose-1-phosphate uridylyltransferase,)  
(db:swissprot) GAL7\_ECOLI P09148 ESCHERICHIA COLI 562 -11532685 124048 galt  
udpoglucose--hexose-1-phosphate uridylyltransferase::galactose-1-phosphate  
uridylyltransferase:utp--hexose-1-phosphate uridylyltransferase  
(cl:udpoglucose--hexose-1-phosphate uridylyltransferase)  
(ec:2.7.7.12:2.7.7.10) (db:pir1.dat) (mp:17 min) XNECUD S00722 Escherichia  
coli 562 -11532685 223193 galt udpoglucose-hexose-1-phosphate uridylyl-  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #179)  
(db:genpept-bct1) (de:escherichia coli genomic dna.(16.8 - 17.1 min).)  
(le:10047) (re:11093) (di:complement) D90714 D90714 g1651343 Escherichia  
coli 562 -11532685 7500882077 galt galactose-1-phosphate  
uridylyltransferase (fn:enzyme; degradation of small molecules: carbon)  
(db:genpept-bct2) (ec:2.7.7.10) (de:escherichia coli k-12 mg1655 section 68  
of 400 of the completegenome.) (nt:f348; 99 pct identical to gal7\_ecoli sw:  
p09148;) (le:5133) (re:6179) (di:complement) AE000178 AE000178 g1786973  
Escherichia coli 562 -11532685 5000690090 galt  
udpoglucose-hexose-1-phosphate (sr:escherichia coli(strain:k12) dna,  
clone:kohara clone #179) (db:genpept) (de:escherichia coli genomic dna.  
(16.8 - 17.1 min).) (nt:orf\_id:o179#9; similar to pir accession number)  
(le:10047) (re:11093) (di:complement) D90714 D90714 g1651343 Escherichia  
coli 562 -11532685

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821634	7240	29396	321	106
<u>Description</u>				
6500728828 gale:gald:b0759 udp-glucose 4-epimerase:galactowaldenase:udp-galactose 4-epimerase (gtcfc:4.3:1.6) (ec:5.1.3.2) (keggfc:1.6:4.3) (rileyfc:1.1.1) (db:gtc-escherichia coli) b0759 b0759 Escherichia coli 562 -11532686 304570 gale:gald (ec:5.1.3.2) (de:galactose 4-epimerase)) (db:swissprot) GALE_ECOLI P09147 ESCHERICHIA COLI 562 -11532686 125739 gale udpglucose 4-epimerase::udpgalactose 4-epimerase (cl:escherichia coli udpglucose 4-epimerase:udpglucose 4-epimerase homology) (ec:5.1.3.2) (db:pir1.dat) (mp:17 min) XUECUG S02089 Escherichia coli 562 -11532686 223194 gale udp-glucose 4-epimerase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #179) (db:genpept-bct1) (de:escherichia coli genomic dna. (16.8 - 17.1 min).) (le:11103) (re:12119) (di:complement) D90714 D90714 g1651344 Escherichia coli 562 -11532686 5000690091 (db:genpept-bct1) (de:e. coli genes gale and galt for udp-galactose-4-epimerase andgalactose-1-p uridyltransferase.) (nt:udp-galactose-4-epimerase) (le:1) (re:1017) (di:direct) ECGALET X06226 g41523 Escherichia coli 562 -11532686 232956 gale udp-galactose-4-epimerase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:5.1.3.2) (de:escherichia coli k-12 mg1655 section 68 of 400 of the completegenome.) (nt:f338; 100 pct identical to gale_ecoli sw: p09147;) (le:6189) (re:7205) (di:complement) AE000178 AE000178 g1786974 Escherichia coli 562 -11532686 7502851802 gald udp-glucose 4-epimerase ec 5.1.3.2 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #179) (db:genpept) (de:escherichia coli genomic dna. (16.8 - 17.1 min).) (nt:orf_id:o179#10; similar to swissprot accession) (le:11103) (re:12119) (di:complement) D90714 D90714 g1651344 Escherichia coli 562 -11532686 73070 gale:gald (ec:5.1.3.2) (de:galactose 4-epimerase)) (db:swissprot) GALE_ECOLI P09147 ESCHERICHIA COLI 562 -11532686				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821637	7241	29397	594	198
<u>Description</u>				
6500728829 poxb:b0871 cytochrome:pyruvate oxidase:pox:pyruvate dehydrogenase:ubiquinone (gtcfc:1.4:1.8:9.12) (ec:1.2.2.2) (keggfc:1.8) (rileyfc:1.1.1) (db:gtc-escherichia coli) b0871 b0871 Escherichia coli 562 -11532687 7500888297 poxb (ec:1.2.2.2) (de:(pox) (pyruvate dehydrogenase (ubiquinone))) (db:swissprot) POXB_ECOLI P07003 ESCHERICHIA COLI 562 -11532687 125546 poxb pyruvate dehydrogenase cytochrome::pyruvate oxidase (cl:acetolactate synthase large chain:thiamine pyrophosphate-binding domain homology) (ec:1.2.2.2) (db:pir1.dat) (mp:19 min) DEECPC A23648 Escherichia coli 562 -11532687 223239 poxb pyruvate dehydrogenase cytochrome (sr:escherichia coli(strain:k12) dna, clone:kohara clone #211) (db:genpept-bct1) (de:escherichia coli genomic dna.(19.3 - 19.7 min).) (le:11610) (re:13328) (di:complement) D90724 D90724 g1651398 Escherichia coli 562 -11532687 5000690101 pyruvate oxidase (db:genpept-bct1) (de:e. coli poxb gene for pyruvate oxidase.) (le:179) (re:1897) (di:direct) ECPOXB X04105 g42473 Escherichia coli 562 -11532687 237864 poxb pyruvate oxidase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:1.2.2.2) (de:escherichia coli k-12 mg1655 section 78 of 400 of the completegenome.) (nt:f572; 100 pct identical to poxb_ecoli sw: p07003) (le:9617) (re:11335) (di:complement) AE000188 AE000188 g1787096 Escherichia coli 562 -11532687 7502851803 poxb pyruvate dehydrogenase cytochrome ec (sr:escherichia coli(strain:k12) dna, clone:kohara clone #211) (db:genpept) (de:escherichia coli genomic dna. (19.4 - 19.8 min).) (nt:orf_id:o211#14; similar to pir accession number) (le:11610) (re:13328) (di:complement) D90724 D90724 g1651398 Escherichia coli 562 -11532687 90613 poxb (ec:1.2.2.2) (de:(pox) (pyruvate dehydrogenase (ubiquinone))) (db:swissprot) POXB_ECOLI P07003 ESCHERICHIA COLI 562 -11532687				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821648	7242	29398	390	129

Description

6500728830 mana:pmi:b1613 mannose-6-phosphate isomerase:phosphomannose isomerase:pmi:phosphohexomutase (gtcfc:1.4:1.5) (ec:5.3.1.8) (keggfc:1.5) (rileyfc:1.1.1) (db:gtc-escherichia coli) b1613 b1613 Escherichia coli 562 -11532688 82934 mana:pmi (ec:5.3.1.8) (de:(pmi) (phosphohexomutase)) (db:swissprot) MANA\_ECOLI P00946 ESCHERICHIA COLI 562 -11532688 125798 mana mannose-6-phosphate isomerase::phosphohexomutase:phosphomannose isomerase (cl:mannose-6-phosphate isomerase) (ec:5.3.1.8) (db:pir1.dat) (mp:35.5 min) ISECMP A01172 Escherichia coli 562 -11532688 224039 mana:pmi mannose-6-phosphate isomerase ec 5.3.1.8 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #313(36.1-36.4 min.)) (nt:orf\_id:o312#13; similar to (swissprot accession) (le:12396) (re:13571) (di:direct) D90804 D90804 g1742663 Escherichia coli 562 -11532688 300738 mana:pmi mannose-6-phosphate isomerase ec 5.3.1.8 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #314(36.3-36.7 min.)) (nt:orf\_id:o312#13; similar to (swissprot accession) (le:3260) (re:4435) (di:direct) D90805 D90805 g1742668 Escherichia coli 562 -11532688 300734 mana (sr:e.coli (strain gm242) dna, clone pgs57) (db:genpept-bct1) (de:e.coli mana gene encoding phosphomannose isomerase, complete cds.) (nt:phosphomannose isomerase) (le:392) (re:1567) (di:direct) ECOMANAA M15380 g146722 Escherichia coli 562 -11532688 235054 mana mannose-6-phosphate isomerase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:5.3.1.8) (de:escherichia coli k-12 mg1655 section 147 of 400 of the completegenome.) (nt:o391; 100 pct identical to mana\_ecoli sw: p00946) (le:153) (re:1328) (di:direct) AE000257 AE000257 g1787899 Escherichia coli 562 -11532688 224043 mana:pmi mannose-6-phosphate isomerase ec 5.3.1.8 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #314(36.3-36.7 min.)) (nt:orf\_id:o312#13; similar to (swissprot accession) (le:3260) (re:4435) (di:direct) D90805 D90805 g1742668 Escherichia coli 562 -11532688 5000690073 (de:(ecoli\_1572) (pn:mannose-6-phosphate isomerase) (gn:mana) (gtcfc:1.5) (ec:5.3.1.8) (mana\_ecoli) (keggfc:1.5) (rileyfc:1.1.1) (db:gtc-escherichia coli)) ECOLI\_1572 ECOLI\_1572 Escherichia coli 562 10025154

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821650	7243	29399	426	141

# Description

6500728831 uida:gusa:gura:b1617  
beta-d-glucuronidase:beta-glucuronidase:gus:beta-d-glucuronoside  
glucuronosohydrolase (gtcfc:1.4:7.2:9.10) (ec:3.2.1.31) (keggfc:7.1:9.10)  
(rileyfc:1.1.1) (db:gtc-escherichia coli) b1617 b1617 Escherichia coli 562  
-11532689 61662 uida:gusa:gura (ec:3.2.1.31) (de:glucuronosohydrolase))  
(db:swissprot) BGLR\_ECOLI P05804 ESCHERICHIA COLI 562 -11532689 162783 uida  
beta-glucuronidase:uida:beta-d-glucuronoside glucuronosohydrolase:gusa  
protein (cl:beta-glucuronidase) (ec:3.2.1.31) (db:pir1.dat) (mp:36 min)  
GBECGC C64918 Escherichia coli 562 -11532689 7500877787 uida:gusa:gura  
b-glucuronidase ec 3.2.1.31 gus (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #314(36.3-36.7 min.)) (nt:orf\_id:o314#3; similar to (swissprot  
accession) (le:8944) (re:10755) (di:complement) D90805 D90805 g1742671  
Escherichia coli 562 -11532689 258679 uida beta-glucuronidase  
(db:genpept-bct1) (de:uida=beta-glucuronidase (escherichia coli, genomic,  
1812 nt.)) (nt:glu-279 in previously reported sequence is replaced) (le:1)  
(re:1812) (di:direct) S69414 S69414 g545894 Escherichia coli 562 -11532689  
224046 uida beta-d-glucuronidase (fn:enzyme; degradation of small  
molecules: carbon) (db:genpept-bct2) (ec:3.2.1.31) (de:escherichia coli k-12  
mg1655 section 147 of 400 of the completegenome.) (nt:f603; 100 pct  
identical to bglr\_ecoli sw: p05804;) (le:5837) (re:7648) (di:complement)  
AE000257 AE000257 g1787903 Escherichia coli 562 -11532689 407133 st-ls1  
gluceronidase (db:genpept-syn) (de:artificial sequences t-dna of binary  
vector pmog553.) (le:115:689) (re:499:2115) (di:directjoin) ASTDNABV X84105  
g642973 unidentified 32644 -11532689 7000684703 uida  
beta-glucuronidase::beta-d-glucuronoside glucuronosohydrolase  
(cl:beta-glucuronidase) (ec:3.2.1.31) (db:pir) (mp:36 min) GBECGC I53717  
Escherichia coli 562 -11532689 300741 st-ls1 gluceronidase (db:genpept-syn)  
(de:artificial sequences t-dna of binary vector pmog553.) (le:115:689)  
(re:499:2115) (di:directjoin) ASTDNABV X84105 g642973 unidentified 32644  
-11532689 5000690543 (de:(ecoli\_1576) (pn:beta-d-glucuronidase) (gn:uida)  
(gtcfc:7.2:9.10) (ec:3.2.1.31) (bglr\_ecoli) (keggfc:7.1:9.10)  
(rileyfc:1.1.1) (db:gtc-escherichia coli)) ECOLI\_1576 ECOLI\_1576 Escherichia  
coli 562 10004371



ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501821651	7244	29400	390	129

# Description

6500728832 mali:b1620 repressor protein:maltose regulon regulatory protein mali (gtcfc:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b1620 b1620 Escherichia coli 562 -11532690 82901 mali (de:maltose regulon regulatory protein mali) (db:swissprot) MALI\_ECOLI P18811 ESCHERICHIA COLI 562 -11532690 7000685782 mali maltose regulon repressor mali (cl:lac repressor) (db:pir1.dat) (mp:36 min) RPECML F64918 Escherichia coli 562 -11532690 224049 mali maltose regulon regulatory protein mali. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #314(36.3-36.7 min.)) (nt:orf\_id:o314#6; similar to (swissprot accession) (le:12836) (re:13864) (di:complement) D90805 D90805 g1742674 Escherichia coli 562 -11532690 224056 mali maltose regulon regulatory protein mali. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #315(36.6-36.9 min.)) (nt:orf\_id:o314#6; similar to (swissprot accession) (le:1148) (re:2176) (di:complement) D90806 D90806 g1742682 Escherichia coli 562 -11532690 300769 mali maltose regulon regulatory protein mali. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #317(36.6-36.9 min.)) (nt:orf\_id:o314#6; similar to (swissprot accession) (le:1249) (re:2277) (di:complement) D90808 D90808 g1742714 Escherichia coli 562 -11532690 300744 mali repressor of malx and y genes (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 147 of 400 of the completegenome.) (nt:f342; this 342 aa orf is 97 pct identical (1 gap)) (le:9729) (re:10757) (di:complement) AE000257 AE000257 g1787906 Escherichia coli 562 -11532690 224086 mali maltose regulon regulatory protein mali. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #317(36.6-36.9 min.)) (nt:orf\_id:o314#6; similar to (swissprot accession) (le:1249) (re:2277) (di:complement) D90808 D90808 g1742714 Escherichia coli 562 -11532690

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821652	7245	29401	555	184

Description

6500728833 maly:b1622 maly protein (gtcfc:1.4:5.11:5.8) (ec:2.6.1.-)  
(keggfc:5.8:5.11) (rileyfc:1.1.1) (db:gtc-escherichia coli) b1622 b1622  
Escherichia coli 562 -11532691 82919 maly (ec:2.6.1.-) (de:maly protein,)  
(db:swissprot) MALY\_ECOLI P23256 ESCHERICHIA COLI 562 -11532691 164027 maly  
maly protein (ec:2.6.1.-) (db:pir2.dat) C42477 C42477 Escherichia coli 562  
-11532691 224051 maly maly protein (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #314(36.3-36.7 min.)) (nt:orf\_id:o314#8; similar to (pir  
accession number) (le:15641) (re:16813) (di:direct) D90805 D90805 g1742676  
Escherichia coli 562 -11532691 224058 maly maly protein (sr:escherichia  
coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #315(36.6-36.9 min.))  
(nt:orf\_id:o314#8; similar to (pir accession number) (le:3953) (re:5125)  
(di:direct) D90806 D90806 g1742684 Escherichia coli 562 -11532691 300771  
maly maly protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara  
lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#317(36.6-36.9 min.)) (nt:orf\_id:o314#8; similar to (pir accession number)  
(le:4054) (re:5226) (di:direct) D90808 D90808 g1742716 Escherichia coli 562  
-11532691 300746 maly (fn:degrades the inducer of the maltose system or)  
(sr:e.coli, cdna to mrna) (db:genpept-bct1) (de:e.coli mali, malx, and maly  
genes, complete cds.) (le:3015) (re:4187) (di:direct) ECOMALAA M60722  
g146693 Escherichia coli 562 -11532691 235037 maly enzyme that may degrade  
or block biosynthesis of (fn:enzyme; degradation of small molecules: carbon)  
(db:genpept-bct2) (ec:2.6.1.-) (de:escherichia coli k-12 mg1655 section 148  
of 400 of the completegenome.) (nt:o390; 100 pct identical to maly\_ecoli sw:  
p23256;) (le:1678) (re:2850) (di:direct) AE000258 AE000258 g1787909  
Escherichia coli 562 -11532691 224088 maly maly protein (sr:escherichia  
coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #317(36.6-36.9 min.))  
(nt:orf\_id:o314#8; similar to (pir accession number) (le:4054) (re:5226)  
(di:direct) D90808 D90808 g1742716 Escherichia coli 562 -11532691  
5000690376 (de:(ecoli\_1581) (pn:enzyme that may degrade or block  
biosynthesis of endogenous mal inducer, probably aminotrasferase) (gn:maly)  
(gtcfc:5.11:5.8) (ec:2.6.1.-) (maly\_ecoli) (keggfc:5.8:5.11) (rileyfc:1.1.1)  
(db:gtc-escherichia c) ECOLI\_1581 ECOLI\_1581 Escherichia coli 562 10025139

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821653	7246	29402	183	60
<u>Description</u>				
6500728834 nlpc:b1708 probable lipoprotein nlpc precursor:orf-17 (gtcfc:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b1708 b1708 Escherichia coli 562 -11532692 86104 nlpc (de:probable lipoprotein nlpc precursor (orf-17)) (db:swissprot) NLPC_ECOLI P23898 ESCHERICHIA COLI 562 -11532692 7000685975 nlpc probable lipoprotein nlpc precursor (cl:conserved hypothetical protein hi1314) (db:pir2.dat) D64929 D64929 Escherichia coli 562 -11532692 224155 nlpc probable lipoprotein nlpc precursor orf-17 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #322(38.4-38.8 min.)) (nt:orf_id:o322#9; similar to (swissprot accession) (le:9012) (re:9476) (di:complement) D90813 D90813 g1742788 Escherichia coli 562 -11532692 224167 nlpc probable lipoprotein nlpc precursor orf-17 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #323(38.6-39.0 min.)) (nt:orf_id:o322#9; similar to (swissprot accession) (le:1852) (re:2316) (di:complement) D90814 D90814 g1742801 Escherichia coli 562 -11532692 300824 (sr:e.coli (k12) dna, clone plcd25) (db:genpept-bct1) (de:e.coli btuced genes encoding vitamin b12 transport mechanisms,complete cds, orf17 encoding a protein of unknown function, andhima gene encoding integration host factor (ihf) alpha-subunit,partia... ECOBTUCED M14031 g145446 Escherichia coli 562 -11532692 233926 nlpc lipoprotein (fn:membrane; macromolecule synthesis,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 156 of 400 of the completegenome.) (nt:f154; 100 pct identical to nlpc_ecoli sw: p23898;) (le:2750) (re:3214) (di:complement) AE000266 AE000266 g1788001 Escherichia coli 562 -11532692				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821657	7247	29403	210	69
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821658	7248	29404	198	65
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821677	7249	29405	552	183
<u>Description</u>				
6500728835 celf:b1734 phospho-beta-glucosidase b:6-phospho-beta-glucosidase (gtcf:1.4) (ec:3.2.1.86) (keggfc:14.1) (rileyfc:1.1.1) (db:gtc-escherichia coli) b1734 b1734 Escherichia coli 562 -11532693 63806 celf (ec:3.2.1.86) (de:6-phospho-beta-glucosidase,) (db:swissprot) CELF_ECOLI P17411 ESCHERICHIA COLI 562 -11532693 7000684791 celf 6-phospho-beta-glucosidase:celf (ec:3.2.1.86) (db:pir2.dat) F64932 F64932 Escherichia coli 562 -11532693 224195 celf 6-phospho-b-glucosidase ec 3.2.1.86 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #325(38.9-39.2 min.)) (nt:orf_id:o326#3; similar to (swissprot accession) (le:9737) (re:11089) (di:complement) D90816 D90816 g1742831 Escherichia coli 562 -11532693 224203 celf 6-phospho-b-glucosidase ec 3.2.1.86 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #326(39.1-39.4 min.)) (nt:orf_id:o326#3; similar to (swissprot accession) (le:2508) (re:3860) (di:complement) D90817 D90817 g1742840 Escherichia coli 562 -11532693 300845 celf phospho-beta-glucosidase:cryptic (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:3.2.1.86) (de:escherichia coli k-12 mg1655 section 158 of 400 of the completegenome.) (nt:f450; 100 pct identical to 371 residues) (le:7055) (re:8407) (di:complement) AE000268 AE000268 g1788029 Escherichia coli 562 -11532693				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821680	7250	29406	1356	451

Description

6500728836 celd:b1735 cel operon repressor (gtcfc:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b1735 b1735 Escherichia coli 562 -11532694 233950 celd (de:cel operon repressor) (db:swissprot) CELD\_ECOLI P17410 ESCHERICHIA COLI 562 -11532694 164465 celd regulatory protein celd:cel operon repressor (db:pir2.dat) S10873 S10873 Escherichia coli 562 -11532694 224196 celd regulatory protein celd (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #325(38.9-39.2 min.)) (nt:orf\_id:o326#4; similar to (pir accession number) (le:11194) (re:12036) (di:complement) D90816 D90816 g1742832 Escherichia coli 562 -11532694 224204 celd regulatory protein celd (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #326(39.1-39.4 min.)) (nt:orf\_id:o326#4; similar to (pir accession number) (le:3965) (re:4807) (di:complement) D90817 D90817 g1742841 Escherichia coli 562 -11532694 300846 (db:genpept-bct1) (de:escherichia coli dna for cel operon including cela, celb, celc, celd and celf genes.) (nt:celd product, repressor of the cel operon) (le:2447) (re:3289) (di:direct) ECCELOPE X52890 g41100 Escherichia coli 562 -11532694 7502851804 celd (sr:e.coli dna) (db:genpept-bct1) (de:e.coli cellobiose permease proteins cela, celb, celc, cellobioseoperon repressor protein celd and cellobiose phospho-b-glucosidaseprotein celf gene, complete cds.) (nt:putative) (le:2447) (re:3289) (di:direct) ECOCELA M64438 g145481 Escherichia coli 562 -11532694 232509 celd negative transcriptional regulator of cel (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 158 of 400 of the completegenome.) (nt:f280; 100 pct identical to celd\_ecoli sw: p17410;) (le:8512) (re:9354) (di:complement) AE000268 AE000268 g1788030 Escherichia coli 562 -11532694 63804 celd (de:cel operon repressor) (db:swissprot) CELD\_ECOLI P17410 ESCHERICHIA COLI 562 -11532694

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821688	7251	29407	234	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821693	7252	29408	516	171

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821697	7253	29409	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821704	7254	29410	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821706	7255	29411	483	161

Description

6500728837 gatr\_1 (gtcfc:1.4) (keggfc:14.2) (rileyfc:1.1.1)  
(db:gtc-escherichia coli) b2087 b2087 Escherichia coli 562 -11532695  
7000690887 gatr\_1 gatr\_1 protein (db:pir2.dat) F64975 F64975 Escherichia  
coli 562 -11532695 224623 gatr galactitol utilization operon repressor  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #357(46.5-46.8  
min.)) (nt:orf\_id:o357#10; similar to (swissprot accession) (le:12445)  
(re:12891) (di:complement) D90846 D90846 g1736793 Escherichia coli 562  
-11532695 301274 gatr galactitol utilization operon repressor  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #358(46.6-46.9  
min.)) (nt:orf\_id:o357#10; similar to (swissprot accession) (le:7090)  
(re:7536) (di:complement) D90847 D90847 g1736805 Escherichia coli 562  
-11532695 301263 gatr\_1 split galactitol utilization operon repressor  
(fn:regulator; degradation of small molecules:) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 188 of 400 of the completegenome.)  
(nt:fl48; residues 1-78 are 93 pct identical to) (le:4649) (re:5095)  
(di:complement) AE000298 AE000298 g1788403 Escherichia coli 562 -11532695  
224634 gatr galactitol utilization operon repressor (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #358(46.6-46.9 min.))  
(nt:orf\_id:o357#10; similar to (swissprot accession) (le:7090) (re:7536)  
(di:complement) D90847 D90847 g1736805 Escherichia coli 562 -11532695

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821710	7256	29412	435	144

Description

6500728838 gatr\_2:b2090 galactitol utilization operon repressor (gtcfc:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b2090 b2090  
 Escherichia coli 562 -11532696 7000690884 gatr\_2:gatr galactitol utilization operon repressor (db:pir2.dat) A64976 A64976 Escherichia coli 562 -11532696 224625 gatr galactitol utilization operon repressor (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #357(46.5-46.8 min.)) (nt:orf\_id:o357#14; similar to (swissprot accession) (le:14147) (re:14485) (di:complement) D90846 D90846 g1736795 Escherichia coli 562 -11532696 301276 gatr galactitol utilization operon repressor (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #358(46.6-46.9 min.)) (nt:orf\_id:o357#14; similar to (swissprot accession) (le:8792) (re:9130) (di:complement) D90847 D90847 g1736807 Escherichia coli 562 -11532696 301265 gatr\_2 split galactitol utilization operon repressor (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 188 of 400 of the completegenome.) (nt:f112; residues 1-102 are 99 pct identical to) (le:6351) (re:6689) (di:complement) AE000298 AE000298 g1788406 Escherichia coli 562 -11532696 224636 gatr galactitol utilization operon repressor (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #358(46.6-46.9 min.)) (nt:orf\_id:o357#14; similar to (swissprot accession) (le:8792) (re:9130) (di:complement) D90847 D90847 g1736807 Escherichia coli 562 -11532696

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821712	7257	29413	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821713	7258	29414	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821729	7259	29415	1530	509

Description

6500728839 gals:b2151 mgl repressor and galactose ultrainduction factor (gtcfc:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b2151 b2151 Escherichia coli 562 -11532697 73091 gals (de:mgl repressor and galactose ultrainduction factor) (db:swissprot) GALS\_ECOLI P25748 ESCHERICHIA COLI 562 -11532697 7000685365 gals isorepressor gals (cl:lac repressor) (db:pir2.dat) F64983 F64983 Escherichia coli 562 -11532697 7500882100 gals (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (le:48373) (re:49413) (di:complement) ECOHU47 U00007 g405897 Escherichia coli 562 -11532697 234758 gals mgl repressor:galactose operon inducer (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 194 of 400 of the completegenome.) (nt:f346; 99 pct identical to gals\_ecoli sw: p25748) (le:4037) (re:5077) (di:complement) AE000304 AE000304 g1788474 Escherichia coli 562 -11532697

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821735	7260	29416	1698	565

Description

6500728840 pta:b2297 phosphate acetyltransferase:phosphotransacetylase (gtcfc:1.4:1.8) (ec:2.3.1.8) (keggfc:1.8) (rileyfc:1.1.1) (db:gtc-escherichia coli) b2297 b2297 Escherichia coli 562 -11532698 7000691882 pta phosphate acetyltransferase (cl:phosphate acetyltransferase pta) (ec:2.3.1.8) (db:pir2.dat) G65001 G65001 Escherichia coli 562 -11532698 7500960411 pta phosphotransacetylase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:2.3.1.8) (de:escherichia coli k-12 mg1655 section 209 of 400 of the completegenome.) (nt:o714; 99 pct identical to pta\_ecoli sw: p39184) (le:68) (re:2212) (di:direct) AE000319 AE000319 g1788635 Escherichia coli 562 -11532698 5000690108 (de:(ecoli\_2246) (pn:phosphotransacetylase) (gn:pta) (gtcfc:1.8) (ec:2.3.1.8) (pta\_ecoli) (keggfc:1.8) (rileyfc:1.1.1) (db:gtc-escherichia coli)) ECOLI\_2246 ECOLI\_2246 Escherichia coli 562 10123633

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821740	7261	29417	246	81

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821751	7262	29418	231	76

Description

6500728841 nlpb:dapx:b2477 lipoprotein-34 precursor (gtcfc:1.4:11.1) (keggfc:14.2) (rileyfc:1.1.1:3.3.1) (db:gtc-escherichia coli) b2477 b2477 Escherichia coli 562 -11532699 7000691857 nlpb lipoprotein-34 precursor:lipoprotein nlpb (db:pir2.dat) D65023 D65023 Escherichia coli 562 -11532699 7500960374 nlpb lipoprotein-34 (fn:membrane; macromolecule synthesis,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 225 of 400 of the completegenome.) (nt:f345; 100 pct identical to nlpb\_ecoli sw: p21167) (le:137) (re:1174) (di:complement) AE000335 AE000335 g1788822 Escherichia coli 562 -11532699 5000690914 (de:(ecoli\_2417) (pn:lipoprotein-34) (gn:nlpb) (gtcfc:11.1) (ec:) (nlpb\_ecoli) (keggfc:11.2:11.2) (rileyfc:1.1.1:3.3.1) (db:gtc-escherichia coli)) ECOLI\_2417 ECOLI\_2417 Escherichia coli 562 10123703

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821752	7263	29419	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501821759	7264	29420	1281	426
Description				
<p>6500728842 gutm:srlm:b2706 gutm:glucitol operon activator protein (gtcfc:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b2706 b2706 Escherichia coli 562 -11532700 234598 gutm:srlm (de:glucitol operon activator protein) (db:swissprot) GUTM_ECOLI P15081 ESCHERICHIA COLI 562 -11532700 164468 gutm regulatory protein gutm:glucitol operon protein m (db:pir2.dat) S01831 S01831 Escherichia coli 562 -11532700 225258 gutm glucitol operon activator protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #446(60.5-60.9 min.)) (nt:similar to (swissprot accession number p15081)) (le:17527) (re:17886) (di:direct) D90892 D90892 g1800092 Escherichia coli 562 -11532700 7500882857 (db:genpept-bct1) (de:escherichia coli gutm gene and gutr gene for activator and repressor proteins.) (nt:gut m protein (aa 1-119)) (le:353) (re:712) (di:direct) ECGUTMR X13463 g41629 Escherichia coli 562 -11532700 239279 (db:genpept-bct1) (de:e.coli glucitol (gut) operon: glucitol-specific enzyme ii (guta), and iii (gutb), glucitol-6-phosphate dehydrogenase (gutd), activator (gutm) and repressor (guttr) genes, complete cds.) (nt:gut operon activator (gutm)) (le:3322) (re:... ECOGUT J02708 g146281 Escherichia coli 562 -11532700 7502851805 gutm (fn:glucitol operon activator) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg site no. 33198; alternate gene name srlm) (le:924) (re:1283) (di:direct) ECU29579 U29579 g882598 Escherichia coli 562 -11532700 233044 gutm glucitol operon activator (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 244 of 400 of the complete genome.) (nt:ol19; 100 pct identical to gutm_ecoli sw: p15081;) (le:6577) (re:6936) (di:direct) AE000354 AE000354 g1789058 Escherichia coli 562 -11532700 75115 gutm:srlm (de:glucitol operon activator protein) (db:swissprot) GUTM_ECOLI P15081 ESCHERICHIA COLI 562 -11532700</p>				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821771	7265	29421	276	91

Description

6500728843 ascg:b2714 asc operon repressor protein:cryptic asc operon repressor (gtcfc:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b2714 b2714 Escherichia coli 562 -11532701 7000690857 ascg asc operon repressor protein (cl:lac repressor) (db:pir2.dat) F65051 F65051 Escherichia coli 562 -11532701 7500959677 ascg (fn:asc operon repressor) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg site no. 33230) (le:10558) (re:11571) (di:complement) ECU29579 U29579 g882607 Escherichia coli 562 -11532701 239288 ascg ascbf operon repressor (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 245 of 400 of the completegenome.) (nt:f337; 92 pct identical (1 gap) to ascg\_ecoli) (le:5864) (re:6877) (di:complement) AE000355 AE000355 g1789068 Escherichia coli 562 -11532701

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821774	7266	29422	225	74

Description

6500728844 ascb:b2716 6-phospho-beta-glucosidase:6-phospho-beta-glucosidase ascb (gtcfc:1.4) (ec:3.2.1.86) (keggfc:14.1) (rileyfc:1.1.1) (db:gtc-escherichia coli) b2716 b2716 Escherichia coli 562 -11532702 60336 ascb (ec:3.2.1.86) (de:6-phospho-beta-glucosidase ascb,) (db:swissprot) ASCB\_ECOLI P24240 ESCHERICHIA COLI 562 -11532702 7000684642 ascb 6-phospho-beta-glucosidase (cl:agrobacterium beta-glucosidase) (ec:3.2.1.86) (db:pir2.dat) (mp:59 min) H65051 H65051 Escherichia coli 562 -11532702 7500877233 ascb 6-phospho-beta-glucosidase:cryptic (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:3.2.1.86) (de:escherichia coli k-12 mg1655 section 245 of 400 of the completegenome.) (nt:o474; 98 pct identical to ascb\_ecoli sw: p24240; cg) (le:8600) (re:10024) (di:direct) AE000355 AE000355 g1789070 Escherichia coli 562 -11532702

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821776	7267	29423	186	61

Description

GTC ORF with score 158 to: (sr:neurospora crassa (clone pcn24, strain 74a-or23-iva) vegetativ) (db:genpept-pln1) (ec:1.15.1.1) (de:neurospora crassa cu/zn-superoxide dismutase (sod1) gene, completecds.) (le:96:396:676:886) (re:108:575:827:1005) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821788	7268	29424	1116	371

Description

6500728845 nlpd:b2742 lipoprotein nlpd precursor (gtcfc:1.4:11.1)  
(keggfc:14.2) (rileyfc:1.1.1:3.3.1) (db:gtc-escherichia coli) b2742 b2742  
Escherichia coli 562 -11532703 86106 nlpd (de:lipoprotein nlpd precursor)  
(db:swissprot) NLPD\_ECOLI P33648 ESCHERICHIA COLI 562 -11532703 164003 nlpd  
lipoprotein d precursor (cl:lipoprotein d) (db:pir2.dat) B55522 B55522  
Escherichia coli 562 -11532703 239316 nlpd lipoprotein precursor  
(sr:escherichia coli (strain mp180) dna) (db:genpept-bct1) (de:escherichia  
coli l-isoaspartyl methyltransferase (pcm) and katfgene, partial cds and  
lipoprotein precursor (nlpd) gene, completecds.) (le:197) (re:1336)  
(di:direct) ECOPCMNLPD L07869 g433185 Escherichia coli 562 -11532703  
7500886497 nlpd lipoprotein nlpd precursor (db:genpept-bct1)  
(de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg  
site no. 33225; orfx of d17549, has different) (le:39919) (re:41058)  
(di:complement) ECU29579 U29579 g882635 Escherichia coli 562 -11532703  
235365 nlpd lipoprotein (fn:membrane; macromolecule synthesis,)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 248 of 400 of the  
completegenome.) (nt:f379; 100 pct identical to nlpd\_ecoli sw: p33648;)  
(le:2588) (re:3727) (di:complement) AE000358 AE000358 g1789099 Escherichia  
coli 562 -11532703 5000690916 (de:(ecoli\_2671) (pn:lipoprotein) (gn:nlpd)  
(gtcfc:11.1) (ec:) (nlpd\_ecoli) (keggfc:11.2:11.2) (rileyfc:1.1.1:3.3.1)  
(db:gtc-escherichia coli)) ECOLI\_2671 ECOLI\_2671 Escherichia coli 562  
10028273

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501821789	7269	29425	681	226

#### Description

6500728846 fuco:b2799 1:2-propanediol oxidoreductase:lactaldehyde reductase:propanediol oxidoreductase (gtcfc:1.4:1.8:1.9) (ec:1.1.1.77) (keggfc:1.8:1.9) (rileyfc:1.1.1) (db:gtc-escherichia coli) b2799 b2799 Escherichia coli 562 -11532704 72506 fuco (ec:1.1.1.77) (de:lactaldehyde reductase, (propanediol oxidoreductase)) (db:swissprot) FUCO\_ECOLI P11549 ESCHERICHIA COLI 562 -11532704 122562 fuco lactaldehyde reductase (cl:lactaldehyde reductase:lactaldehyde reductase homology) (ec:1.1.1.77) (db:pir1.dat) (mp:60 min) RDECLA A32883 Escherichia coli 562 -11532704 234417 (sr:e.coli k12 dna) (db:genpept-bct1) (de:e.coli nad+-linked oxiredutase (fuco) and fucose-1-phosphatealdolase (fuca) genes, complete cds, and l-fucose utilizationprotein (fucp) gene, 5' end.) (nt:oxiredutase (fuco)) (le:1312) (re:2463) (di:direct) ECOFUCAO M31059 g146043 Escherichia coli 562 -11532704 239373 fuco 1:2-propanediol oxidoreductase (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli (dh5-alpha strain) fuco gene, complete cds.) (le:354) (re:1505) (di:direct) ECOFUCO M27177 g146045 Escherichia coli 562 -11532704 7500881905 fuco 1:2-propanediol oxidoreductase lactaldehyde (db:genpept-bct1) (ec:1.1.1.77) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:cg site no. 17698; orf\_f383) (le:13420) (re:14571) (di:complement) ECU29581 U29581 g882694 Escherichia coli 562 -11532704 234416 fuco l-1:2-propanediol oxidoreductase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:1.1.1.77) (de:escherichia coli k-12 mg1655 section 253 of 400 of the completegenome.) (nt:f383; 100 pct identical to fuco\_ecoli sw: p11549;) (le:9578) (re:10729) (di:complement) AE000363 AE000363 g1789163 Escherichia coli 562 -11532704 5000690109 (de:(ecoli\_2730) (pn:l-1,2-propanediol oxidoreductase) (gn:fuco) (gtcfc:1.8:1.9) (ec:1.1.1.77) (fuco\_ecoli) (keggfc:1.8:1.9) (rileyfc:1.1.1) (db:gtc-escherichia coli)) ECOLI\_2730 ECOLI\_2730 Escherichia coli 562 10015057

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501821806	7270	29426	1992	664

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821823	7271	29427	342	113
<u>Description</u>				
<p>6500728847 fuca:fucc:prd:b2800 fucose-1-phosphate aldolase:l-fucose phosphate aldolase (gtcfc:1.4:1.8) (ec:4.1.2.17) (keggfc:1.8) (rileyfc:1.1.1) (db:gte-escherichia coli) b2800 b2800 Escherichia coli 562 -11532705 234415 fuca:fucc:prd (ec:4.1.2.17) (de:l-fucose phosphate aldolase,) (db:swissprot) FUCA_ECOLI P11550 ESCHERICHIA COLI 562 -11532705 125747 fuca l-fucose-phosphate aldolase (cl:l-ribulose-phosphate 4-epimerase) (ec:4.1.2.17) (db:pir1.dat) (mp:60 min) ADECFP B33495 Escherichia coli 562 -11532705 5000690110 (db:genpept-bct1) (de:escherichia coli fucose operon.) (nt:fuca orf (aa 1-215)) (le:1414) (re:2061) (di:complement) ECFUCOSE X15025 g41503 Escherichia coli 562 -11532705 239374 (sr:e.coli k12 dna) (db:genpept-bct1) (de:e.coli nad+-linked oxiredutase (fuco) and fucose-1-phosphatealdolase (fuca) genes, complete cds, and l-fucose utilizationprotein (fucp) gene, 5' end.) (nt:fucose-1-phosphate aldolase (fuca)) (le:640) (re:1... ECOFUCAO M31059 g146042 Escherichia coli 562 -11532705 7500881899 fuca fucose-1-phosphate aldolase (db:genpept-bct1) (ec:4.1.2.17) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:cg site no. 17701; alternate gene names fucc, prd;) (le:14596) (re:15243) (di:complement) ECU29581 U29581 g882695 Escherichia coli 562 -11532705 232930 fuca l-fucose-1-phosphate aldolase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:4.1.2.17) (de:escherichia coli k-12 mg1655 section 253 of 400 of the completegenome.) (nt:f215; 100 pct identical to fuca_ecoli sw: p11550 cg) (le:10754) (re:11401) (di:complement) AE000363 AE000363 g1789164 Escherichia coli 562 -11532705 72497 fuca:fucc:prd (ec:4.1.2.17) (de:l-fucose phosphate aldolase,) (db:swissprot) FUCA_ECOLI P11550 ESCHERICHIA COLI 562 -11532705</p>				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821830	7272	29428	717	238

Description

6500728848 fuci:b2802 l-fucose isomerase:l-fucose isomerase  
 (gtcfc:1.4:1.6) (ec:5.3.1.-) (keggfc:1.6) (rileyfc:1.1.1)  
 (db:gtc-escherichia coli) b2802 b2802 Escherichia coli 562 -11532706 239376  
 fuci (ec:5.3.1.25) (de:l-fucose isomerase,) (db:swissprot) FUCI\_ECOLI P11552  
 ESCHERICHIA COLI 562 -11532706 125870 fuci l-fucose isomerase  
 (cl:isomerase fuci) (ec:5.3.1.-) (db:pir1.dat) (mp:60 min) ISECFI JS0185  
 Escherichia coli 562 -11532706 5000690093 (db:genpept-bct1) (de:escherichia  
 coli fucose operon.) (nt:fuci orf (aa 1-591)) (le:3957) (re:5732)  
 (di:direct) ECFUCOSE X15025 g41505 Escherichia coli 562 -11532706  
 7500881901 fuci l-fucose isomerase (db:genpept-bct1) (ec:5.3.1.-)  
 (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:cg  
 site no. 10878; orf\_o591) (le:17139) (re:18914) (di:direct) ECU29581 U29581  
 g882697 Escherichia coli 562 -11532706 232932 fuci l-fucose isomerase  
 (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2)  
 (ec:5.3.1.-) (de:escherichia coli k-12 mg1655 section 254 of 400 of the  
 completegenome.) (nt:o591; 100 pct identical to fuci\_ecoli sw: p11552;)  
 (le:1653) (re:3428) (di:direct) AE000364 AE000364 g1789167 Escherichia coli  
 562 -11532706 72499 fuci (ec:5.3.1.25) (de:l-fucose isomerase,)  
 (db:swissprot) FUCI\_ECOLI P11552 ESCHERICHIA COLI 562 -11532706

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821831	7273	29429	267	88

Description

6500728849 fuck:b2803 l-fucose kinase:l-fuculokinase (gtcfc:1.4:1.8)  
 (ec:2.7.1.51) (keggfc:1.8) (rileyfc:1.1.1) (db:gtc-escherichia coli) b2803  
 b2803 Escherichia coli 562 -11532707 239377 fuck (ec:2.7.1.51)  
 (de:l-fuculokinase,) (db:swissprot) FUCK\_ECOLI P11553 ESCHERICHIA COLI 562  
 -11532707 123535 fuck fucokinase (cl:xylulokinase) (ec:2.7.1.52)  
 (db:pir1.dat) (mp:60 min) KIECFK JS0186 Escherichia coli 562 -11532707  
 5000690111 (db:genpept-bct1) (de:escherichia coli fucose operon.) (nt:fuck  
 orf (aa 1-482)) (le:5811) (re:7259) (di:direct) ECFUCOSE X15025 g41506  
 Escherichia coli 562 -11532707 7500881903 fuck l-fucose kinase  
 (db:genpept-bct1) (ec:2.7.1.51) (de:escherichia coli k-12 genome;  
 approximately 63 to 64 minutes.) (nt:cg site no. 19878) (le:18993)  
 (re:20441) (di:direct) ECU29581 U29581 g882698 Escherichia coli 562  
 -11532707 232933 fuck l-fuculokinase (fn:enzyme; degradation of small  
 molecules: carbon) (db:genpept-bct2) (ec:2.7.1.51) (de:escherichia coli k-12  
 mg1655 section 254 of 400 of the completegenome.) (nt:o482; 100 pct  
 identical to fuck\_ecoli sw: p11553;) (le:3507) (re:4955) (di:direct)  
 AE000364 AE000364 g1789168 Escherichia coli 562 -11532707 72501 fuck  
 (ec:2.7.1.51) (de:l-fuculokinase,) (db:swissprot) FUCK\_ECOLI P11553  
 ESCHERICHIA COLI 562 -11532707

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821836	7274	29430	1323	440

Description

6500728850 fucr:b2805 l-fucose operon activator (gtcfc:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b2805 b2805 Escherichia coli 562 -11532708 239379 fucr (de:l-fucose operon activator) (db:swissprot) FUCR\_ECOLI P11554 ESCHERICHIA COLI 562 -11532708 131528 fucr fuc operon regulatory protein (cl:fuc operon regulatory protein) (db:pir1.dat) (mp:60 min) RGECEO JS0188 Escherichia coli 562 -11532708 7500881908 (db:genpept-bct1) (de:escherichia coli fucose operon.) (nt:fucr orf (aa 1-243)) (le:7740) (re:8471) (di:direct) ECFUCOSE X15025 g41508 Escherichia coli 562 -11532708 7502851806 fucr (fn:positive regulatory gene) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:cg site no. 10884) (le:20923) (re:21654) (di:direct) ECU29581 U29581 g882700 Escherichia coli 562 -11532708 232935 fucr positive regulator of the fuc operon (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 254 of 400 of the completegenome.) (nt:o243; 100 pct identical to fucr\_ecoli sw: p11554;) (le:5437) (re:6168) (di:direct) AE000364 AE000364 g1789170 Escherichia coli 562 -11532708 72511 fucr (de:l-fucose operon activator) (db:swissprot) FUCR\_ECOLI P11554 ESCHERICHIA COLI 562 -11532708



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821839	7275	29431	765	254

Description

6500728851 galr:b2837 galactose operon repressor (gtcfc:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b2837 b2837 Escherichia coli 562 -11532709 234429 galr (de:galactose operon repressor) (db:swissprot) GALR\_ECOLI P03024 ESCHERICHIA COLI 562 -11532709 130808 galr gal operon repressor (cl:lac repressor) (db:pir1.dat) (mp:62 min) RPECG A93910 Escherichia coli 562 -11532709 239408 (db:genpept-bct1) (de:e. coli gene galr coding for galactose repressor.) (nt:repressor) (le:81) (re:1112) (di:direct) ECGALR V00280 g41534 Escherichia coli 562 -11532709 7500882093 galr operon repressor (sr:escherichia coli (1): k-12 bmh71-18(lac-pro)-del/f' pro-laci-q-zml) (db:genpept-bct1) (de:e.coli galr, lysa, and lysr genes coding for galetk operonrepressor protein (gal repressor), diaminopimelate decarboxylaseand lysa activatory protein.) (le:81... ECOGALLYS J01614 g146068 Escherichia coli 562 -11532709 7502851807 galr (fn:repressor of galetk operon) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:cg site no. 721; alternate gene name rgal) (le:58154) (re:59185) (di:direct) ECU29581 U29581 g882730 Escherichia coli 562 -11532709 232964 galr repressor of galetk operon (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 257 of 400 of the completgenome.) (nt:o343; 100 pct identical to galr\_ecoli sw: p03024;) (le:7310) (re:8341) (di:direct) AE000367 AE000367 g1789202 Escherichia coli 562 -11532709 73088 galr (de:galactose operon repressor) (db:swissprot) GALR\_ECOLI P03024 ESCHERICHIA COLI 562 -11532709

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821847	7276	29432	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821853	7277	29433	756	252

Description

6500728852 ebgr:b3075 ebg operon repressor (gtcfc:1.4) (keggfc:14.2)  
(rileyfc:1.1.1) (db:gtc-escherichia coli) b3075 b3075 Escherichia coli 562  
-11532710 234218 ebgr (de:ebg operon repressor) (db:swissprot) EBGR\_ECOLI  
P06846 ESCHERICHIA COLI 562 -11532710 130805 ebgr ebg repressor (cl:lac  
repressor) (db:pir1.dat) (mp:68 min) RPECEG A25752 Escherichia coli 562  
-11532710 236312 (db:genpept-bct1) (de:escherichia coli wildtype ebg operon  
dna for beta-galactosidasealpha and beta subunits and repressor proteins.)  
(nt:ebgr product, repressor (aa 1-126)) (le:126) (re:1109) (di:direct) ECEBG  
X52031 g41308 Escherichia coli 562 -11532710 7500880810 ebgr ebg repressor  
(sr:e.coli dna) (db:genpept-bct1) (de:e.coli ebgr, ebga, ebgc genes complete  
cds.) (nt:putative) (le:126) (re:1109) (di:direct) ECOEBGRA M64441 g145820  
Escherichia coli 562 -11532710 7502851808 ebgr (fn:ebg repressor)  
(db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to  
76.0 minutes.) (nt:cg site no. 829) (le:2219) (re:3202) (di:direct) ECOUW67  
U18997 g606013 Escherichia coli 562 -11532710 232723 ebgr regulator of ebg  
operon (fn:regulator; degradation of small molecules:) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 279 of 400 of the completegenome.)  
(nt:o327; 100 pct to ebgr\_ecoli sw: p06846; cg site) (le:4861) (re:5844)  
(di:direct) AE000389 AE000389 g1789456 Escherichia coli 562 -11532710 69653  
ebgr (de:ebg operon repressor) (db:swissprot) EBGR\_ECOLI P06846 ESCHERICHIA  
COLI 562 -11532710

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821855	7278	29434	600	200

Description

6500728853 ebga:b3076  
phospho-beta-d-galactosidase:alpha-subunit:phospho-beta-d-galactosidase:alpha-subunit (gtcfc:1.4:1.6:8.1:8.5) (ec:3.2.1.23) (keggfc:1.6:8.1:8.5) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3076 b3076 Escherichia coli 562 -11532711 7000688878 ebga beta-galactosidase:alpha chain:beta-d-galactoside galactohydrolase:lactase:phospho-beta-d-galactosidase alpha-subunit (cl:beta-galactosidase) (ec:3.2.1.23) (db:pir1.dat) (mp:68 min) GBECE A65096 Escherichia coli 562 -11532711 7500953302 ebga  
phospho-beta-d-galactosidase:alpha-subunit (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 830) (le:3350) (re:6478) (di:direct) ECOUW67 U18997 g606014 Escherichia coli 562 -11532711 236313 ebga evolved beta-d-galactosidase:alpha subunit (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 279 of 400 of the completegenome.) (nt:o1042; this 1042 aa orf is 99 pct identical (1) (le:5992) (re:9120) (di:direct) AE000389 AE000389 g1789457 Escherichia coli 562 -11532711 5000690094 (de:(ecoli\_2998) (pn:evolved beta-d-galactosidase, alpha subunit; cryptic gene) (gn:ebga) (gtcfc:1.6:8.4:8.5) (ec:3.2.1.23) (bga2\_ecoli) (keggfc:1.6:8.5) (rileyfc:1.1.1) (db:gtc-escherichia coli))  
ECOLI\_2998 ECOLI\_2998 Escherichia coli 562 10123971

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501821860	7279	29435	1347	448

#### Description

6500728854 ebgc:b3077 phospho-beta-d-galactosidase:beta-subunit:evolved beta-galactosidase beta-subunit (gtcfc:1.4:1.6:8.1:8.5) (ec:3.2.1.23) (keggfc:1.6:8.1:8.5) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3077 b3077 Escherichia coli 562 -11532712 69652 ebgc (de:evolved beta-galactosidase beta-subunit) (db:swissprot) EBGC\_ECOLI P24225 ESCHERICHIA COLI 562 -11532712 7000685133 ebgc beta-galactosidase:beta chain:phospho-beta-d-galactosidase:beta-subunit (ec:3.2.1.23) (db:pir2.dat) B65096 B65096 Escherichia coli 562 -11532712 7500880809 ebgc phospho-beta-d-galactosidase:beta-subunit (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 18412; difference near end makes this) (le:6475) (re:6924) (di:direct) ECOUW67 U18997 g606015 Escherichia coli 562 -11532712 236314 ebgc evolved beta-d-galactosidase:beta subunit (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 279 of 400 of the completegenome.) (nt:o149; cg site no. 18412; difference near end makes) (le:9117) (re:9566) (di:direct) AE000389 AE000389 g1789458 Escherichia coli 562 -11532712 5000690095 (de:(ecoli\_2999) (pn:evolved beta-d-galactosidase, beta subunit; cryptic gene) (gn:ebgc) (gtcfc:1.6:8.4:8.5) (ec:3.2.1.23) (ebgc\_ecoli) (keggfc:1.6:8.5) (rileyfc:1.1.1) (db:gtc-escherichia coli)) ECOLI\_2999 ECOLI\_2999 Escherichia coli 562 10012234

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501821898	7280	29436	588	195

#### Description

6500728855 exur:b3094 exu regulon regulator (gtcfc:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3094 b3094 Escherichia coli 562 -11532713 7000690876 exur exu regulon regulator (cl:regulatory protein uxur 2) (db:pir2.dat) C65098 C65098 Escherichia coli 562 -11532713 7500959736 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf\_o263) (le:27389) (re:28180) (di:direct) ECOUW67 U18997 g606035 Escherichia coli 562 -11532713 236334 exur negative regulator of exu regulon:exut:uxaac (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 281 of 400 of the completegenome.) (nt:o263; 100 pct identical amino acid sequence and) (le:8227) (re:9018) (di:direct) AE000391 AE000391 g1789480 Escherichia coli 562 -11532713

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501821899	7281	29437	189	62

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821915	7282	29438	588	195

#### Description

6500728856 nlp:sfs7:b3188 ner-like protein (gtcfc:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3188 b3188 Escherichia coli 562 -11532714 236425 nlp:sfs7 (de:ner-like protein) (db:swissprot) NLP\_ECOLI P18837 ESCHERICHIA COLI 562 -11532714 128618 nlp nlp protein:ner-like protein (cl:phage d108 dna-binding protein) (db:pir1.dat) (mp:69 min) BVECNP JV0027 Escherichia coli 562 -11532714 7500886498 nlp (db:genpept-bct1) (de:e.coli nlp gene for ner-like protein.) (nt:ner-like protein,homologous to ner protein of) (le:627) (re:905) (di:direct) ECNLP X68873 g42129 Escherichia coli 562 -11532714 7502851809 nlp ner-like protein (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (le:115661) (re:115939) (di:direct) ECOUW67 U18997 g606126 Escherichia coli 562 -11532714 233490 nlp regulatory factor of maltose metabolism:similar (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 289 of 400 of the completengenome.) (nt:o92; 100 pct identical amino acid sequence and) (le:6182) (re:6460) (di:direct) AE000399 AE000399 g1789579 Escherichia coli 562 -11532714 86111 nlp:sfs7 (de:ner-like protein) (db:swissprot) NLP\_ECOLI P18837 ESCHERICHIA COLI 562 -11532714

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821932	7283	29439	723	240

#### Description

6500728857 malp:b3417 maltodextrin phosphorylase (gtcfc:1.4:7.2) (ec:2.4.1.1) (keggfc:7.1) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3417 b3417 Escherichia coli 562 -11532715 7000688859 malp maltodextrin phosphorylase (cl:phosphorylase) (ec:2.4.1.1) (db:pir1.dat) (mp:75 min) PHECGM D65137 Escherichia coli 562 -11532715 7500953239 malp maltodextrin phosphorylase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:2.4.1.1) (de:escherichia coli k-12 mg1655 section 307 of 400 of the completengenome.) (nt:f797; cg site no. 528; alternate name mala; 99 pct) (le:7042) (re:9435) (di:complement) AE000417 AE000417 g2367221 Escherichia coli 562 -11532715

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821933	7284	29440	918	305

Description

6500728858 malt:mala:b3418 malt:malt regulatory protein (gtcfc:1.4)  
 (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3418 b3418  
 Escherichia coli 562 -11532716 7000688988 malt regulatory protein malt  
 (cl:regulatory protein malt) (db:pir1.dat) (mp:75 min) RGE CMT E65137  
 Escherichia coli 562 -11532716 7500953663 malt positive regulator of mal  
 regulon (fn:regulator; degradation of small molecules:) (db:genpept-bct2)  
 (de:escherichia coli k-12 mg1655 section 308 of 400 of the completegenome.)  
 (nt:o901; cg site no. 526; alternate name mala; 99 pct) (le:212) (re:2917)  
 (di:direct) AE000418 AE000418 g2367223 Escherichia coli 562 -11532716

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821938	7285	29441	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821943	7286	29442	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501821950	7287	29443	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501821952	7288	29444	384	128

#### Description

6500728859 tref:b3519 probable cytoplasmic trehalase:alpha:alpha-trehalase:alpha:alpha-trehalose glucohydrolase (gtcfc:1.4:7.2) (ec:3.2.1.28) (keggfc:7.1) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3519 b3519 Escherichia coli 562 -11532717 102166 tref (ec:3.2.1.28) (de:(alpha,alpha-trehalose glucohydrolase)) (db:swissprot) TREF\_ECOLI P37196 ESCHERICHIA COLI 562 -11532717 164762 tref probable alpha:alpha-trehalase::cytoplasmic (ec:3.2.1.28) (db:pir2.dat) S47739 S47739 Escherichia coli 562 -11532717 7500893379 tref (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:83851) (re:85500) (di:direct) ECOUW76 U00039 g466656 Escherichia coli 562 -11532717 236755 tref cytoplasmic trehalase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:3.2.1.28) (de:escherichia coli k-12 mg1655 section 318 of 400 of the completegenome.) (nt:o549; 100 pct identical amino acid sequence and) (le:5914) (re:7563) (di:direct) AE000428 AE000428 g1789936 Escherichia coli 562 -11532717 5000690554 (de:(ecoli\_3438) (pn:cytoplasmic trehalase) (gn:tref) (gtcfc:7.2) (ec:3.2.1.28) (tref\_ecoli) (keggfc:7.1) (rileyfc:1.1.1) (db:gtc-escherichia coli)) ECOLI\_3438 ECOLI\_3438 Escherichia coli 562 10043986

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501821955	7289	29445	816	271

#### Description

6500728860 xy1r:b3569 xylose operon regulatory protein (gtcfc:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3569 b3569 Escherichia coli 562 -11532718 108239 xy1r (de:xylose operon regulatory protein) (db:swissprot) XYLR\_ECOLI P37390 ESCHERICHIA COLI 562 -11532718 164841 xy1r xylose operon regulatory protein (db:pir2.dat) S47790 S47790 Escherichia coli 562 -11532718 7500894495 xy1r (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:149230) (re:150408) (di:direct) ECOUW76 U00039 g466707 Escherichia coli 562 -11532718 236806 xy1r putative regulator of xyl operon (fn:putative regulator; degradation of small) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 324 of 400 of the completegenome.) (nt:o392; 100 pct identical amino acid sequence and) (le:4122) (re:5300) (di:direct) AE000434 AE000434 g1789993 Escherichia coli 562 -11532718

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501821967	7290	29446	198	65

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821981	7291	29447	1218	405

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501821996	7292	29448	1584	528

Description

6500728861 mtld:b3600 mannitol-1-phosphate  
dehydrogenase:mannitol-1-phosphate 5-dehydrogenase (gtcfc:1.4:1.5)  
(ec:1.1.1.17) (keggfc:1.5) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3600  
b3600 Escherichia coli 562 -11532719 84553 mtld (ec:1.1.1.17)  
(de:mannitol-1-phosphate 5-dehydrogenase,) (db:swissprot) MTLD\_ECOLI P09424  
ESCHERICHIA COLI 562 -11532719 7000685878 mtld mannitol-1-phosphate  
5-dehydrogenase (cl:mannitol-1-phosphate 5-dehydrogenase) (ec:1.1.1.17)  
(db:pir2.dat) (mp:81 min) B65160 B65160 Escherichia coli 562 -11532719  
7500886036 mtld mannitol-1-phosphate dehydrogenase (sr:escherichia coli  
(sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1)  
(ec:1.1.1.17) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.)  
(nt:cg site no. 479) (le:188674) (re:189822) (di:direct) ECOUW76 U00039  
g466738 Escherichia coli 562 -11532719 236837 mtld mannitol-1-phosphate  
dehydrogenase (fn:enzyme; degradation of small molecules: carbon)  
(db:genpept-bct2) (ec:1.1.1.17) (de:escherichia coli k-12 mg1655 section 328  
of 400 of the completegenome.) (nt:o382; 100 pct identical to mtld\_ecoli sw:  
p09424;) (le:2220) (re:3368) (di:direct) AE000438 AE000438 g1790028  
Escherichia coli 562 -11532719 5000690081 (de:(ecoli\_3520)  
(pn:mannitol-1-phosphate dehydrogenase) (gn:mtld) (gtcfc:1.5) (ec:1.1.1.17)  
(mtld\_ecoli) (keggfc:1.5) (rileyfc:1.1.1) (db:gtc-escherichia coli))  
ECOLI\_3520 ECOLI\_3520 Escherichia coli 562 10026749

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822004	7293	29449	285	94

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822012	7294	29450	429	142

#### Description

6500728862 mtlr:b3601 mannitol operon repressor:mannitol repressor protein (gtcfc:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3601 b3601 Escherichia coli 562 -11532720 84557 mtlr (de:mannitol operon repressor (mannitol repressor protein)) (db:swissprot) MTLR\_ECOLI P36563 ESCHERICHIA COLI 562 -11532720 164028 mtlr mannitol operon repressor (db:pir2.dat) B36970 B36970 Escherichia coli 562 -11532720 236838 mtlr mannitol repressor (db:genpept-bct1) (de:escherichia coli k12 mannitol-phosphate dehydrogenase (mtld) gene,partial cds, and mannitol repressor (mtlr) gene, complete cds.) (le:47) (re:634) (di:direct) ECOMTLR U03845 g434583 Escherichia coli 562 -11532720 7500886038 mtlr (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:189822) (re:190409) (di:direct) ECOUW76 U00039 g466739 Escherichia coli 562 -11532720 235189 mtlr repressor for mtl (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 328 of 400 of the completegenome.) (nt:o195; 100 pct identical amino acid sequence and) (le:3368) (re:3955) (di:direct) AE000438 AE000438 g1790029 Escherichia coli 562 -11532720

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822014	7295	29451	783	260

#### Description

6500728863 nlpa:b3661 lipoprotein-28 precursor (gtcfc:1.4:11.1) (keggfc:14.2) (rileyfc:1.1.1:3.3.1) (db:gtc-escherichia coli) b3661 b3661 Escherichia coli 562 -11532721 86101 nlpa (de:lipoprotein-28 precursor) (db:swissprot) NLPA\_ECOLI P04846 ESCHERICHIA COLI 562 -11532721 130868 nlpa lipoprotein-28 precursor (cl:lipoprotein-28) (db:pir1.dat) LPEC28 A26286 Escherichia coli 562 -11532721 236898 (sr:e.coli (strain k-12) dna, clone pfy107) (db:genpept-bct1) (de:e.coli nlpa gene coding for lipoprotein-28, complete cds.) (nt:lipoprotein-28 precursor) (le:309) (re:1127) (di:direct) ECOLP28 M12163 g146649 Escherichia coli 562 -11532721 7500886494 nlpa lipoprotein-28 (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:28567) (re:29385) (di:complement) ECOUW82 L10328 g290510 Escherichia coli 562 -11532721 235002 nlpa lipoprotein-28 (fn:membrane; macromolecule synthesis,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 333 of 400 of the completegenome.) (nt:f272; 100 pct identical amino acid sequence and) (le:10508) (re:11326) (di:complement) AE000443 AE000443 g1790093 Escherichia coli 562 -11532721 5000690918 (de:(ecoli\_3580) (pn:regulatory factor of maltose metabolism; similar to ner repressor protein of phage mu) (gn:nlpa) (gtcfc:11.1) (ec:) (nlpa\_ecoli) (keggfc:11.2:11.2) (rileyfc:1.1.1:3.3.1) (db:gtc-escherichia coli)) ECOLI\_3580 ECOLI\_3580 Escherichia coli 562 10028268

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822017	7296	29452	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822040	7297	29453	186	61

Description

6500728864 bglb:b3721 phospho-beta-glucosidase:6-phospho-beta-glucosidase  
bglb (gtcfc:1.4) (ec:3.2.1.86) (keggfc:14.1) (rileyfc:1.1.1)  
(db:gtc-escherichia coli) b3721 b3721 Escherichia coli 562 -11532722 61658  
bglb (ec:3.2.1.86) (de:6-phospho-beta-glucosidase bglb,) (db:swissprot)  
BGLB\_ECOLI P11988 ESCHERICHIA COLI 562 -11532722 7000684702 bglb  
6-phospho-beta-glucosidase:bglb (cl:agrobacterium beta-glucosidase)  
(ec:3.2.1.86) (db:pir2.dat) (mp:84 min) B65175 B65175 Escherichia coli 562  
-11532722 7500877785 bglb phospho-beta-glucosidase b:cryptic (fn:enzyme;  
degradation of small molecules: carbon) (db:genpept-bct2) (ec:3.2.1.86)  
(de:escherichia coli k-12 mg1655 section 339 of 400 of the completegenome.)  
(nt:f470; 99 pct identical amino acid sequence and) (le:3673) (re:5085)  
(di:complement) AE000449 AE000449 g2367270 Escherichia coli 562 -11532722

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822045	7298	29454	468	156
<u>Description</u>				
6500728865 bglg:bglc:b3723 positive regulatory protein:cryptic beta-glucoside bgl operon antiterminator:cryptic beta-glucoside bgl operon antiterminator (gtcfc:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3723 b3723 Escherichia coli 562 -11532723 61661 bglg:bglc (de:cryptic beta-glucoside bgl operon antiterminator) (db:swissprot) BGLG_ECOLI P11989 ESCHERICHIA COLI 562 -11532723 162782 bglg:bglc beta-glucoside positive regulatory protein:cryptic beta-glucoside bgl operon antiterminator (cl:bacillus subtilis transcription antiterminator lict) (db:pir2.dat) (mp:84 min) B25977 B25977 Escherichia coli 562 -11532723 236959 bglc positive regulatory protein (sr:e.coli k12 dna, clone pfdx733) (db:genpept-bct1) (de:e.coli bgl operon encoding a positive regulatory protein, atransport protein, and phospho-beta-glucosidase, complete cds, andphou gene, 3' end.) (le:582) (re:1418) (di:direct) ECOBGLO M16487 g145417 Escherichia coli 562 -11532723 7500877786 bglg::cg site no. 963 positive regulatory protein (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:alternate gene name bglc) (le:95122) (re:95958) (di:complement) ECOUW82 L10328 g290571 Escherichia coli 562 -11532723 233905 bglg positive regulation of bgl operon (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 339 of 400 of the completegenome.) (nt:f278; 100 pct identical to bglg_ecoli sw: p11989;) (le:7115) (re:7951) (di:complement) AE000449 AE000449 g1790160 Escherichia coli 562 -11532723				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822058	7299	29455	531	176
<u>Description</u>				
6500728866 rbsr:b3753 rbs repressor:ribose operon repressor (gtcfc:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3753 b3753 Escherichia coli 562 -11532724 7000691903 rbsr ribose operon repressor (cl:lac repressor) (db:pir2.dat) B65179 B65179 Escherichia coli 562 -11532724 235700 rbsr regulator for rbs operon (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 342 of 400 of the completegenome.) (nt:o330; 99 pct identical amino acid sequence and) (le:5232) (re:6224) (di:direct) AE000452 AE000452 g1790194 Escherichia coli 562 -11532724 7500960453 rbsr rbs repressor (sr:escherichia coli (strain:k-12) dna, clone:puh25) (db:genpept-bct2) (de:escherichia coli gene for rbs repressor, complete cds.) (le:52) (re:1044) (di:direct) ECORBSR D10466 g471110 Escherichia coli 562 -11532724				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822060	7300	29456	507	168

#### Description

6500728867 rhad:b3902 rhamnulose-1-phosphate aldolase (gtcfc:1.4:1.5) (ec:4.1.2.19) (keggfc:1.5) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3902 b3902 Escherichia coli 562 -11532725 7500889732 rhad (ec:4.1.2.19) (de:rhamnulose-1-phosphate aldolase,) (db:swissprot) RHAD\_ECOLI P32169 ESCHERICHIA COLI 562 -11532725 164530 rhad rhamnulose-1-phosphate aldolase (ec:4.1.2.19) (db:pir2.dat) C48649 C48649 Escherichia coli 562 -11532725 238064 rhad rhamnulose-1-phosphate aldolase (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 289) (le:55085) (re:55909) (di:complement) ECOUW87 L19201 g305006 Escherichia coli 562 -11532725 5000690084 rhad rhamnulose-1-phosphate aldolase (db:genpept-bct1) (ec:4.1.2.19) (de:e.coli rhab, rha, rhad genes for rhamnulokinase, l-rhamnoseisomerase, and rammulose-1-phosphate aldolase.) (le:3417) (re:4241) (di:direct) ECRHABAD X60472 g396681 Escherichia coli 562 -11532725 237120 rhad rhamnulose-phosphate aldolase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:4.1.2.19) (de:escherichia coli k-12 mg1655 section 355 of 400 of the completegenome.) (nt:f274; 100 pct identical to rhad\_ecoli sw: p32169;) (le:7626) (re:8450) (di:complement) AE000465 AE000465 g1790336 Escherichia coli 562 -11532725 94261 rhad (ec:4.1.2.19) (de:rhamnulose-1-phosphate aldolase,) (db:swissprot) RHAD\_ECOLI P32169 ESCHERICHIA COLI 562 -11532725

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822076	7301	29457	345	115

#### Description

6500728868 rhaa:b3903 l-rhamnose isomerase (gtcfc:1.4:1.5) (ec:5.3.1.14) (keggfc:1.5) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3903 b3903 Escherichia coli 562 -11532726 94257 rhaa (ec:5.3.1.14) (de:l-rhamnose isomerase,) (db:swissprot) RHAA\_ECOLI P32170 ESCHERICHIA COLI 562 -11532726 163984 rhaa l-rhamnose isomerase (ec:5.3.1.14) (db:pir2.dat) S40847 S40847 Escherichia coli 562 -11532726 7500889730 rhaa l-rhamnose isomerase (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 292; matches ps00102: phosphorylase;) (le:56356) (re:57615) (di:complement) ECOUW87 L19201 g305007 Escherichia coli 562 -11532726 237121 rhaa l-rhamnose isomerase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:5.3.1.14) (de:escherichia coli k-12 mg1655 section 355 of 400 of the completegenome.) (nt:f419; 100 pct identical to rhaa\_ecoli sw: p32170;) (le:8901) (re:10160) (di:complement) AE000465 AE000465 g1790337 Escherichia coli 562 -11532726 5000690085 (de:(ecoli\_3802) (pn:l-rhamnose isomerase) (gn:rhaa) (gtcfc:1.5) (ec:5.3.1.14) (rhaa\_ecoli) (keggfc:1.5) (rileyfc:1.1.1) (db:gtc-escherichia coli)) ECOLI\_3802 ECOLI\_3802 Escherichia coli 562 10036240

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822077	7302	29458	675	224

Description

6500728869 rhab:b3904 rhamnulokinase:rhamnulose kinase (gtcfc:1.4:1.5) (ec:2.7.1.5) (keggfc:1.5) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3904 b3904 Escherichia coli 562 -11532727 94259 rhab (ec:2.7.1.5) (de:rhamnulokinase, (rhamnulose kinase)) (db:swissprot) RHAB\_ECOLI P32171 ESCHERICHIA COLI 562 -11532727 164529 rhab rhamnulokinase (cl:rhamnulokinase) (ec:2.7.1.5) (db:pir2.dat) S40848 S40848 Escherichia coli 562 -11532727 7500889731 rhab rhamnulokinase (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 291; similar to s. typhimurium rhab) (le:57612) (re:59081) (di:complement) ECOUW87 L19201 g305008 Escherichia coli 562 -11532727 237122 rhab rhamnulokinase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:2.7.1.5) (de:escherichia coli k-12 mg1655 section 355 of 400 of the completegenome.) (nt:f489; 100 pct identical to rhab\_ecoli sw: p32171;) (le:10157) (re:11626) (di:complement) AE000465 AE000465 g1790338 Escherichia coli 562 -11532727 5000690086 (de:(ecoli\_3803) (pn:rhamnulokinase) (gn:rhab) (gtcfc:1.5) (ec:2.7.1.5) (rhab\_ecoli) (keggfc:1.5) (rileyfc:1.1.1) (db:gtc-escherichia coli)) ECOLI\_3803 ECOLI\_3803 Escherichia coli 562 10036242

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822092	7303	29459	450	149

Description

6500728870 rhas:rhac2:b3905 l-rhamnose operon regulatory protein rhas (gtcfc:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3905 b3905 Escherichia coli 562 -11532728 7500889734 rhas:rhac2 (de:l-rhamnose operon regulatory protein rhas) (db:swissprot) RHAS\_ECOLI P09377 ESCHERICHIA COLI 562 -11532728 164527 rhas l-rhamnose operon regulatory protein rhas (db:pir2.dat) S40849 S40849 Escherichia coli 562 -11532728 238067 rhas (fn:transcription regulator for the rha operon) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 17950) (le:59369) (re:60205) (di:direct) ECOUW87 L19201 g305009 Escherichia coli 562 -11532728 7502851810 (db:genpept-bct1) (de:e. coli rhac gene (rhas and rhar) (positive activator of genesrequired for l-rhamnose utilization).) (nt:rhas (aa 1-278)) (le:121) (re:957) (di:direct) ECRHAC X06058 g42724 Escherichia coli 562 -11532728 237123 rhas positive regulator for rhabad operon (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 355 of 400 of the completegenome.) (nt:o278; 100 pct identical to rhas\_ecoli sw: p09377;) (le:11914) (re:12750) (di:direct) AE000465 AE000465 g1790339 Escherichia coli 562 -11532728 94264 rhas:rhac2 (de:l-rhamnose operon regulatory protein rhas) (db:swissprot) RHAS\_ECOLI P09377 ESCHERICHIA COLI 562 -11532728

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822096	7304	29460	345	114

#### Description

6500728871 rhar:rhacl:b3906 l-rhamnose operon transcriptional activator:l-rhamnose operon transcriptional activator rhar (gtcfc:10.2:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b3906 b3906 Escherichia coli 562 -11532729 7500889733 rhar:rhacl (de:l-rhamnose operon transcriptional activator rhar) (db:swissprot) RHAR\_ECOLI P09378 ESCHERICHIA COLI 562 -11532729 164526 rhar transcription activator of l-rhamnose operon rhar (db:pir2.dat) S40850 S40850 Escherichia coli 562 -11532729 238068 rhar (fn:transcription regulator for the rha operon) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 290) (le:60189) (re:61127) (di:direct) ECOUW87 L19201 g305010 Escherichia coli 562 -11532729 7502851811 (db:genpept-bct1) (de:e. coli rhac gene (rhas and rhar) (positive activator of genesrequired for l-rhamnose utilization).) (nt:rhar (aa 1-312)) (le:941) (re:1879) (di:direct) ECRHAC X06058 g42725 Escherichia coli 562 -11532729 237124 rhar positive regulator for rhars operon (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 355 of 400 of the completegenome.) (nt:o312; 100 pct identical to rhar\_ecoli sw: p09378;) (le:12734) (re:13672) (di:direct) AE000465 AE000465 g1790340 Escherichia coli 562 -11532729 94262 rhar:rhacl (de:l-rhamnose operon transcriptional activator rhar) (db:swissprot) RHAR\_ECOLI P09378 ESCHERICHIA COLI 562 -11532729

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822101	7305	29461	1029	342

#### Description

6500728872 malm:mola:b4037 maltose operon periplasmic protein:maltose operon periplasmic protein precursor (gtcfc:1.4:12.6) (keggfc:11.1) (rileyfc:1.1.1) (db:gtc-escherichia coli) b4037 b4037 Escherichia coli 562 -11532730 7500885273 malm:mola (de:maltose operon periplasmic protein precursor) (db:swissprot) MALM\_ECOLI P03841 ESCHERICHIA COLI 562 -11532730 130774 malm:mola maltose operon periplasmic protein malm (cl:malm protein) (db:pir1.dat) (mp:92 min) BVECMM A25787 Escherichia coli 562 -11532730 7502851812 (db:genpept-bct1) (de:e.coli malm gene encoding a periplasmic protein.) (nt:periplasmic protein (aa 1-306)) (le:242) (re:1162) (di:direct) ECMALM X04477 g41961 Escherichia coli 562 -11532730 233347 malm periplasmic protein of mal regulon (fn:phenotype; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 367 of 400 of the completegenome.) (nt:o306; cg site no. 18178; alternate gene name mola) (le:1649) (re:2569) (di:direct) AE000477 AE000477 g1790470 Escherichia coli 562 -11532730 82906 malm:mola (de:maltose operon periplasmic protein precursor) (db:swissprot) MALM\_ECOLI P03841 ESCHERICHIA COLI 562 -11532730

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822116	7306	29462	858	285
<u>Description</u>				
6500728873 melr:b4118 melibiose operon regulatory protein (gtcfc:1.4) (keggfc:14.2) (rileyfc:1.1.1) (db:gtc-escherichia coli) b4118 b4118 Escherichia coli 562 -11532731 83420 melr (de:melibiose operon regulatory protein) (db:swissprot) MELR_ECOLI P10411 ESCHERICHIA COLI 562 -11532731 131451 melr melibiose operon regulatory protein (cl:arabinose operon regulatory protein) (db:pir1.dat) (mp:93 min) RGECEMB A29625 Escherichia coli 562 -11532731 7500885472 melr (fn:regulatory gene) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 18166) (le:31548) (re:32456) (di:complement) ECOUW93 U14003 g536963 Escherichia coli 562 -11532731 237327 melr regulator of melibiose operon (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 374 of 400 of the completegenome.) (nt:f302; cg site no. 18166) (le:5093) (re:6001) (di:complement) AE000484 AE000484 g1790559 Escherichia coli 562 -11532731				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822118	7307	29463	462	153
<u>Description</u>				
6500728874 mela:mel-7:b4119 alpha-galactosidase:melibiase (gtcfc:1.4:1.6:8.1:8.5) (ec:3.2.1.22) (keggfc:1.6:8.1:8.5) (rileyfc:1.1.1) (db:gtc-escherichia coli) b4119 b4119 Escherichia coli 562 -11532732 237328 mela:mel-7 (ec:3.2.1.22) (de:alpha-galactosidase, (melibiase)) (db:swissprot) AGAL_ECOLI P06720 ESCHERICHIA COLI 562 -11532732 124681 mela alpha-galactosidase::melibiose-specific:alpha-d-galactoside galactohydrolase:melibiase (cl:melibiose-specific alpha-galactosidase) (ec:3.2.1.22) (db:pir1.dat) (mp:93 min) GBECAG A26571 Escherichia coli 562 -11532732 5000690097 (db:genpept-bct1) (de:e. coli mela gene for alpha-galactosidase.) (nt:alpha-galactosidase (aa 1-451)) (le:288) (re:1643) (di:direct) ECMELA X04894 g41991 Escherichia coli 562 -11532732 7500876661 mela alpha-galactosidase (db:genpept-bct1) (ec:3.2.1.22) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 522; alternate gene name mel-7) (le:32739) (re:34094) (di:direct) ECOUW93 U14003 g536964 Escherichia coli 562 -11532732 233367 mela alpha-galactosidase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:3.2.1.22) (de:escherichia coli k-12 mg1655 section 374 of 400 of the completegenome.) (nt:o451; 100 pct identical to agal_ecoli sw: p06720;) (le:6284) (re:7639) (di:direct) AE000484 AE000484 g1790560 Escherichia coli 562 -11532732 58927 mela:mel-7 (ec:3.2.1.22) (de:alpha-galactosidase, (melibiase)) (db:swissprot) AGAL_ECOLI P06720 ESCHERICHIA COLI 562 -11532732				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822134	7308	29464	234	77

Description

6500728875 trec:olgh:b4239 trehalose-6-phosphate  
hydrolase:alpha:alpha-phosphotrehalase (gtcfc:1.4:7.2) (ec:3.2.1.93)  
(keggfc:7.1) (rileyfc:1.1.1) (db:gtc-escherichia coli) b4239 b4239  
Escherichia coli 562 -11532733 102165 trec:olgh (ec:3.2.1.93)  
(de:phosphotrehalase)) (db:swissprot) TREC\_ECOLI P28904 ESCHERICHIA COLI 562  
-11532733 164764 trec alpha:alpha-phosphotrehalase::trehalose-6-phosphate  
hydrolase (cl:alpha-glucosidase:alpha-amylase core homology) (ec:3.2.1.93)  
(db:pir2.dat) S56465 S56465 Escherichia coli 562 -11532733 7500893378 trec  
trehalose-6-phosphate hydrolase (db:genpept-bct1) (de:escherichia coli k-12  
chromosomal region from 92.8 to 00.1 minutes.) (nt:amylotrehalase)  
(le:153883) (re:155538) (di:complement) ECOUW93 U14003 g537081 Escherichia  
coli 562 -11532733 237445 trec trehalase 6-p hydrolase (fn:enzyme;  
degradation of small molecules: carbon) (db:genpept-bct2) (ec:3.2.1.93)  
(de:escherichia coli k-12 mg1655 section 385 of 400 of the completegenome.)  
(nt:f551; 100 pct identical amino acid sequence and) (le:3696) (re:5351)  
(di:complement) AE000495 AE000495 g1790687 Escherichia coli 562 -11532733  
5000690556 (de:(ecoli\_4122) (pn:trehalase 6-p hydrolase) (gn:trec)  
(gtcfc:7.2) (ec:3.2.1.93) (trec\_ecoli) (keggfc:7.1) (rileyfc:1.1.1)  
(db:gtc-escherichia coli)) ECOLI\_4122 ECOLI\_4122 Escherichia coli 562  
10043985

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822142	7309	29465	411	136

Description

6500728876 uxur:b4324 uxu operon regulator (gtcfc:1.4) (keggfc:14.2)  
(rileyfc:1.1.1) (db:gtc-escherichia coli) b4324 b4324 Escherichia coli 562  
-11532734 104082 uxur (de:uxu operon transcriptional regulator)  
(db:swissprot) UXUR\_ECOLI P39161 ESCHERICHIA COLI 562 -11532734 164480 uxur  
regulatory protein uxur (cl:regulatory protein uxur 2) (db:pir2.dat) S56549  
S56549 Escherichia coli 562 -11532734 237529 uxur uxu regulon repressor  
(sr:escherichia coli (strain:k12) cell\_line:w3110 dna) (db:genpept-bct1)  
(de:escherichia coli uxua, uxub and uxur genes for mannonatedehydratase,  
mannonate oxidoreductase and uxu regulon repressor,complete cds.) (le:3520)  
(re:4293) (di:direct) D13329 D13329 g1160324 Escherichia coli 562 -11532734  
301664 uxur (fn:regulatory gene for uxu operon) (db:genpept-bct1)  
(de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.)  
(nt:cg site no. 12) (le:245408) (re:246181) (di:direct) ECOUW93 U14003  
g537165 Escherichia coli 562 -11532734 237622 uxur regulator for uxu operon  
(fn:regulator; degradation of small molecules:) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 393 of 400 of the completegenome.)  
(nt:o257; 100 pct identical to uxur\_ecoli sw: p39161;) (le:3116) (re:3889)  
(di:direct) AE000503 AE000503 g1790780 Escherichia coli 562 -11532734



ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822143	7310	29466	903	300

#### Description

6500728877 murg:b0090 udp-n-acetylglucosamine:n-acetylmuramyl-pentapeptide pyrophosphoryl-undecaprenol n-acetylglucosamine transferase (gtcfc:11.4:11.3:1.5:7.1:8.5) (ec:2.4.1.-) (keggfc:1.5:7.2:7.3:8.5) (rileyfc:3.3.4) (db:gtc-escherichia coli) b0090 b0090 Escherichia coli 562 -11532735 131351 murg udp-n-acetylglucosamine--n-acetylmuramyl-pentapeptide pyrophosphoryl-undecaprenol n-acetylgl... (cl:murg protein) (ec:2.4.1.-) (db:pir1.dat) (mp:2 min) BVECMG JQ0544 Escherichia coli 562 -11532735 233428 udp-n-acetylglucosamine (db:genpept-bct1) (de:escherichia coli cell-envelope murg gene.) (nt:murg protein (aa 1-355)) (le:82) (re:1149) (di:direct) ECMURG X52540 g42052 Escherichia coli 562 -11532735 233614 murg protein aa 1-355 (db:genpept-bct1) (de:escherichia coli murg and murc genes for an unidentified readingframe and udp-n-acetylmuramate:l-alanine ligase (ec 6.3.2.8)respectively.) (le:82) (re:1149) (di:direct) ECMURGC X52644 g42055 Escherichia coli 562 -11532735 7500953640 murg murg protein (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (le:99298) (re:100365) (di:direct) ECO110K D10483 g216504 Escherichia coli 562 -11532735 233426 murg udp-n-acetylglucosamine:n-acetylmuramyl- (fn:enzyme; murein sacculus, peptidoglycan) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 8 of 400 of the completegenome.) (nt:o355; 100 pct identical to murg\_ecoli sw: p17443) (le:16099) (re:17166) (di:direct) AE000118 AE000118 g1786278 Escherichia coli 562 -11532735 5000690580 (de:(ecoli\_90) (pn:transferase in peptidoglycan synthesis) (gn:murg) (gtcfc:8.4:8.5:11.4) (ec:2.4.1.-) (murg\_ecoli) (keggfc:7.2:7.3:8.5) (rileyfc:3.3.4) (db:gtc-escherichia coli)) ECO1I\_90 ECO1I\_90 Escherichia coli 562 10068095

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822145	7311	29467	456	151

#### Description

GTC ORF with score 107 to: (sr:mus musculus (strain dba/2) lymphoid tumor cdna to mrna) (db:genpept-rod) (de:mus musculus serine/threonine kinase (sak-b) mrna, complete cds.) (nt:sak-a and sak-b are alternate splices with) (le:206) (re:1600) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822149	7312	29468	357	118

# Description

6500728878 kdsb:b0918 3-deoxy-manno-octulosonate  
cytidyltransferase:cmp-kdo synthetase:cmp-2-keto-3-deoxyoctulosonic acid  
synthetase:cks (gtcfc:1.5:11.2) (ec:2.7.7.38) (keggfc:1.5) (rileyfc:3.3.2)  
(db:gtc-escherichia coli) b0918 b0918 Escherichia coli 562 -11532736 162611  
kdsb 3-deoxy-manno-octulosonate  
cytidyltransferase::cmp-3-deoxy-d-manno-octulosonate  
pyrophosphorylase:cmp-kdo synthetase (cl:3-deoxy-manno-octulosonate  
cytidyltransferase) (ec:2.7.7.38) (db:pir2.dat) A26322 A26322 Escherichia  
coli 562 -11532736 223279 kdsb 3-deoxy-manno-octulosonate cytidyl-  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #218)  
(db:genpept-bct1) (de:escherichia coli genomic dna. (20.8 - 21.2 min).)  
(le:3206) (re:3952) (di:direct) D90730 D90730 g1651444 Escherichia coli 562  
-11532736 7500959664 kdsb cmp-kdo synthetase (sr:escherichia coli (strain  
k-12) (clone: ptjb101.) dna) (db:genpept-bct1) (de:e.coli kdsb gene  
encodingctp:cmp-3-deoxy-d-manno-octulosonate-cytidyl-transferase  
(cmp-kdosynthetase), complete cds.) (le:266) (re:1012) (di:direct) ECOKDSB  
J02614 g146554 Escherichia coli 562 -11532736 234929 kdsb  
ctp:cmp-3-deoxy-d-manno-octulosonate (fn:enzyme; surface polysaccharides and  
antigens) (db:genpept-bct2) (ec:2.7.7.38) (de:escherichia coli k-12 mg1655  
section 83 of 400 of the completegenome.) (nt:o248; 100 pct identical to  
kdsb\_ecoli sw: p04951) (le:14181) (re:14927) (di:direct) AE000193 AE000193  
g1787147 Escherichia coli 562 -11532736 5000690071 kdsb  
3-deoxy-manno-octulosonate cytidyltransferase (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #218) (db:genpept) (de:escherichia  
coli genomic dna. (20.9 - 21.3 min).) (nt:orf\_id:o218#4; similar to pir  
accession number) (le:3206) (re:3952) (di:direct) D90730 D90730 g1651444  
Escherichia coli 562 -11532736

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822158	7313	29469	630	209

Description

6500728879 kdsa:b1215 2-dehydro-3-deoxyphosphooctonate aldolase:phospho-2-dehydro-3-deoxyoctonate aldolase:3-deoxy-d-manno-octulosonic acid 8-phosphate synthetase:kdo 8-p synthase (gtcfc:1.5) (ec:4.1.2.16) (keggfc:1.5) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1215 b1215 Escherichia coli 562 -11532737 80596 kdsa (ec:4.1.2.16) (de:8-phosphate synthetase) (kdo 8-p synthase)) (db:swissprot) KDSA\_ECOLI P17579 ESCHERICHIA COLI 562 -11532737 162609 kdsa 2-dehydro-3-deoxyphosphooctonate aldolase::3-deoxy-d-manno-octulosonic acid 8-phosphate synthetase:phospho-2-dehydro-3-deoxyoctonate aldolase (cl:phospho-2-dehydro-3-deoxyoctonate aldolase) (ec:4.1.2.16) (db:pir1.dat) (mp:27 min) SYECOL I83573 Escherichia coli 562 -11532737 223415 kdsa 2-dehydro-3-deoxyphosphooctonate aldolase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #247) (db:genpept-bct1) (de:escherichia coli genomic dna. (27.0 -27.4 min).) (le:12427) (re:13281) (di:direct) D90756 D90756 g1651603 Escherichia coli 562 -11532737 223422 kdsa 2-dehydro-3-deoxyphosphooctonate aldolase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #248) (db:genpept-bct1) (de:escherichia coli genomic dna (27.2-27.6 min).) (le:3289) (re:4143) (di:direct) D90757 D90757 g1651611 Escherichia coli 562 -11532737 238750 kdsa 2-dehydro-3-deoxyphosphooctulonate aldolase (fn:enzyme; surface polysaccharides and antigens) (db:genpept-bct2) (ec:4.1.2.16) (de:escherichia coli k-12 mg1655 section 109 of 400 of the completegenome.) (nt:o284; 99 pct identical to kdsa\_ecoli sw: p17579) (le:11859) (re:12713) (di:direct) AE000219 AE000219 g1787466 Escherichia coli 562 -11532737 7500884572 kdsa 3-deoxy-d-manno-octulosonic acid 8-phosphate (db:genpept-bct2) (de:escherichia coli kdsa operon genes, complete cds.) (le:6307) (re:7161) (di:direct) ECU18555 U18555 g968934 Escherichia coli 562 -11532737 5000690072 kdsa 3-deoxy-d-manno-octulosonic acid 8-phosphate (sr:escherichia coli(strain:k12) dna, clone:kohara clone #247) (db:genpept) (de:escherichia coli genomic dna. (27.1 - 27.5 min).) (nt:orf\_id:o248#5; similar to pir accession number) (le:12427) (re:13281) (di:direct) D90756 D90756 g1651603 Escherichia coli 562 -11532737 7502851813 kdsa 3-deoxy-d-manno-octulosonic acid 8-phosphate (sr:escherichia coli(strain:k12) dna, clone:kohara clone #248) (db:genpept) (de:escherichia coli genomic dna. (27.3 - 27.7 min).) (nt:orf\_id:o248#5; similar to pir accession number) (le:3289) (re:4143) (di:direct) D90757 D90757 g1651611 Escherichia coli 562 -11532737

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822159	7314	29470	426	141

# Description

6500728880 rfbc:b2038 dtdp-4-dehydrorhamnose  
3:5-epimerase:dtdp-4-keto-6-deoxyglucose 3:5-epimerase:dtdp-1-rhamnose  
synthetase (gtcfc:1.5:4.3) (ec:5.1.3.13) (keggfc:1.5:4.3) (rileyfc:1.3.3)  
(db:gtc-escherichia coli) b2038 b2038 Escherichia coli 562 -11532738 94155  
rfbc (ec:5.1.3.13) (de:deoxyglucose 3,5-epimerase) (dtdp-1-rhamnose  
synthetase)) (db:swissprot) RFBC\_ECOLI P37745 ESCHERICHIA COLI 562 -11532738  
162972 rfbc dtdp-4-dehydrorhamnose  
3:5-epimerase::dtdp-6-deoxy-d-glucose-3:5  
epimerase:dtdp-6-deoxy-l-xylo-4-hexulose  
4-reductase:dtdp-6-deoxy-d-glucose-3:5  
epimerase:dtdp-6-deoxy-l-xylo-4-hexulose 4-reductase  
(cl:dtdp-4-dehydrorhamnose 3,5-epimerase) (sr:strain k-12, , strain k-12)  
(sr:strain k-12, ) (ec:5.1.3.13) (db:pir2.dat) (mp:45 min) I69651 I69651  
Escherichia coli 562 -11532738 301203 rfbc dtdp-4-dehydrorhamnose  
3:5-epimerase ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara  
lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#351(45.1-45.5 min.)) (nt:orf\_id:o351#14; similar to (swissprot accession)  
(le:15881) (re:16438) (di:complement) D90841 D90841 g1736728 Escherichia  
coli 562 -11532738 301215 rfbc dtdp-4-dehydrorhamnose 3:5-epimerase ec  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #352(45.3-45.7  
min.)) (nt:orf\_id:o351#14; similar to (swissprot accession) (le:6670)  
(re:7227) (di:complement) D90842 D90842 g1736741 Escherichia coli 562  
-11532738 238581 rmlc dtdp-6-deoxy-d-glucose-3:5 epimerase  
(db:genpept-bct1) (de:escherichia coli k-12 dtdp-d-glucose 4,6-dehydratase  
(rmlb),dtdp-6-deoxy-l-mannose-dehydrogenase (rmlc),  
glucose-1-phosphatethymidyltransferase (rmla), dtdp-6-deoxy-d-glucose-3,5  
epimerase(rmlc), putative o-antigen transporter (... ECU09876 U09876 g508240  
Escherichia coli 562 -11532738 238051 rfbc dtdp-6-deoxy-d-glucose-3:5  
epimerase (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2)  
(ec:5.1.3.13) (de:escherichia coli k-12 mg1655 section 184 of 400 of the  
completegenome.) (nt:f185; 100 pct identical to rfbc\_ecoli sw: p37745;)  
(le:12338) (re:12895) (di:complement) AE000294 AE000294 g1788350 Escherichia  
coli 562 -11532738 297654 rmlc dtdp-6-deoxy-l-xylo-4-hexulose 4-reductase  
(fn:synthesis of dtdp-rhamnose) (db:genpept-bct2) (de:escherichia coli k12  
glucose-1-phosphate thymidyltransferase (rmla)gene, partial cds;  
dtdp-6-deoxy-l-xylo-4-hexulose 4-reductase(rmlc), membrane protein (wzx),  
dehydrogenase (glf), o-antigenpolymera... ECRFBA U03041 g510251 Escherichia  
coli 562 -11532738 224563 rfbc dtdp-4-dehydrorhamnose 3:5-epimerase ec  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #351(45.1-45.5  
min.)) (nt:orf\_id:o351#14; similar to (swissprot accession) (le:15881)  
(re:16438) (di:complement) D90841 D90841 g1736728 Escherichia coli 562  
-11532738 224575 rfbc dtdp-4-dehydrorhamnose 3:5-epimerase ec  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #352(45.3-45.7

(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #352(45.3-45.7 min.)) (nt:orf\_id:o351#14; similar to (swissprot accession) (le:6670)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822163	7315	29471	1263	420

# Description

6500728881 rfbd:b2040 (gtcfc:1.5:4.3) (ec:1.1.1.133) (keggfc:1.5:4.3) (rileyfc:1.3.3) (db:gtc-escherichia coli) b2040 b2040 Escherichia coli 562 -11532739 94160 rfbd (ec:1.1.1.133) (de:rhamnose synthetase)) (db:swissprot) RBD1\_ECOLI P37760 ESCHERICHIA COLI 562 -11532739 7000686276 rfbd dtdp-4-dehydrorhamnose reductase::dtdp-4-keto-1-rhamnose reductase:dtdp-6-deoxy-1-mannose dehydrogenase:dtdp-4-keto-1-rhamnose reductase:dtdp-6-deoxy-1-mannose dehydrogenase (cl:dtdp-dihydrostreptose synthase) (sr:strain k-12, , strain k-12) (sr:strain k-12, ) (ec:1.1.1.133) (db:pir2.dat) G64969 G64969 Escherichia coli 562 -11532739 224565 rfbd dtdp-4-dehydrorhamnose reductase ec 1.1.1.133 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #351(45.1-45.5 min.)) (nt:orf\_id:o351#16; similar to (swissprot accession) (le:17377) (re:18276) (di:complement) D90841 D90841 g1736730 Escherichia coli 562 -11532739 224577 rfbd dtdp-4-dehydrorhamnose reductase ec 1.1.1.133 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #352(45.3-45.7 min.)) (nt:orf\_id:o351#16; similar to (swissprot accession) (le:8166) (re:9065) (di:complement) D90842 D90842 g1736743 Escherichia coli 562 -11532739 7000686277 rmlb dtdp-6-deoxy-1-mannose-dehydrogenase (db:genpept-bct1) (de:escherichia coli k-12 dtdp-d-glucose 4,6-dehydratase (rmlb), dtdp-6-deoxy-1-mannose-dehydrogenase (rmlb), glucose-1-phosphatethymidyltransferase (rmla), dtdp-6-deoxy-d-glucose-3,5 epimerase(rmlc), putative o-antigen transporter (... ECU09876 U09876 g2665490 Escherichia coli 562 -11532739 301205 rfbd dtdp-6-deoxy-1-mannose-dehydrogenase (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 184 of 400 of the completegenome.) (nt:f299; 99 pct identical to rfbd\_ecoli sw: p37760) (le:13834) (re:14733) (di:complement) AE000294 AE000294 g1788352 Escherichia coli 562 -11532739 301217 rmlb dtdp-6-deoxy-1-mannose-dehydrogenase (db:genpept-bct1) (de:escherichia coli k-12 dtdp-d-glucose 4,6-dehydratase (rmlb), dtdp-6-deoxy-1-mannose-dehydrogenase (rmlb), glucose-1-phosphatethymidyltransferase (rmla), dtdp-6-deoxy-d-glucose-3,5 epimerase(rmlc), putative o-antigen transporter (... ECU09876 U09876 g2665490 Escherichia coli 562 -11532739 5000690075 (de:(ecoli\_1988) (pn:dtdp-4-dehydrorhamnose reductase) (gn:rfbd) (gtcfc:1.5:4.3) (ec:1.1.1.133) (rfbd\_ecoli) (keggfc:1.5:4.3) (rileyfc:1.3.3) (db:gtc-escherichia coli)) ECOLI\_1988 ECOLI\_1988 Escherichia coli 562 10119970

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822177	7316	29472	1446	482

Description

6500728882 rfbb:b2041 dtdp-glucose 4:6-dehydratase (gtcfc:1.5:4.3)  
(ec:4.2.1.46) (keggfc:1.5:4.3) (rileyfc:1.3.3) (db:gtc-escherichia coli)  
b2041 b2041 Escherichia coli 562 -11532740 93156 rfbb (ec:4.2.1.46)  
(de:dtdp-glucose 4,6-dehydratase,) (db:swissprot) RBB1\_ECOLI P37759  
ESCHERICHIA COLI 562 -11532740 7000686274 rfbb dtdpglucose 4:6-dehydratase  
(cl:escherichia coli udpglucose 4-epimerase:udpglucose 4-epimerase homology)  
(sr:strain k-12, , strain k-12) (sr:strain k-12, ) (ec:4.2.1.46)  
(db:pir2.dat) H64969 H64969 Escherichia coli 562 -11532740 224566 rfbb  
dtdp-glucose 4:6-dehydratase ec 4.2.1.46 . (sr:escherichia coli (strain:k12)  
dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic  
dna, kohara clone #351(45.1-45.5 min.)) (nt:orf\_id:o351#17; similar to  
(swissprot accession) (le:18276) (re:19361) (di:complement) D90841 D90841  
g1736731 Escherichia coli 562 -11532740 224578 rfbb dtdp-glucose  
4:6-dehydratase ec 4.2.1.46 . (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #352(45.3-45.7 min.)) (nt:orf\_id:o351#17; similar to  
(swissprot accession) (le:9065) (re:10150) (di:complement) D90842 D90842  
g1736744 Escherichia coli 562 -11532740 7000686275 rmlb dtdp-d-glucose  
4:6-dehydratase (db:genpept-bct1) (de:escherichia coli k-12 dtdp-d-glucose  
4,6-dehydratase (rmlb),dtdp-6-deoxy-1-mannose-dehydrogenase (rmlb),  
glucose-1-phosphatethymidylyltransferase (rmla), dtdp-6-deoxy-d-glucose-3,5  
epimerase(rmlc), putative o-antigen transporter (... ECU09876 U09876  
g2665489 Escherichia coli 562 -11532740 301206 rfbb dtdp-glucose 4:6  
dehydratase (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2)  
(ec:4.2.1.46) (de:escherichia coli k-12 mg1655 section 184 of 400 of the  
completegenome.) (nt:f361; 99 pct identical to rfbb\_ecoli sw: p37759)  
(le:14733) (re:15818) (di:complement) AE000294 AE000294 g1788353 Escherichia  
coli 562 -11532740 301218 rmlb dtdp-d-glucose 4:6-dehydratase  
(db:genpept-bct1) (de:escherichia coli k-12 dtdp-d-glucose 4,6-dehydratase  
(rmlb),dtdp-6-deoxy-1-mannose-dehydrogenase (rmlb),  
glucose-1-phosphatethymidylyltransferase (rmla), dtdp-6-deoxy-d-glucose-3,5  
epimerase(rmlc), putative o-antigen transporter (... ECU09876 U09876  
g2665489 Escherichia coli 562 -11532740 5000690076 (de:(ecoli\_1989)  
(pn:dtdp-glucose 4,6 dehydratase) (gn:rfbb) (gtcfc:1.5:4.3) (ec:4.2.1.46)  
(rbb1\_ecoli) (keggfc:1.5:4.3) (rileyfc:1.3.3) (db:gtc-escherichia coli))  
ECOLI\_1989 ECOLI\_1989 Escherichia coli 562 10119971

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822183	7317	29473	1797	599

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822194	7318	29474	2736	912

Description

6500728883 manb:cpsg:rdbl:b2048 phosphomannomutase:pmm (gtcfc:1.5:2.3) (ec:5.4.2.8) (keggfc:1.5) (rileyfc:1.3.1) (db:gtc-escherichia coli) b2048 b2048 Escherichia coli 562 -11532741 66185 manb:cpsg:rdbl (ec:5.4.2.8) (de:phosphomannomutase, (pmm)) (db:swissprot) MANB\_ECOLI P24175 ESCHERICHIA COLI 562 -11532741 162868 cpsg phosphomannomutase::cpsg protein (ec:5.4.2.8) (db:pir2.dat) B55239 B55239 Escherichia coli 562 -11532741 301227 cpsg phosphomannomutase ec 5.4.2.8 pmm . (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #353(45.6-46.0 min.)) (nt:orf\_id:o353#1; similar to (swissprot accession) (le:3377) (re:4747) (di:complement) D90843 D90843 g1736754 Escherichia coli 562 -11532741 239546 pgm phosphoglucomutase (sr:escherichia coli (strain dg101) (library: dg101:puc18) dna) (db:genpept-bct1) (de:escherichia coli phosphoglucomutase (pgm) gene, 3' end, andphosphomannose isomerase (pmi) gene, complete cds.) (le:565) (re:1935) (di:direct) ECOPGMPMI M77127 g147165 Escherichia coli 562 -11532741 235398 cpsg phosphomannomutase (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (ec:5.4.2.8) (de:escherichia coli k-12 mg1655 section 185 of 400 of the completegenome.) (nt:f456; 100 pct identical to cpsg\_ecoli sw: p24175;) (le:8392) (re:9762) (di:complement) AE000295 AE000295 g1788361 Escherichia coli 562 -11532741 296205 manb phosphomannomutase (db:genpept-bct2) (de:escherichia coli k-12 wca gene cluster.) (nt:referred to as cpsg in reference (2)) (le:13994) (re:15364) (di:direct) ECU38473 U38473 g1407617 Escherichia coli 562 -11532741 224587 cpsg phosphomannomutase ec 5.4.2.8 pmm . (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #353(45.6-46.0 min.)) (nt:orf\_id:o353#1; similar to (swissprot accession) (le:3377) (re:4747) (di:complement) D90843 D90843 g1736754 Escherichia coli 562 -11532741 5000690077 (de:(ecoli\_1996) (pn:phosphomannomutase) (gn:cpsg) (gtcfc:1.5) (ec:5.4.2.8) (cpsg\_ecoli) (keggfc:1.5) (rileyfc:1.3.1) (db:gtc-escherichia coli)) ECOLI\_1996 ECOLI\_1996 Escherichia coli 562 10008816

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822212	7319	29475	264	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822233	7320	29476	402	133

Description

6500728884 manc:cpsb:rfbm:b2049 mannose-1-phosphate  
guanylyltransferase:gdp:gdp-mannose pyrophosphorylase:gmp (gtcfc:1.5:4.3)  
(ec:2.7.7.22) (keggfc:1.5) (rileyfc:1.3.3) (db:gtc-escherichia coli) b2049  
b2049 Escherichia coli 562 -11532742 7000691858 cpsb mannose-1-phosphate  
guanylyltransferase gdp (cl:helicobacter mannose-6-phosphate isomerase)  
(ec:2.7.7.22) (db:pir2.dat) H64970 H64970 Escherichia coli 562 -11532742  
224588 cpsb mannose-1-phosphate guanylyltransferase gdp (sr:escherichia  
coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #353(45.6-46.0 min.)).)  
(nt:orf\_id:o353#2; similar to (swissprot accession) (le:4852) (re:6288)  
(di:complement) D90843 D90843 g1736755 Escherichia coli 562 -11532742  
301228 cpsb mannose-1-phosphate guanyltransferase (fn:enzyme; central  
intermediary metabolism:) (db:genpept-bct2) (ec:2.7.7.22) (de:escherichia  
coli k-12 mg1655 section 185 of 400 of the completegenome.) (nt:f478; 99 pct  
identical to cpsb\_ecoli sw: p24174; cg) (le:9867) (re:11303) (di:complement)  
AE000295 AE000295 g1788362 Escherichia coli 562 -11532742 5000690078  
(de:(ecoli\_1997) (pn:mannose-1-phosphate guanyltransferase) (gn:cpsb)  
(gtcfc:1.5) (ec:2.7.7.22) (cpsb\_ecoli) (keggfc:1.5) (rileyfc:1.3.3)  
(db:gtc-escherichia coli)) ECOLI\_1997 ECOLI\_1997 Escherichia coli 562  
10119976

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822252	7321	29477	186	61

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822255	7322	29478	747	249
<u>Description</u>				
6500728885 yefa:gmd:b2053 gdp-mannose 4:6-dehydratase:gdp-d-mannose dehydratase (gtcfc:1.5) (ec:4.2.1.47) (keggfc:1.5) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2053 b2053 Escherichia coli 562 -11532743 111544 gmd (ec:4.2.1.47) (de:gdp-mannose 4,6-dehydratase, (gdp-d-mannose dehydratase)) (db:swissprot) GM4D_ECOLI P32054 ESCHERICHIA COLI 562 -11532743 7000685434 yefa gdp-d-mannose dehydratase (cl:gdp-d-mannose dehydratase) (db:pir2.dat) D64971 D64971 Escherichia coli 562 -11532743 301232 yefa dtdp-glucose 4:6-dehydratase ec 4.2.1.46 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #353(45.6-46.0 min..)) (nt:orf_id:o353#6; similar to (swissprot accession) (le:8961) (re:10082) (di:complement) D90843 D90843 g1736759 Escherichia coli 562 -11532743 239541 gmd gdp-d-mannose dehydratase (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 185 of 400 of the completgenome.) (nt:f373; formerly designated yefa) (le:13976) (re:15097) (di:complement) AE000295 AE000295 g1788366 Escherichia coli 562 -11532743 296200 gmd gdp-d-mannose dehydratase (db:genpept-bct2) (de:escherichia coli k-12 wca gene cluster.) (nt:referred to as orf0.0 in reference (2)) (le:8659) (re:9780) (di:direct) ECU38473 U38473 g1407612 Escherichia coli 562 -11532743 224592 yefa dtdp-glucose 4:6-dehydratase ec 4.2.1.46 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #353(45.6-46.0 min..)) (nt:orf_id:o353#6; similar to (swissprot accession) (le:8961) (re:10082) (di:complement) D90843 D90843 g1736759 Escherichia coli 562 -11532743 5000692663 (de:(ecoli_2001) (pn:gdp-d-mannose dehydratase:orf0) (gn:yefa) (gtcfc:13.7:14.1) (ec:) (yefa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2001 ECOLI_2001 Escherichia coli 562 10119978				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822259	7323	29479	504	167
<u>Description</u>				
6500728886 srld:gutd:b2705 sorbitol-6-phosphate 2-dehydrogenase:glucitol-6-phosphate dehydrogenase:ketosephosphate reductase (gtcfc:1.5:1.4) (ec:1.1.1.140) (keggfc:1.5) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2705 b2705 Escherichia coli 562 -11532744 99471 srld:gutd (ec:1.1.1.140) (de:phosphate dehydrogenase) (ketosephosphate reductase)) (db:swissprot) SRLD_ECOLI P05707 ESCHERICHIA COLI 562 -11532744 7000686678 srld:gutd sorbitol-6-phosphate 2-dehydrogenase::glucitol-6-phosphate dehydrogenase (cl:ribitol dehydrogenase:short-chain alcohol dehydrogenase homology) (ec:1.1.1.140) (db:pirl.dat) (mp:58 min) DEECSP E65050 Escherichia coli 562 -11532744 225257 gutd sorbitol-6-phosphate 2-dehydrogenase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #446(60.5-60.9 min.)) (nt:similar to (swissprot accession number p05707)) (le:16643) (re:17422) (di:direct) D90892 D90892 g1800091 Escherichia coli 562 -11532744 7500892077 gutd glucitol-6-phosphate dehydrogenase sorbitol-6- (db:genpept-bct1) (ec:1.1.1.140) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg site no. 153; alternate gene name srld) (le:39) (re:818) (di:direct) ECU29579 U29579 g882597 Escherichia coli 562 -11532744 239278 srld glucitol sorbitol -6-phosphate dehydrogenase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:1.1.1.140) (de:escherichia coli k-12 mg1655 section 244 of 400 of the completegenome.) (nt:o259; 99 pct identical to srld_ecoli sw: p05707; cg) (le:5693) (re:6472) (di:direct) AE000354 AE000354 g1789057 Escherichia coli 562 -11532744 5000690080 (de:(ecoli_2633) (pn:glucitol:sorbitol-6-phosphate dehydrogenase) (gn:srld) (gtcfc:1.5) (ec:1.1.1.140) (srld_ecoli) (keggfc:1.5) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2633 ECOLI_2633 Escherichia coli 562 10041329				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822262	7324	29480	309	102

Description

6500728887 rfad:htrm:b3619 adp-l-glycero-d-mannoheptose-6-epimerase  
(gtcf:1.5) (ec:5.1.3.-) (keggfc:1.5) (rileyfc:3.3.2) (db:gtc-escherichia  
coli) b3619 b3619 Escherichia coli 562 -11532745 235757 rfad:htrm  
(ec:5.1.3.20) (de:glyceromanno-heptose 6-epimerase)) (db:swissprot)  
RFAD\_ECOLI P17963 ESCHERICHIA COLI 562 -11532745 162679 rfad:htrm  
adp-l-glycero-d-mannoheptose-6-epimerase (ec:5.1.3.-) (db:pir2.dat) (mp:81  
min) JU0299 JU0299 Escherichia coli 562 -11532745 5000690082 htrm acidic  
34:893da htrm protein (db:genpept-bct1) (de:e.coli htrm (heat shock gene  
family) gene.) (le:227) (re:1159) (di:direct) ECHTRMG X54492 g41763  
Escherichia coli 562 -11532745 236856 (sr:e.coli (strain k12) dna)  
(db:genpept-bct1) (de:e.coli rfad gene, complete cds.) (nt:rfad protein)  
(le:946) (re:1878) (di:direct) ECORFADA M33577 g147576 Escherichia coli 562  
-11532745 7500889669 rfad adp-l-glycero-d-mannoheptose-6-epimerase  
(sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda)  
(db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.)  
(nt:alternate gene name htrm; heat shock regulated; cg) (le:208251)  
(re:209183) (di:direct) ECOUW76 U00039 g466757 Escherichia coli 562  
-11532745 233166 rfad adp-l-glycero-d-mannoheptose-6-epimerase (fn:enzyme;  
surface polysaccharides and antigens) (db:genpept-bct2) (ec:5.1.3.-)  
(de:escherichia coli k-12 mg1655 section 330 of 400 of the completegenome.)  
(nt:o310; 100 pct identical to rfad\_ecoli sw: p17963;) (le:1353) (re:2285)  
(di:direct) AE000440 AE000440 g1790049 Escherichia coli 562 -11532745 94117  
rfad:htrm (ec:5.1.3.20) (de:glyceromanno-heptose 6-epimerase))  
(db:swissprot) RFAD\_ECOLI P17963 ESCHERICHIA COLI 562 -11532745

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822267	7325	29481	453	150

Description

6500728888 rfab:b3628 udp-d-galactose  
glucosyllipopolysaccharide-alpha-1:3-d-galactosyltransferase:lipopolysaccharide 1:6-galactosyltransferase (gtcfc:11.2:1.6:7.1:8.5) (ec:2.4.1.-) (keggfc:1.5:7.2:7.3:8.5) (rileyfc:3.3.2) (db:gtc-escherichia coli) b3628 b3628 Escherichia coli 562 -11532746 94113 rfab (ec:2.4.1.-) (de:galactosyltransferase)) (db:swissprot) RFAB\_ECOLI P27127 ESCHERICHIA COLI 562 -11532746 164798 rfab udp-d-galactose--glucosyl lipopolysaccharide-alpha-1:3-d-galactosyltransferase::rfab (ec:2.4.1.-) (db:pir2.dat) B42982 B42982 Escherichia coli 562 -11532746 236865 rfab lipopolysaccharide core biosynthesis protein (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli lipopolysaccharide core biosynthesis proteinoperon (rfaq, rfap, rfag, rfas, rfab, rfai, and rfaj) genes,complete cds.) (le:4375) (re:5484) (di:direct) ECOLPOSACR M80599 gl46655 Escherichia coli 562 -11532746 7500889667 rfab udp-d-galactose:glucosyl lipopolysaccharide (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 17617) (le:217322) (re:218431) (di:complement) ECOUW76 U00039 g912480 Escherichia coli 562 -11532746 235010 rfab udp-d-galactose:glucosyl lipopolysaccharide-1 (fn:enzyme; surface polysaccharides and antigens) (db:genpept-bct2) (ec:2.4.1.-) (de:escherichia coli k-12 mg1655 section 330 of 400 of the completegenome.) (nt:f369; 100 pct identical to rfab\_ecoli sw: p27127;cg) (le:10424) (re:11533) (di:complement) AE000440 AE000440 g1790058 Escherichia coli 562 -11532746 5000690582 (de:(ecoli\_3548) (pn:udp-d-galactose:udp-d-galactose,:glucosyllipopolysaccharide-1,6-d-galactosyltransferase) (gn:rfab) (gtcfc:8.4:8.5:11.4) (ec:2.4.1.-) (rfab\_ecoli) (keggfc:7.2:7.3:8.5) (rileyfc:3.3.2) (db:gtc-escherichia col) ECOLI\_3548 ECOLI\_3548 Escherichia coli 562 10036096

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822274	7326	29482	573	191

Description

6500728889 rfe:b3784 putative undecaprenyl-phosphate  
alpha-n-acetylglucosaminyltransferase (gtcfc:1.5:7.1:8.5:11.2:11.3:11.4)  
(ec:2.4.1.-) (keggfc:1.5:7.2:7.3:8.5) (rileyfc:3.3.2) (db:gtc-escherichia  
coli) b3784 b3784 Escherichia coli 562 -11532747 94199 rfe (ec:2.4.1.-)  
(de:(ec 2.4.1.-)) (db:swissprot) RFE\_ECOLI P24235 ESCHERICHIA COLI 562  
-11532747 7000686313 rfe probable undecaprenyl-phosphate  
alpha-n-acetylglucosaminyltransferase:rfe protein (db:pir2.dat) (mp:85 min)  
C65182 C65182 Escherichia coli 562 -11532747 7500889696 rfe  
udp-glcnac:undecaprenylphosphate (fn:enzyme; central intermediary  
metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 344  
of 400 of the completegenome.) (nt:o367; 99 pct identical to 257 amino  
acids) (le:10001) (re:11104) (di:direct) AE000454 AE000454 g1790218  
Escherichia coli 562 -11532747 5000690583 (de:(ecoli\_3694) (pn:synthesis of  
enterobacterial common antigen:eca, udp- glcnac:undecaprenylphosphate  
glcnac-1-phosphate transferase; synt) (gn:rfe) (gtcfc:8.4:8.5:11.4)  
(ec:2.4.1.-) (rfe\_ecoli) (keggfc:7.2:7.3:8.5) (rileyfc:3) ECOLI\_3694  
ECOLI\_3694 Escherichia coli 562 10124094

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822278	7327	29483	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822290	7328	29484	354	117

Description

6500728890 rffg:b3788 udp-n-acetylglucosamine  
epimerase:udp-glcnac-2-epimerase:dtdp-glucose 4:6-dehydratase  
(gtcfc:11.3:1.5:4.3) (ec:4.2.1.46) (keggfc:1.5:4.3) (rileyfc:5.8.0)  
(db:gtc-escherichia coli) b3788 b3788 Escherichia coli 562 -11532748 94205  
rffg (ec:4.2.1.46) (de:dtdp-glucose 4,6-dehydratase,) (db:swissprot)  
RFFG\_ECOLI P27830 ESCHERICHIA COLI 562 -11532748 7000686314 rffg  
dtdpglucose 4:6-dehydratase (cl:escherichia coli udpglucose  
4-epimerase:udpglucose 4-epimerase homology) (ec:4.2.1.46) (db:pir2.dat)  
G65182 G65182 Escherichia coli 562 -11532748 7500889702 rffg dtdp-glucose  
4:6-dehydratase (fn:enzyme; central intermediary metabolism:)  
(db:genpept-bct2) (ec:5.1.3.-) (de:escherichia coli k-12 mg1655 section 345  
of 400 of the completengenome.) (nt:100 pct identical to rffe\_ecoli sw:  
p27830) (le:2439) (re:3506) (di:direct) AE000455 AE000455 g1790223  
Escherichia coli 562 -11532748 5000690083 (de:(ecoli\_3698) (pn:dtdp-glucose  
4,6-dehydratase) (gn:rffg) (gtcfc:1.5:4.3) (ec:4.2.1.46) (rffg\_ecoli)  
(keggfc:1.5:4.3) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_3698  
ECOLI\_3698 Escherichia coli 562 10124097

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822291	7329	29485	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822298	7330	29486	252	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822318	7331	29487	1674	558

Description

6500728891 rfft:b3793 4-alpha-1-fucosyltransferase  
 (gtcfc:1.5:7.1:8.5:11.3:11.4) (ec:2.4.1.-) (keggfc:1.5:7.2:7.3:8.5)  
 (rileyfc:3.3.2) (db:gtc-escherichia coli) b3793 b3793 Escherichia coli 562  
 -11532749 7500894381 wecf:rfft (ec:2.4.1.-) (de:transferase))  
 (db:swissprot) WECF\_ECOLI P27835 ESCHERICHIA COLI 562 -11532749 7000690841  
 rfft 4-alpha-1-fucosyltransferase (ec:2.4.1.-) (db:pir2.dat) F65183 F65183  
 Escherichia coli 562 -11532749 7500894383 wecf tdp-fuc4nac:lipidii  
 transferase:synthesis of (fn:enzyme; central intermediary metabolism:)  
 (db:genpept-bct2) (ec:2.4.1.-) (de:escherichia coli k-12 mg1655 section 345  
 of 400 of the completegenome.) (nt:o450; formerly designated rfft) (le:8519)  
 (re:9871) (di:direct) AE000455 AE000455 g2367288 Escherichia coli 562  
 -11532749

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822319	7332	29488	414	137

Description

GTC ORF with score 218 to: (db:genpept-bct1) (de:methanobacterium  
 thermoautotrophicum from bases 481808 to 494891(section 43 of 148) of the  
 complete genome.) (nt:function code:14.01 - unknown, conserved protein;)  
 (le:7639) (re:8022) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822331	7333	29489	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822349	7334	29490	342	113
<u>Description</u>				
6500728892 rffm:b3794 probable udp-n-acetyl-d-mannosaminuronic acid transferase:udp-mannaca transferase (gtcfc:11.3:11.4:1.5:7.1:8.5) (ec:2.4.1.-) (keggfc:1.5:7.2:7.3:8.5) (rileyfc:3.3.2) (db:gtc-escherichia coli) b3794 b3794 Escherichia coli 562 -11532750 7500894384 wecg:rffm (ec:2.4.1.-) (de:(udp-mannaca transferase)) (db:swissprot) WECG_ECOLI P27836 ESCHERICHIA COLI 562 -11532750 7000691900 rffm probable udp-n-acetyl-d-mannosaminuronic acid transferase:hypothetical protein o246 (db:pir2.dat) G65183 G65183 Escherichia coli 562 -11532750 7500894386 wecg probable udp-n-acetyl-d-mannosaminuronic acid (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 345 of 400 of the completegenome.) (nt:o246; formerly designated rffm) (le:9874) (re:10614) (di:direct) AE000455 AE000455 g2367289 Escherichia coli 562 -11532750				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822352	7335	29491	699	232
<u>Description</u>				
6500728893 yjhk:sgce:b4301 hypothetical 23.2 kd protein in feci-fimb intergenic region:sgce protein (gtcfc:14.3) (ec:5.1.3.-) (keggfc:1.5) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4301 b4301 Escherichia coli 562 -11532751 113799 sgce (ec:5.1.3.-) (de:sgce protein,) (db:swissprot) SGCE_ECOLI P39362 ESCHERICHIA COLI 562 -11532751 163588 yjhk hypothetical 23.2k protein feci-fimb intergenic region:hypothetical protein f210 (cl:yeast ribulose-5-phosphate-epimerase) (db:pir2.dat) S56526 S56526 Escherichia coli 562 -11532751 7500891599 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f210) (le:217737) (re:218369) (di:complement) ECOUW93 U14003 g537142 Escherichia coli 562 -11532751 237506 sgce putative epimerase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 390 of 400 of the completegenome.) (nt:f210; formerly designated yjhk) (le:10215) (re:10847) (di:complement) AE000500 AE000500 g1790754 Escherichia coli 562 -11532751 5000694005 (de:(ecoli_4184) (pn:hypothetical 23) (gn:yjhk) (gtcfc:13.7:14.1) (ec:) (yjhk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4184 ECOLI_4184 Escherichia coli 562 10055527				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822357	7336	29492	267	88

#### Description

6500728894 bglx:b2132 periplasmic beta-glucosidase precursor:gentiobiase:cellobiase:beta-d-glucoside glucohydrolase (gtcfc:7.1:11.1:1.6) (ec:3.2.1.21) (keggfc:1.6:5.13:6.5:7.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2132 b2132 Escherichia coli 562 -11532752 61676 bglx (ec:3.2.1.21) (de:(cellobiase) (beta-d-glucoside glucohydrolase)) (db:swissprot) BGLX\_ECOLI P33363 ESCHERICHIA COLI 562 -11532752 7000684704 bglx beta-glucosidase:precursor:periplasmic (ec:3.2.1.21) (db:pir2.dat) C64981 C64981 Escherichia coli 562 -11532752 7500877789 bglx beta-glucosidase precursor (db:genpept-bct1) (de:escherichia coli beta-glucosidase precursor (bglx) gene, completecds.) (nt:bglx; periplasmic protease similar to yoha, a) (le:201) (re:2498) (di:direct) ECU15049 U15049 g555956 Escherichia coli 562 -11532752 238680 bglx beta-d-glucoside glucohydrolase:periplasmic (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:3.2.1.21) (de:escherichia coli k-12 mg1655 section 192 of 400 of the completegenome.) (nt:f765; 100 pct identical bglx\_ecoli sw: p33363) (le:4967) (re:7264) (di:complement) AE000302 AE000302 g1788453 Escherichia coli 562 -11532752 5000690092 (de:(ecoli\_2081) (pn:beta-d-glucoside glucohydrolase, periplasmic) (gn:bglx) (gtcfc:1.6:6.5:7.2) (ec:3.2.1.21) (bglx\_ecoli) (keggfc:1.6:6.5:7.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2081 ECOLI\_2081 Escherichia coli 562 10004385

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822372	7337	29493	312	103

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822374	7338	29494	198	65

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822383	7339	29495	1197	398

#### Description

GTC ORF with score 486 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f09d1.) (nt:similar to peptidase family c19 (ubiquitin) (le:<901:2323:3335:4374) (re:993:2636:3578:4655) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822384	7340	29496	306	101

Description

GTC ORF with score 207 to: (sr:thale cress) (db:genpept-pln1)  
 (de:arabidopsis thaliana dna chromosome 4, bac clone t10i14  
 (essaiiproject).) (nt:similarity to probable membrane protein yfr005c,)  
 (le:64831:65039:65307) (re:64927:65213:65478) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822392	7341	29497	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822396	7342	29498	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822409	7343	29499	756	251

Description

6500728895 agai:b3141 putative galactosamine-6-phosphate isomerase  
 (gtcfc:1.6) (ec:5.3.1.-) (keggfc:1.6) (rileyfc:5.8.0) (db:gtc-escherichia  
 coli) b3141 b3141 Escherichia coli 562 -11532753 58924 agai (ec:5.3.1.-)  
 (de:(galactosamine-6-phosphate deaminase)) (db:swissprot) AGAI\_ECOLI P42912  
 ESCHERICHIA COLI 562 -11532753 7000684534 agai probable  
 galactosamine-6-phosphate isomerase (cl:glucosamine-6-phosphate isomerase)  
 (ec:5.3.1.-) (db:pir2.dat) A65104 A65104 Escherichia coli 562 -11532753  
 7500876660 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region  
 from 67.4 to 76.0 minutes.) (nt:orf\_o251) (le:67022) (re:67777) (di:direct)  
 ECOUW67 U18997 g606081 Escherichia coli 562 -11532753 236380 agai putative  
 galactosamine-6-phosphate isomerase (fn:putative enzyme; not classified)  
 (db:genpept-bct2) (ec:5.3.1.-) (de:escherichia coli k-12 mg1655 section 285  
 of 400 of the completegenome.) (nt:o251; 100 pct identical amino acid  
 sequence and) (le:4505) (re:5260) (di:direct) AE000395 AE000395 g1789530  
 Escherichia coli 562 -11532753 5000690096 (de:(ecoli\_3065) (pn:putative  
 galactosamine-6-phosphate isomerase:galactosamine- 6-phosphate deaminase)  
 (gn:agai) (gtcfc:1.6) (ec:5.3.1.-) (agai\_ecoli) (keggfc:1.6) (rileyfc:5.7.0)  
 (db:gtc-escherichia coli)) ECOLI\_3065 ECOLI\_3065 Escherichia coli 562  
 10001668

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822431	7344	29500	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822433	7345	29501	699	232

Description

6500728896 mhpc:b0349 hypothetical  
protein:2-hydroxy-6-ketonona-2:4-dienedioic acid hydrolase (gtcfc:1.7:5.13)  
(ec:3.7.1.-) (keggfc:1.7:5.13) (rileyfc:5.7.0) (db:gtc-escherichia coli)  
b0349 b0349 Escherichia coli 562 -11532754 120051 mhpc (ec:3.7.1.-)  
(de:2-hydroxy-6-ketonona-2,4-dienedioic acid hydrolase,) (db:swissprot)  
MHPC\_ECOLI P77044 ESCHERICHIA COLI 562 -11532754 7000685842 mhpc probable  
2:6-dioxo-6-phenylhexa-3-enoate hydrolase (cl:tropinesterase) (ec:3.7.1.8)  
(db:pir2.dat) E64762 E64762 Escherichia coli 562 -11532754 7500885609  
(db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:similar  
to pseudomonas sp. pcbd) (le:78971) (re:79900) (di:direct) ECU73857 U73857  
g1657545 Escherichia coli 562 -11532754 239966 mhpc  
2-hydroxy-6-ketonona-2:4-dienedioic acid (fn:enzyme; degradation of small  
molecules: carbon) (db:genpept-bct2) (de:escherichia coli k-12 mg1655  
section 32 of 400 of the completengenome.) (nt:o309; this 309 aa orf is 51  
pct identical (2 gaps)) (le:2634) (re:3563) (di:direct) AE000142 AE000142  
g1786545 Escherichia coli 562 -11532754 5000691527 (de:(ecoli\_333)  
(pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2)  
(rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_333 ECOLI\_333 Escherichia  
coli 562 10060201

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822435	7346	29502	210	69
<u>Description</u>				
6500728897 ubix:dedf:b2311 3-octaprenyl-4-hydroxybenzoate carboxy-lyase:polyprenyl p-hydroxybenzoate decarboxylase (gtcfc:1.7:1.8:5.10:5.12:5.13:5.14:9.12:9.3) (ec:4.1.1.-) (keggfc:1.7:1.8:5.10:5.12:5.13:5.14:9.3:9.13) (rileyfc:1.7.11) (db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-ascorbate and aldarate metabolism:carbohydrate metabolism-pyruvate and ace... b2311 b2311 Escherichia coli 562 -11532755 103144 ubix:dedf (ec:4.1.1.-) (de:p-hydroxybenzoate decarboxylase)) (db:swissprot) UBIX_ECOLI P09550 ESCHERICHIA COLI 562 -11532755 7000686849 dedf:ubix 3-octaprenyl-4-hydroxybenzoate carboxy-lyase (cl:dedf protein) (ec:4.1.1.-) (db:pir1.dat) (mp:50 min) XMECFD E65003 Escherichia coli 562 -11532755 224844 dedf 3-octaprenyl-4-hydroxybenzoate carboxy-lyase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #406(52.2-52.5 min.)) (nt:similar to (swissprot accession number p09550)) (le:11634) (re:12203) (di:complement) D90862 D90862 g1799692 Escherichia coli 562 -11532755 7500893695 ubix 3-octaprenyl-4-hydroxybenzoate carboxy-lyase (fn:putative enzyme; not classified) (db:genpept-bct2) (ec:4.1.1.-) (de:escherichia coli k-12 mg1655 section 210 of 400 of the completegenome.) (nt:f189; 93 pct identical to ubix_ecoli sw: p09550;) (le:2126) (re:2695) (di:complement) AE000320 AE000320 g1788650 Escherichia coli 562 -11532755 5000690098 (de:(ecoli_2260) (pn:3-octaprenyl-4-hydroxybenzoate carboxy-lyase:polyprenyl p- hydroxybenzoate decarboxylase) (gn:ubix) (gtcfc:1.7:1.8:5.10:5.12:5.13:9.12:9.3) (ec:4.1.1.-) (ubix_ecoli) (keggfc:1.7:1.8:5.10:5.12:5.13:9.3:9.13)) ECOLI_2260 ECOLI_2260 Escherichia coli 562 10120108				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822446	7347	29503	1107	369

#### Description

6500728898 ygcx:b2787 hypothetical protein:probable glucarate dehydratase 1:gdh (gtcfc:1.7:1.4) (ec:4.2.1.40) (keggfc:1.7) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2787 b2787 Escherichia coli 562 -11532756 5500685317 ygcx (ec:4.2.1.40) (de:probable glucarate dehydratase 1, (gdh)) (db:swissprot) GUD1\_ECOLI P76637 ESCHERICHIA COLI 562 -11532756 7000685475 probable glucarate dehydratase (cl:glucarate dehydratase) (ec:4.2.1.40) (db:pir2.dat) G65060 G65060 Escherichia coli 562 -11532756 7500882846 ygcx putative glucarate dehydratase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 252 of 400 of the completgenome.) (nt:f446; realign with gudh\_bacsu (sw: p42238);) (le:8295) (re:9635) (di:complement) AE000362 AE000362 g1789150 Escherichia coli 562 -11532756 5000693162 (de:(ecoli\_2718) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2718 ECOLI\_2718 Escherichia coli 562 10123831

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822452	7348	29504	237	78

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822476	7349	29505	711	237

#### Description

6500728899 ygcy:b2788 hypothetical protein:probable glucarate dehydratase 2:gdh (gtcfc:1.7:1.4) (ec:4.2.1.40) (keggfc:1.7) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2788 b2788 Escherichia coli 562 -11532757 5500685318 ygcy (ec:4.2.1.40) (de:probable glucarate dehydratase 2, (gdh)) (db:swissprot) GUD2\_ECOLI Q46915 ESCHERICHIA COLI 562 -11532757 7000685476 glucarate dehydratase homolog (cl:glucarate dehydratase) (db:pir2.dat) H65060 H65060 Escherichia coli 562 -11532757 7500882847 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:orf\_f446) (le:961) (re:2301) (di:complement) ECU29581 U29581 g882683 Escherichia coli 562 -11532757 239362 ygcy putative glucarate dehydratase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 252 of 400 of the completgenome.) (nt:f446; this 446 aa orf is 66 pct identical (5 gaps)) (le:9656) (re:10996) (di:complement) AE000362 AE000362 g1789151 Escherichia coli 562 -11532757 5000693163 (de:(ecoli\_2719) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2719 ECOLI\_2719 Escherichia coli 562 10123832

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822477	7350	29506	450	149

Description

GTC ORF with score 107 to: (fn:ethylene signal transduction) (sr:common tobacco) (db:genpept-pln1) (de:nicotiana tabacum pk12 protein kinase (pk12) mrna, complete cds.) (nt:component of the lammer family of protein kinases;) (le:73) (re:1368) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822481	7351	29507	1692	563

Description

6500728900 leua:b0074 2-isopropylmalate synthase:alpha-isopropylmalate synthase:alpha-ipm synthetase (gtcfc:1.8:5.7) (ec:4.1.3.12) (keggfc:1.8:5.7) (rileyfc:1.4.7) (db:gtc-escherichia coli) b0074 b0074 Escherichia coli 562 -11532758 7000690838 leua 2-isopropylmalate synthase::alpha-isopropylmalate synthase (cl:2-isopropylmalate synthase leua) (ec:4.1.3.12) (db:pir2.dat) B64729 B64729 Escherichia coli 562 -11532758 7500959663 leua 2-isopropylmalate synthase (fn:enzyme; amino acid biosynthesis: leucine) (db:genpept-bct2) (ec:4.1.3.12) (de:escherichia coli k-12 mgl655 section 7 of 400 of the completengenome.) (nt:f523; 99 pct identical to leul\_ecoli sw: p09151) (le:11771) (re:13342) (di:complement) AE000117 AE000117 gl786261 Escherichia coli 562 -11532758 5000690099 (de:(ecoli\_74) (pn:2-isopropylmalate synthase) (gn:leua) (gtcfc:1.8:5.7) (ec:4.1.3.12) (leul\_ecoli) (keggfc:1.8:5.7) (rileyfc:1.4.7) (db:gtc-escherichia coli)) ECOLI\_74 ECOLI\_74 Escherichia coli 562 10122647

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822510	7352	29508	285	94

Description

6500728901 glob:b0212 hypothetical protein:probable hydroxyacylglutathione hydrolase:glyoxalase ii (gtcfc:6.16:1.4) (ec:3.1.2.6) (keggfc:1.8) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0212 b0212 Escherichia coli 562 -11532759 500684911 glob (ec:3.1.2.6) (de:ii) (glx ii)) (db:swissprot) GLO2\_ECOLI Q47677 ESCHERICHIA COLI 562 -11532759 7000685412 glob probable hydroxyacylglutathione hydrolase:glob:probable glyoxalase ii:protein b0212 (cl:glyoxalase) (ec:3.1.2.6) (db:pir2.dat) F64745 F64745 Escherichia coli 562 -11532759 239833 unknown (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (nt:orf161) (le:43568) (re:44323) (di:complement) ECOTSF D83536 g1208973 Escherichia coli 562 -11532759 303268 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical protein) (le:65102) (re:65857) (di:complement) ECU70214 U70214 g1552782 Escherichia coli 562 -11532759 236191 glob probable hydroxyacylglutathione hydrolase (fn:putative enzyme; central intermediary) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 20 of 400 of the completegenome.) (nt:f251; 100 pct identical to gb: ecotsf\_31) (le:3056) (re:3811) (di:complement) AE000130 AE000130 g1786406 Escherichia coli 562 -11532759 5000691427 (de:(ecoli\_206) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_206 ECOLI\_206 Escherichia coli 562 10060537

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822511	7353	29509	627	208

Description

6500728902 mhpe:mhpf:b0352 hypothetical protein:4-hydroxy-2-oxovalerate aldolase:hoa (gtcfc:1.8:5.15:5.9:9.12) (ec:4.1.3.-) (keggfc:1.8:5.9:5.15:9.13) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0352 b0352 Escherichia coli 562 -11532760 83676 mhpe:mhpf (ec:4.1.3.-) (de:4-hydroxy-2-oxovalerate aldolase, (hoa)) (db:swissprot) MHPE\_ECOLI P51020 ESCHERICHIA COLI 562 -11532760 7000685844 4-hydroxy-2-oxovalerate aldolase (ec:4.1.3.-) (db:pir2.dat) H64762 H64762 Escherichia coli 562 -11532760 222962 mhpf mhpf (sr:escherichia coli (strain:k-12, sub\_strain:w3110) dna) (db:genpept-bct1) (de:escherichia coli genes for mhpr, mhpa, mhpb, mhpc, mhpD, mhpe andmhpf, complete sequence of the mhp operon.) (le:6281) (re:7294) (di:direct) D86239 D86239 g1665751 Escherichia coli 562 -11532760 7500885612 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:similar to p. put4-hydroxy-2-oxovalerate) (le:81663) (re:82676) (di:direct) ECU73857 U73857 g1657548 Escherichia coli 562 -11532760 239969 mhpe 4-hydroxy-2-ketovalerate aldolase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:4.1.3.-) (de:escherichia coli k-12 mg1655 section 32 of 400 of the completegenome.) (nt:o337; this 337 aa orf is 29 pct identical (18 gaps)) (le:5326) (re:6339) (di:direct) AE000142 AE000142 g1786548 Escherichia coli 562 -11532760 5000691529 (de:(ecoli\_336) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_336 ECOLI\_336 Escherichia coli 562 10119247

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822512	7354	29510	792	263

#### Description

6500728903 ldha:hsli:htph:b1380 d-lactate dehydrogenase:d-ldh  
 (gtcfc:1.1:1.8) (ec:1.1.1.28) (keggfc:1.8) (rileyfc:1.2.7)  
 (db:gtc-escherichia coli) b1380 b1380 Escherichia coli 562 -11532761 81647  
 ldha:hsli:htph (ec:1.1.1.28) (de:d-lactate dehydrogenase, (d-ldh))  
 (db:swissprot) LDHD\_ECOLI P52643 ESCHERICHIA COLI 562 -11532761 7000685720  
 ldha d-lactate dehydrogenase (ec:1.1.1.28) (db:pir2.dat) G64888 G64888  
 Escherichia coli 562 -11532761 223663 ldha:hsli:htph d-lactate  
 dehydrogenase ec 1.1.1.28 d-ldh . (sr:escherichia coli (strain:k12) dna,  
 clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
 kohara clone #265(30.9-31.2 min.)) (nt:orf\_id:o265#1; similar to (swissprot  
 accession) (le:5931) (re:6920) (di:complement) D90776 D90776 g1742259  
 Escherichia coli 562 -11532761 300436 ldha d-lactate dehydrogenase  
 (sr:escherichia coli strain=k-12) (db:genpept-bct1) (de:escherichia coli  
 d-lactate dehydrogenase (ldha) gene, complete cds.) (le:1201) (re:2190)  
 (di:direct) ECU36928 U36928 g1049265 Escherichia coli 562 -11532761 239522  
 ldha fermentative d-lactate dehydrogenase (fn:enzyme; energy metabolism,  
 carbon:) (db:genpept-bct2) (ec:1.1.1.28) (de:escherichia coli k-12 mg1655  
 section 125 of 400 of the completegenome.) (nt:f329; 100 pct identical to  
 ldhd\_ecoli sw: p52643;) (le:832) (re:1821) (di:complement) AE000235 AE000235  
 g1787645 Escherichia coli 562 -11532761 5000690102 (de:(ecoli\_1340)  
 (pn:d-lactate dehydrogenase, nad-dependent) (gn:ldha) (gtcfc:1.8)  
 (ec:1.1.1.28) (ldhd\_ecoli) (keggfc:1.8) (rileyfc:1.2.7) (db:gtc-escherichia  
 coli) ECOLI\_1340 ECOLI\_1340 Escherichia coli 562 10023882

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822522	7355	29511	300	99

#### Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822523	7356	29512	405	134

#### Description

GTC ORF with score 179 to: (fn:involved in production of the virulence  
 factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide  
 synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703)  
 (re:1524:2083:2661:3353) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822531	7357	29513	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822548	7358	29514	1110	370

Description

6500728904 alda:ald:b1415 lactaldehyde dehydrogenase a:aldehyde dehydrogenase a:lactaldehyde dehydrogenase (gtcfc:1.4:1.8) (ec:1.2.1.22) (keggfc:1.8) (rileyfc:1.2.7) (db:gtc-escherichia coli) b1415 b1415 Escherichia coli 562 -11532762 162695 alda lactaldehyde dehydrogenase:alda (cl:aldehyde dehydrogenase (nad+):aldehyde dehydrogenase homology) (ec:1.2.1.22) (db:pir2.dat) A38165 A38165 Escherichia coli 562 -11532762 223707 alda aldehyde dehydrogenase nad+ ec 1.2.1.3 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #269(31.8-32.1 min.).) (nt:orf\_id:o270#3; similar to (pir accession number) (le:11084) (re:12523) (di:direct) D90780 D90780 g1742307 Escherichia coli 562 -11532762 223712 alda aldehyde dehydrogenase nad+ ec 1.2.1.3 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #270(32.0-32.3 min.).) (nt:orf\_id:o270#3; similar to (pir accession number) (le:3900) (re:5339) (di:direct) D90781 D90781 g1742313 Escherichia coli 562 -11532762 300477 ald lactaldehyde dehydrogenase (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli lactaldehyde dehydrogenase (ald) gene, completecds.) (le:199) (re:1638) (di:direct) ECOALD M64541 g145222 Escherichia coli 562 -11532762 233757 alda aldehyde dehydrogenase:nad-linked (fn:enzyme; energy metabolism, carbon:) (db:genpept-bct2) (ec:1.2.1.22) (de:escherichia coli k-12 mg1655 section 129 of 400 of the completegenome.) (nt:o479; 100 pct identical to alda\_ecoli sw: p25553;) (le:1163) (re:2602) (di:direct) AE000239 AE000239 g1787684 Escherichia coli 562 -11532762 5000690103 (de:(ecoli\_1375) (pn:aldehyde dehydrogenase, nad-linked) (gn:alda) (gtcfc:1.8) (ec:1.2.1.22) (alda\_ecoli) (keggfc:1.8) (rileyfc:1.2.7) (db:gtc-escherichia coli)) ECOLI\_1375 ECOLI\_1375 Escherichia coli 562 10086586

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822551	7359	29515	855	284

# Description

6500728905 sfca:maea:b1479 nad-linked malic enzyme:malate oxidoreductase:probable malate oxidoreductase:nad malic enzyme (gtcfc:1.8:1.2) (ec:1.1.1.38) (keggfc:1.8) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1479 b1479 Escherichia coli 562 -11532763 98446 sfca:maea (ec:1.1.1.38) (de:probable malate oxidoreductase (nad), (malic enzyme)) (db:swissprot) SFCA\_ECOLI P26616 ESCHERICHIA COLI 562 -11532763 7000686590 sfca:maea malate dehydrogenase oxaloacetate-decarboxylating::nad-linked:malic enzyme:pyruvic-malic carboxylase:sfca protein (cl:malate dehydrogenase (oxaloacetate-decarboxylating)) (ec:1.1.1.38) (db:pir2.dat) B64901 B64901 Escherichia coli 562 -11532763 223803 sfca:maea sfca protein fragment . (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #277(33.2-33.6 min.)) (nt:orf\_id:o277#10; similar to (swissprot accession) (le:11776) (re:13500) (di:complement) D90788 D90788 g1742411 Escherichia coli 562 -11532763 223812 sfca:maea sfca protein fragment . (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #278(33.3-33.7 min.)) (nt:orf\_id:o277#10; similar to (swissprot accession) (le:8152) (re:9876) (di:complement) D90789 D90789 g1742421 Escherichia coli 562 -11532763 300559 sfca:maea sfca protein fragment . (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #279(33.5-33.9 min.)) (nt:orf\_id:o277#10; similar to (swissprot accession) (le:255) (re:1979) (di:complement) D90790 D90790 g1742432 Escherichia coli 562 -11532763 300555 sfca nad-linked malate dehydrogenase malic enzyme (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:1.1.1.38) (de:escherichia coli k-12 mg1655 section 135 of 400 of the completegenome.) (nt:f574; 100 pct identical to fragment sfca\_ecoli) (le:1208) (re:2932) (di:complement) AE000245 AE000245 g1787754 Escherichia coli 562 -11532763 223822 sfca:maea sfca protein fragment . (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #279(33.5-33.9 min.)) (nt:orf\_id:o277#10; similar to (swissprot accession) (le:255) (re:1979) (di:complement) D90790 D90790 g1742432 Escherichia coli 562 -11532763 5000690104 (de:(ecoli\_1439) (pn:nad-linked malate dehydrogenase) (gn:sfca) (gtcfc:1.8:2.4) (ec:1.1.1.38) (sfca\_ecoli) (keggfc:1.8:2.3) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_1439 ECOLI\_1439 Escherichia coli 562 10119635

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822553	7360	29516	582	193

Description

6500728906 gloa:b1651 hypothetical protein:lactoylglutathione  
lyase:methylglyoxalase:aldoketomutase:glyoxalase i (gtcfc:1.8:6.16:1.4)  
(ec:4.4.1.5) (keggfc:1.8) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1651  
b1651 Escherichia coli 562 -11532764 118369 gloa (ec:4.4.1.5)  
(de:(s-d-lactoylglutathione methylglyoxal lyase)) (db:swissprot) LGUL\_ECOLI  
Q59384 ESCHERICHIA COLI 562 -11532764 7000685740 gloa lactoylglutathione  
lyase:gloa (ec:4.4.1.5) (db:pir2.dat) E64922 E64922 Escherichia coli 562  
-11532764 239733 gloa lactoylglutathione lyase (fn:enzyme; central  
intermediary metabolism: pool,) (db:genpept-bct2) (de:escherichia coli k-12  
mg1655 section 150 of 400 of the completegenome.) (nt:o135; 74 pct identical  
amino acid sequence and) (le:3172) (re:3579) (di:direct) AE000260 AE000260  
g1787940 Escherichia coli 562 -11532764 297237 gloa s-d-lactoylglutathione  
methylglyoxal lyase (db:genpept-bct2) (ec:4.4.1.5) (de:escherichia coli  
s-d-lactoylglutathione methylglyoxal lyase (gloa)gene, complete cds.)  
(nt:homodimeric enzyme; not activated by zinc; one) (le:1) (re:408)  
(di:direct) ECU57363 U57363 g1354845 Escherichia coli 562 -11532764  
5000692402 (de:(ecoli\_1610) (pn:function not assigned) (gtcfc:13.7:14.1)  
(ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_1610  
ECOLI\_1610 Escherichia coli 562 10060529

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822555	7361	29517	615	204

# Description

6500728907 pabb:b1812 para-aminobenzoate synthase component i:adc synthase  
 (gtcfc:1.8:5.15:5.9:9.12:9.6) (ec:4.1.3.-) (keggfc:1.8:5.9:5.15:9.13)  
 (rileyfc:1.7.2) (db:gtc-escherichia coli) (gtcfc:carbohydrate  
 metabolism-pyruvate and acetyl-coa metabolism:l-amino acid  
 metabolism-phenylalanine--tyrosine and tryptophan biosynthesi... b1812 b1812  
 Escherichia coli 562 -11532765 88416 pabb (ec:4.1.3.-)  
 (de:para-aminobenzoate synthase component i, (adc synthase)) (db:swissprot)  
 PABB\_ECOLI P05041 ESCHERICHIA COLI 562 -11532765 125567 pabb  
 p-aminobenzoate synthase:component i (cl:anthranilate synthase component i)  
 (ec:4.1.3.-) (db:pir1.dat) (mp:40 min) AGEC1 A30251 Escherichia coli 562  
 -11532765 224300 pabb p-aminobenzoate synthase ec 4.1.3.- component  
 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
 (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #334(40.6-41.0  
 min.)) (nt:orf\_id:o334#4; similar to (pir accession number) (le:7511)  
 (re:8872) (di:direct) D90825 D90825 g1736449 Escherichia coli 562 -11532765  
 300942 pabb (sr:e.coli dna, clone ppg3) (db:genpept-bct1) (de:e.coli pabb  
 gene, coding for p-aminobenzoate synthetase, completecoding sequence.)  
 (nt:p-aminobenzoate synthetase) (le:135) (re:1496) (di:direct) ECOPABB  
 K02673 g147058 Escherichia coli 562 -11532765 235324 pabb p-aminobenzoate  
 synthetase:component i (fn:enzyme; biosynthesis of cofactors, carriers:)  
 (db:genpept-bct2) (ec:4.1.3.-) (de:escherichia coli k-12 mg1655 section 165  
 of 400 of the completegenome.) (nt:o453; 100 pct identical to pabb\_ecoli sw:  
 p05041;) (le:6809) (re:8170) (di:direct) AE000275 AE000275 g1788114  
 Escherichia coli 562 -11532765 5000690106 (de:(ecoli\_1769)  
 (pn:p-aminobenzoate synthetase, component i) (gn:pabb)  
 (gtcfc:1.8:5.15:5.9:9.12) (ec:4.1.3.-) (pabb\_ecoli)  
 (keggfc:1.8:5.9:5.15:9.13) (rileyfc:1.7.2) (db:gtc-escherichia coli))  
 ECOLI\_1769 ECOLI\_1769 Escherichia coli 562 10030545

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822556	7362	29518	636	211

Description

6500728908 dld:b2133 d-lactate dehydrogenase (gtcfc:1.8:2.8) (ec:1.1.1.28) (keggfc:1.8) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2133 b2133  
 Escherichia coli 562 -11532766 122512 dld d-lactate dehydrogenase (cl:d-lactate dehydrogenase) (ec:1.1.1.28) (db:pir1.dat) (mp:47 min) DEECDL A21893 Escherichia coli 562 -11532766 234171 d-lactate dehydrogenase (db:genpept-bct1) (de:e. coli gene dld for d-lactate dehydrogenase.) (le:244) (re:1959) (di:direct) ECDLD X01067 g41287 Escherichia coli 562 -11532766 7500953170 dld d-lactate dehydrogenase (sr:e.coli dna, clone piy2) (db:genpept-bct1) (de:e.coli dld gene encoding d-lactate dehydrogenase, complete cds.) (le:244) (re:1959) (di:direct) ECODLDH M10038 g145753 Escherichia coli 562 -11532766 232689 dld d-lactate dehydrogenase:fad protein:nadh (fn:enzyme; energy metabolism, carbon: aerobic) (db:genpept-bct2) (ec:1.1.1.28) (de:escherichia coli k-12 mg1655 section 192 of 400 of the completegenome.) (nt:o571; 100 pct identical to ldhd\_ecoli sw: p06149;) (le:7460) (re:9175) (di:direct) AE000302 AE000302 g1788454 Escherichia coli 562 -11532766 5000690107 (de:(ecoli\_2082) (pn:d-lactate dehydrogenase, fad protein, nadh independent) (gn:dld) (gtcfc:1.8) (ec:1.1.1.28) (dld\_ecoli) (keggfc:1.8) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI\_2082 ECOLI\_2082 Escherichia coli 562 10065499

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822568	7363	29519	375	124

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822584	7364	29520	1482	494

Description

6500728909 glcb:glc:b2976 malate synthase:malate synthase g:msg  
 (gtcfc:1.8:1.9:2.3) (ec:4.1.3.2) (keggfc:1.8:1.9) (rileyfc:1.3.1)  
 (db:gtc-escherichia coli) b2976 b2976 Escherichia coli 562 -11532767 205553  
 glcb malate synthase:isoenzyme g (ec:4.1.3.2) (db:pir2.dat) S51788 S51788  
 Escherichia coli 562 -11532767 239189 glcb malate synthase  
 (db:genpept-bct1) (ec:4.1.3.2) (de:e.coli glcb gene for malate synthase.)  
 (nt:malate synthase (isoenzyme g)) (le:254) (re:2425) (di:direct) ECGLCBMS  
 X74547 g517247 Escherichia coli 562 -11532767 7500960376 glcb malate  
 synthase (db:genpept-bct1) (ec:4.1.3.2) (de:escherichia coli k-12 genome;  
 approximately 65 to 68 minutes.) (le:76026) (re:78197) (di:complement)  
 ECU28377 U28377 g882505 Escherichia coli 562 -11532767 232990 glcb malate  
 synthase g (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2)  
 (ec:4.1.3.2) (de:escherichia coli k-12 mg1655 section 270 of 400 of the  
 completegenome.) (nt:f723; 100 pct identical to masz\_ecoli sw: p37330)  
 (le:7151) (re:9322) (di:complement) AE000380 AE000380 g1789348 Escherichia  
 coli 562 -11532767 5000690112 (de:(ecoli\_2898) (pn:malate synthase g)  
 (gn:glcb) (gtcfc:1.8:1.9) (ec:4.1.3.2) (masz\_ecoli) (keggfc:1.8:1.9)  
 (rileyfc:1.3.1) (db:gtc-escherichia coli)) ECOLI\_2898 ECOLI\_2898 Escherichia  
 coli 562 10087135

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822593	7365	29521	1353	451

#### Description

6500728910 paba:b3360 para-aminobenzoate synthetase:coii:para-aminobenzoate synthase glutamine amidotransferase component ii  
(gtcfc:1.8:5.15:5.9:9.12:9.6) (ec:4.1.3.-) (keggfc:1.8:5.9:5.15:9.13)  
(rileyfc:1.7.2) (db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-pyruvate and acetyl-coa metabolism:l-amino acid metabolism-phenylalanine--tyrosine and tryptophan biosynthesi... b3360 b3360 Escherichia coli 562 -11532768 88410 paba (ec:4.1.3.-) (de:(ec 4.1.3.-)) (db:swissprot) PABA\_ECOLI P00903 ESCHERICHIA COLI 562 -11532768 125572 paba p-aminobenzoate synthase:component ii (cl:glutamine amidotransferase:trpg homology) (ec:4.1.3.-) (db:pir1.dat) (mp:74 min) AGE2 A01124 Escherichia coli 562 -11532768 235322 (sr:escherichia coli, strain bn101 dna) (db:genpept-bct1) (de:e.coli paba gene coding for p-aminobenzoate synthetase.) (nt:p-aminobenzoate synthetase (paba)) (le:83) (re:646) (di:direct) ECOPABA K00030 g147050 Escherichia coli 562 -11532768 236593 (sr:e.coli dna, clone pszd3) (db:genpept-bct1) (de:e.coli glutamine amidotransferase subunit of para-aminobenzoatesynthase (paba) and pot. cell division protein (fic) genes,complete cds.) (nt:glutamine amidotransferase) (le:1360) (re:1923) (di:direct) ECOPABAA M32354 g147055 Escherichia coli 562 -11532768 7500887588 paba para-aminobenzoate synthetase:coii (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no.429) (le:271013) (re:271576) (di:complement) ECOUW67 U18997 g606294 Escherichia coli 562 -11532768 235318 paba p-aminobenzoate synthetase:component ii (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 302 of 400 of the completegenome.) (nt:f187; cg site no.429; 100 pct identical amino) (le:1370) (re:1933) (di:complement) AE000412 AE000412 g1789760 Escherichia coli 562 -11532768 5000690113 (de:(ecoli\_3278) (pn:p-aminobenzoate synthetase, component ii) (gn:paba) (gtcfc:1.8:5.15:5.9:9.12) (ec:4.1.3.-) (paba\_ecoli) (keggfc:1.8:5.9:5.15:9.13) (rileyfc:1.7.2) (db:gtc-escherichia coli)) ECOLI\_3278 ECOLI\_3278 Escherichia coli 562 10030539

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822612	7366	29522	423	140

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822625	7367	29523	228	75

#### Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822628	7368	29524	1944	647

Description

6500728911 aldb:b3588 aldehyde dehydrogenase b (gtcfc:1.4:1.8) (ec:1.2.1.22) (keggfc:1.8) (rileyfc:1.2.7) (db:gtc-escherichia coli) b3588 b3588  
 Escherichia coli 562 -11532769 136431 aldb lactaldehyde dehydrogenase:aldb (cl:aldehyde dehydrogenase (nad+):aldehyde dehydrogenase homology) (ec:1.2.1.22) (db:pir2.dat) S47809 S47809 Escherichia coli 562 -11532769 7500953825 (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:169226) (re:170854) (di:complement) ECOUW76 U00039 g912476 Escherichia coli 562 -11532769 236825 aldb aldehyde dehydrogenase b lactaldehyde (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:1.2.1.22) (de:escherichia coli k-12 mg1655 section 326 of 400 of the completegenome.) (nt:f542; 100 pct identical to 512 amino acids) (le:4049) (re:5677) (di:complement) AE000436 AE000436 g1790014 Escherichia coli 562 -11532769 5000690114 (de:(ecoli\_3508) (pn:aldehyde dehydrogenase b:lactaldehyde dehydrogenase) (gn:aldb) (gtcfc:1.8) (ec:1.2.1.22) (aldb\_ecoli) (keggfc:1.8) (rileyfc:1.2.7) (db:gtc-escherichia coli)) ECOLI\_3508 ECOLI\_3508 Escherichia coli 562 10069455

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822666	7369	29525	273	90

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822671	7370	29526	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822672	7371	29527	537	178

Description

6500728912 lldd:lctd:b3605 lctd:l-lactate dehydrogenase:cytochrome  
 (gtcfc:1.8:2.8) (ec:1.1.2.3) (keggfc:1.8) (rileyfc:1.2.6)  
 (db:gtc-escherichia coli) b3605 b3605 Escherichia coli 562 -11532770 82262  
 lldd:lctd (ec:1.1.2.3) (de:l-lactate dehydrogenase (cytochrome),)  
 (db:swissprot) LLDD\_ECOLI P33232 ESCHERICHIA COLI 562 -11532770 163981 lctd  
 l-lactate dehydrogenase::fmn-dependent:lctd protein (cl:(s)-2-hydroxy-acid  
 oxidase:(s)-2-hydroxy-acid oxidase homology) (ec:1.1.1.27) (db:pir2.dat)  
 C49904 C49904 Escherichia coli 562 -11532770 7500885080 lctd l-lactate  
 dehydrogenase (fn:catalysing dehydrogenation reaction of) (sr:escherichia  
 coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli lct operon  
 encoding l-lactate permease (lctp)gene, (lctr) gene, and l-lactate  
 dehydrogenase (lctd) gene,complete cds.) (nt:lctd s... ECOLCTPRD L13970  
 g404695 Escherichia coli 562 -11532770 234961 lldd l-lactate dehydrogenase  
 (fn:enzyme; energy metabolism, carbon: aerobic) (db:genpept-bct2)  
 (de:escherichia coli k-12 mg1655 section 328 of 400 of the completegenome.)  
 (nt:o396) (le:7623) (re:8813) (di:direct) AE000438 AE000438 g1790033  
 Escherichia coli 562 -11532770 5000690115 (de:(ecoli\_3525) (pn:l-lactate  
 dehydrogenase, ferrocyclochrome protein) (gn:lctd) (gtcfc:1.8) (ec:1.1.2.3)  
 (lldd\_ecoli) (keggfc:1.8) (rileyfc:1.2.6) (db:gtc-escherichia coli))  
 ECOLI\_3525 ECOLI\_3525 Escherichia coli 562 10024492

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822673	7372	29528	309	102

#### Description

6500728913 ppc:glu:b3956 phosphoenolpyruvate carboxylase:pepcase:pepc  
 (gtcfc:1.8:2.2:2.4:2.5) (ec:4.1.1.31) (keggfc:1.8:2.3:2.4) (rileyfc:1.2.7)  
 (db:gtc-escherichia coli) (gtcfc:carbohydrate metabolism-pyruvate and  
 acetyl-coa metabolism:energy metabolism-methane metabolism:energy  
 metabolism-carbon fixation:energy metabol... b3956 b3956 Escherichia coli  
 562 -11532771 237866 ppc:glu (ec:4.1.1.31) (de:phosphoenolpyruvate  
 carboxylase, (pepcase) (pepc)) (db:swissprot) CAPP\_ECOLI P00864 ESCHERICHIA  
 COLI 562 -11532771 125344 ppc phosphoenolpyruvate carboxylase  
 (cl:phosphoenolpyruvate carboxylase) (ec:4.1.1.31) (db:pir1.dat) (mp:89 min)  
 QYEC A01083 Escherichia coli 562 -11532771 5000690116 (db:genpept-bct1)  
 (de:e.coli ppc gene for phosphoenolpyruvate carboxylase (ec 4.1.1.31).)  
 (nt:pep carboxylase (aa 1-883)) (le:239) (re:2890) (di:direct) ECPPCG X05903  
 g48666 Escherichia coli 562 -11532771 237174 ppc phosphoenolpyruvate  
 carboxylase (fn:enzyme; energy metabolism, carbon:) (db:genpept-bct2)  
 (ec:4.1.1.31) (de:escherichia coli k-12 mg1655 section 359 of 400 of the  
 completengenome.) (nt:f883; 100 pct identical to capp\_ecoli sw: p00864;)  
 (le:8215) (re:10866) (di:complement) AE000469 AE000469 g1790393 Escherichia  
 coli 562 -11532771 7500878160 ppc phosphoenolpyruvate carboxylase  
 (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda)  
 (db:genpept-bct2) (ec:4.1.1.31) (de:e. coli chromosomal region from 89.2 to  
 92.8 minutes.) (nt:cg site no. 368) (le:15688) (re:18339) (di:complement)  
 ECOUW89 U00006 g396303 Escherichia coli 562 -11532771 62745 ppc:glu  
 (ec:4.1.1.31) (de:phosphoenolpyruvate carboxylase, (pepcase) (pepc))  
 (db:swissprot) CAPP\_ECOLI P00864 ESCHERICHIA COLI 562 -11532771

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822674	7373	29529	198	65

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822685	7374	29530	183	60

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822722	7375	29531	456	151

#### Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822727	7376	29532	1041	346

# Description

6500728914 aceb:mas:b4014 malate synthase a:msa (gtcfc:1.8:1.9:2.3)  
(ec:4.1.3.2) (keggfc:1.8:1.9) (rileyfc:1.3.1) (db:gtc-escherichia coli)  
b4014 b4014 Escherichia coli 562 -11532772 228035 aceb:mas (ec:4.1.3.2)  
(de:malate synthase a, (msa)) (db:swissprot) MASY\_ECOLI P08997 ESCHERICHIA  
COLI 562 -11532772 125524 aceb malate synthase:a (cl:malate synthase)  
(ec:4.1.3.2) (db:pir1.dat) (mp:91 min) SYECMA A32649 Escherichia coli 562  
-11532772 5000690117 (db:genpept-bct1) (de:e. coli genes aceb and acea for  
for malate synthase (ec 4.1.3.2)and isocitrate lyase (ec 4.1.3.1).)  
(nt:malate synthase) (le:581) (re:2182) (di:direct) ECACEB X12431 g40887  
Escherichia coli 562 -11532772 237220 aceb malate synthase a (fn:enzyme;  
central intermediary metabolism:) (db:genpept-bct2) (ec:4.1.3.2)  
(de:escherichia coli k-12 mg1655 section 364 of 400 of the completegenome.)  
(nt:o533; 100 pct identical to masy\_ecoli sw: p08997;) (le:7609) (re:9210)  
(di:direct) AE000474 AE000474 g1790444 Escherichia coli 562 -11532772  
500684695 aceb malate synthase a (sr:escherichia coli (sub\_strain mg1655,  
strain k-12) (library: lambda) (db:genpept-bct2) (ec:4.1.3.2) (de:e. coli  
chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 1051;  
alternate gene name mas) (le:80720) (re:82321) (di:direct) ECOUW89 U00006  
g396349 Escherichia coli 562 -11532772 7502851814 aceb (db:genpept-pat)  
(de:dna expression cassette mtaceb2 with bacterial aceb gene frompatent  
wo9218635.) (le:882) (re:2483) (di:direct) A31765 A31765 g1926481 synthetic  
construct 32630 -11532772 7502851815 aceb (db:genpept-pat) (de:dna  
exprtession cassette mtaceab1 with bacterial genes acea andaceb from patent  
wo9218635.) (le:4037) (re:5638) (di:direct) A31767 A31767 g1926484 synthetic  
construct 32630 -11532772 83017 aceb:mas (ec:4.1.3.2) (de:malate synthase  
a, (msa)) (db:swissprot) MASY\_ECOLI P08997 ESCHERICHIA COLI 562 -11532772  
500684694 aceb malate synthase a (sr:escherichia coli (sub\_strain mg1655,  
strain k-12) (library: lambda) (db:genpept-bct2) (ec:4.1.3.2) (de:e. coli  
chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 1051;  
alternate gene name mas) (le:80720) (re:82321) (di:direct) ECOUW89 U00006  
g396349 Escherichia coli 562 -11532772

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822737	7377	29533	306	101

#### Description

6500728915 ubic:b4039 chorismate lyase (gtcfc:1.8:5.15:5.9:9.12) (ec:4.1.3.-) (keggfc:1.8:5.9:5.15:9.13) (rileyfc:1.7.11) (db:gtc-escherichia coli) b4039 b4039 Escherichia coli 562 -11532773 162625 ubic 4-hydroxybenzoate synthetase:chorismate lyase:chorismate pyruvate-lyase (db:pir2.dat) S25660 S25660 Escherichia coli 562 -11532773 240320 ubic 4-hydroxybenzoate synthetase (db:genpept-bct1) (de:e.coli ubic and ubia genes for chorismate lyase and 4-hydroxybenzoate octaprenyltransferase.) (le:291) (re:899) (di:direct) ECUBIAC X57434 g43234 Escherichia coli 562 -11532773 237245 ubic chorismate lyase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 367 of 400 of the complete genome.) (nt:o202a; cg site no. 48) (le:4490) (re:5098) (di:direct) AE000477 AE000477 g1790472 Escherichia coli 562 -11532773 7500959668 ubic chorismate lyase (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e.coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 48) (le:117637) (re:118245) (di:direct) ECOUW89 U00006 g396374 Escherichia coli 562 -11532773 5000690118 (de:(ecoli\_3925) (pn:chorismate lyase) (gn:ubic) (gtcfc:1.8:5.15:5.9:9.12) (ec:4.1.3.-) (ubic\_ecoli) (keggfc:1.8:5.9:5.15:9.13) (rileyfc:1.7.11) (db:gtc-escherichia coli)) ECOLI\_3925 ECOLI\_3925 Escherichia coli 562 10086555

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822740	7378	29534	333	110

#### Description

6500728916 pdhr:gena:b0113 pyruvate dehydrogenase complex repressor (gtcfc:1.8) (keggfc:1.8:10.2) (rileyfc:1.2.2) (db:gtc-escherichia coli) b0113 b0113 Escherichia coli 562 -11532774 228038 pdhr:gena (de:pyruvate dehydrogenase complex repressor) (db:swissprot) PDHR\_ECOLI P06957 ESCHERICHIA COLI 562 -11532774 7000686105 pdhr pyruvate dehydrogenase complex repressor (cl:pyruvate dehydrogenase complex repressor) (db:pir1.dat) (mp:3 min) BVECA A64734 Escherichia coli 562 -11532774 7500887740 acea (db:genpept-bct1) (de:e.coli genes acee, a, acef and lpd. gene acee encodes the elcomponent of pyruvate dehydrogenase. gene a is an unidentified reading frame. gene acef encodes dihydrolipoamide acetyltransferase component (e2) of the pyruvate dehydroge... ECACEX V01498 g434009 Escherichia coli 562 -11532774 7502851816 pdhr transcriptional regulator for pyruvate (fn:regulator; energy metabolism, carbon: pyruvate) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 10 of 400 of the complete genome.) (nt:o254; 100 pct identical to pdhr\_ecoli sw: p06957) (le:4472) (re:5236) (di:direct) AE000120 AE000120 g1786303 Escherichia coli 562 -11532774 88867 pdhr:gena (de:pyruvate dehydrogenase complex repressor) (db:swissprot) PDHR\_ECOLI P06957 ESCHERICHIA COLI 562 -11532774

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822747	7379	29535	204	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822753	7380	29536	222	74

Description

6500728917 gcl:b0507 glyoxylate carboligase:tartronate-semialdehyde synthase (gtcfc:1.9:2.3) (ec:4.1.1.47) (keggfc:1.9) (rileyfc:1.3.1) (db:gtc-escherichia coli) b0507 b0507 Escherichia coli 562 -11532775 141712 gcl tartronate-semialdehyde synthase::glyoxylate carbo-ligase (cl:acetolactate synthase large chain:thiamine pyrophosphate-binding domain homology) (ec:4.1.1.47) (db:pir2.dat) JT0742 JT0742 Escherichia coli 562 -11532775 7500954401 gcl glyoxylate carboligase (sr:escherichia coli (strain k-12) f- dna) (db:genpept-bct1) (ec:4.1.1.47) (de:escherichia coli glyoxylate carboligase (gcl) gene, andglyoxylate-induced protein gene of unknown function, complete cds.) (le:129) (re:1910) (di:direct) ECOGCL L03845 g146119 Escherichia coli 562 -11532775 234466 gcl glyoxylate carboligase (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (ec:4.1.1.47) (de:escherichia coli k-12 mg1655 section 47 of 400 of the completegenome.) (nt:o593; 100 pct identical to gcl\_ecoli sw: p30146) (le:75) (re:1856) (di:direct) AE000157 AE000157 g1786717 Escherichia coli 562 -11532775 5000690119 (de:(ecoli\_490) (pn:glyoxylate carboligase) (gn:gcl) (gtcfc:1.9) (ec:4.1.1.47) (gcl\_ecoli) (keggfc:1.9) (rileyfc:1.3.1) (db:gtc-escherichia coli)) ECOLI\_490 ECOLI\_490 Escherichia coli 562 10072571

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822778	7381	29537	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822779	7382	29538	231	76

Description

6500728918 fold:ads:b0529 methylenetetrahydrofolate dehydrogenase:methenyltetrahydrofolate cyclohydrolase (gtcfc:10.7:1.9:9.6) (keggfc:1.9:9.8) (rileyfc:1.7.2) (db:gtc-escherichia coli) (gtcfc:metabolism of macromolecules-protein translation and modification:carbohydrate metabolism-glyoxylate and dicarboxylate metabolism:metabolism of cofactors and vitamin... b0529 b0529 Escherichia coli 562 -11532776 162631 fold:ads methylenetetrahydrofolate dehydrogenase nadp+:methenyltetrahydrofolate cyclohydrolase::fold bifunctional enzyme (cl:methylenetetrahydrofolate dehydrogenase (nad+):methylenetetrahydrofolate dehydrogenase (nad+) homology) (ec:1.5.1.5:3.5.4.9) (db:pir1.dat) (mp:12 min) JS0662 H64784 Escherichia coli 562 -11532776 233738 ads::fold 5:10-methylene-tetrahydrofolate (sr:escherichia coli (strain:k-12) cell\_line:mc4100,w3110 dna) (db:genpept-bct1) (de:e. coli ads(fold) gene encoding 5,10-methylene-tetrahydrofolatedehydrogenase/5,10-methenyl-tetrahydrofolate cyclohydrolase.) (le:150) (re:1016) (di:direct) ECOADS D10588 g216521 Escherichia coli 562 -11532776 7500953199 fold 5:10-methylene-tetrahydrofolate dehydrogenase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:1.5.1.5) (de:escherichia coli k-12 mg1655 section 49 of 400 of the completegenome.) (nt:f288; 99 pct identical to fold\_ecoli sw: p24186) (le:298) (re:1164) (di:complement) AE000159 AE000159 g1786741 Escherichia coli 562 -11532776 7000688846 fold:ads methylenetetrahydrofolate dehydrogenase nadp+:methenyltetrahydrofolate cyclohydrolase::fold bifunctional enzyme (cl:methylenetetrahydrofolate dehydrogenase (nad+):methylenetetrahydrofolate dehydrogenase (nad+) homology) (ec:1.5.1.5:3.5.4.9) (db:pir) (mp:12 min) JS0662 JS0662 Escherichia coli 562 -11532776 5000690120 (de:(ecoli\_512) (pn:5,10-methylene-tetrahydrofolate dehydrogenase; 5,10-methylene-tetrahydrofolate cyclohydrolase) (gn:fold) (gtcfc:1.9:9.6) (ec:1.5.1.5) (fold\_ecoli) (keggfc:1.9:9.8) (rileyfc:1.7.2) (db:gtc-escherichia coli)) ECOLI\_512 ECOLI\_512 Escherichia coli 562 10069587

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822796	7383	29539	888	295

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822803	7384	29540	603	200

#### Description

6500728919 hyaa:b0972 hydrogenase-1 small chain precursor:nife  
hydrogenase:membrane-bound hydrogenase 1 small subunit:hyd1  
(gtcfc:1.9:2.6:2.8:11.1) (ec:1.18.99.1) (keggfc:1.9:2.2) (rileyfc:1.2.6)  
(db:gtc-escherichia coli) b0972 b0972 Escherichia coli 562 -11532777 83112  
hyaa (ec:1.18.99.1) (de:(membrane-bound hydrogenase 1 small subunit) (hyd1))  
(db:swissprot) MBHS\_ECOLI P19928 ESCHERICHIA COLI 562 -11532777 123050 hyaa  
hydrogenase:nife 1 small chain precursor (cl:hydrogenase (nife) small chain)  
(ec:1.18.99.1) (db:pir1.dat) (mp:21 min) HQECSN JV0072 Escherichia coli 562  
-11532777 7500885362 (sr:e.coli (strain le392) dna) (db:genpept-bct1)  
(de:e.coli hya operon encoding hydrogenase isozyme 1 large and smallsubunit  
(hyab and a) genes and hyac-f protein genes, complete cds.)  
(nt:hydrogenase-1 small subunit (hyaa) precursor) (le:188) (re:1306...  
ECOHYA M34825 g146420 Escherichia coli 562 -11532777 234820 hyaa  
hydrogenase-1 small subunit (fn:enzyme; energy metabolism, carbon: aerobic)  
(db:genpept-bct2) (ec:1.18.99.1) (de:escherichia coli k-12 mg1655 section 89  
of 400 of the completengenome.) (nt:o372; 100 pct identical to mbhs\_ecoli sw:  
p19928) (le:2196) (re:3314) (di:direct) AE000199 AE000199 g1787206  
Escherichia coli 562 -11532777 5000690121 (de:(ecoli\_937) (pn:hydrogenase-1  
small subunit) (gn:hyaa) (gtcfc:1.9:2.2) (ec:1.18.99.1) (mbhs\_ecoli)  
(keggfc:1.9:2.2) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI\_937  
ECOLI\_937 Escherichia coli 562 10025331

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822804	7385	29541	216	71

#### Description

6500728920 hyab:b0973 hydrogenase-1 large chain:nife  
hydrogenase:membrane-bound hydrogenase 1 large subunit:hyd1  
(gtcfc:1.9:2.6:2.8:11.1) (ec:1.18.99.1) (keggfc:1.9:2.2) (rileyfc:1.2.6)  
(db:gtc-escherichia coli) b0973 b0973 Escherichia coli 562 -11532778 83101  
hyab (ec:1.18.99.1) (de:bound hydrogenase 1 large subunit) (hyd1))  
(db:swissprot) MBHL\_ECOLI P19927 ESCHERICHIA COLI 562 -11532778 7000685793  
hyab hydrogenase:nife 1 large chain (cl:hydrogenase (nife) large chain)  
(ec:1.18.99.1) (db:pir1.dat) (mp:21 min) HQECL C64838 Escherichia coli 562  
-11532778 7500885360 hyab hydrogenase-1 large subunit (fn:enzyme; energy  
metabolism, carbon: aerobic) (db:genpept-bct2) (ec:1.18.99.1)  
(de:escherichia coli k-12 mg1655 section 89 of 400 of the completengenome.)  
(nt:o597; 99 pct identical to mbhl\_ecoli sw: p19927) (le:3311) (re:5104)  
(di:direct) AE000199 AE000199 g1787207 Escherichia coli 562 -11532778  
5000690122 (de:(ecoli\_938) (pn:hydrogenase-1 large subunit) (gn:hyab)  
(gtcfc:1.9:2.2) (ec:1.18.99.1) (mbhl\_ecoli) (keggfc:1.9:2.2) (rileyfc:1.2.6)  
(db:gtc-escherichia coli)) ECOLI\_938 ECOLI\_938 Escherichia coli 562 10123103



ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501822809	7386	29542	495	165

# Description

6500728921 puru:tgs:b1232 formyltetrahydrofolate deformylase:formyl-fh4 hydrolase (gtcfc:10.7:1.9:9.6) (ec:3.5.1.10) (keggfc:1.9:9.8) (rileyfc:1.6.1) (db:gtc-escherichia coli) (gtcfc:metabolism of macromolecules-protein translation and modification:carbohydrate metabolism-glyoxylate and dicarboxylate metabolism:metabolism of cofacto... b1232 b1232 Escherichia coli 562 -11532779 92482 puru:tgs (ec:3.5.1.10) (de:hydrolase)) (db:swissprot) PURU\_ECOLI P37051 ESCHERICHIA COLI 562 -11532779 137834 puru:tgs formyltetrahydrofolate deformylase::formyltetrahydrofolate hydrolase (cl:phosphoribosylglycinamide formyltransferase:phosphoribosylglycinamide formyltransferase homology) (ec:3.5.1.10) (db:pir2.dat) (mp:27 min) C36871 C36871 Escherichia coli 562 -11532779 223435 puru formyltetrahydrofolate deformylase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #249) (db:genpept-bct1) (de:escherichia coli genomic dna (27.5-27.8 min).) (le:9121) (re:9963) (di:complement) D90758 D90758 g1651625 Escherichia coli 562 -11532779 223443 puru formyltetrahydrofolate deformylase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #250) (db:genpept-bct1) (de:escherichia coli genomic dna (27.6-28.0 min).) (le:4778) (re:5620) (di:complement) D90759 D90759 g1651634 Escherichia coli 562 -11532779 224710 puru formyltetrahydrofolate deformylase ec 3.5.1.10 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #251(27.7-28.2 min).) (nt:orf\_id:o249#8; similar to (swissprot accession) (le:4778) (re:5620) (di:complement) D90852 D90852 g1805509 Escherichia coli 562 -11532779 235615 puru formyltetrahydrofolate deformylase:for (fn:enzyme; purine ribonucleotide biosynthesis) (db:genpept-bct2) (ec:3.5.1.10) (de:escherichia coli k-12 mg1655 section 111 of 400 of the completegenome.) (nt:f280; 100 pct identical to puru\_ecoli sw: p37051) (le:8206) (re:9048) (di:complement) AE000221 AE000221 g1787483 Escherichia coli 562 -11532779 301350 puru formyltetrahydrofolate hydrolase (sr:escherichia coli (strain k-12) dna) (db:genpept-bct2) (de:e. coli formyltetrahydrofolate hydrolase (puru) gene, 5'end.) (le:797) (re:1639) (di:direct) ECOPURU L20251 g410155 Escherichia coli 562 -11532779 5000690123 puru formyltetrahydrofolate deformylase ec 3.5.1.10 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #249) (db:genpept) (de:escherichia coli genomic dna. (27.6 - 27.9 min).) (nt:orf\_id:o250#6; similar to swissprot accession) (le:9121) (re:9963) (di:complement) D90758 D90758 g1651625 Escherichia coli 562 -11532779 7502851817 puru formyltetrahydrofolate deformylase ec 3.5.1.10 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #250) (db:genpept) (de:escherichia coli genomic dna. (27.7 - 28.1 min).) (nt:orf\_id:o250#6; similar to swissprot accession) (le:4778) (re:5620) (di:complement) D90759 D90759 g1651634 Escherichia coli 562 -11532779

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822812	7387	29543	1608	535

Description

6500728922 fdng:b1474 alpha subunit of formate dehydrogenase n:formate dehydrogenase:nitrate-inducible:major subunit:formate dehydrogenase-n alpha subunit:fdh-n alpha subunit:anaerobic formate dehydrogenase major subunit (gtcfc:1.9:2.2:2.8:12.13) (ec:1.2.1.2) (keggfc:1.9:2.2:12.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b1474 b1474 Escherichia coli 562 -11532780 223799 fdng formate dehydrogenase:nitrate-inducible:major (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #277(33.2-33.6 min.).) (nt:orf\_id:o277#3; tga codon for selenocysteine;) (le:5205) (re:8252) (di:direct) D90788 D90788 g1742407 Escherichia coli 562 -11532780 223808 fdng formate dehydrogenase:nitrate-inducible:major (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #278(33.3-33.7 min.).) (nt:orf\_id:o277#3; tga codon for selenocysteine;) (le:1581) (re:4628) (di:direct) D90789 D90789 g1742417 Escherichia coli 562 -11532780 300551 fdng formate dehydrogenase-n:nitrate-inducible (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (ec:1.2.1.2) (de:escherichia coli k-12 mg1655 section 134 of 400 of the completegenome.) (nt:selenocysteine) (le:4800) (re:7847) (di:direct) AE000244 AE000244 g3868719 Escherichia coli 562 -11532780 5000690124 fdng formate dehydrogenase-n:nitrate-inducible (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept) (ec:1.2.1.2) (de:escherichia coli k-12 mg1655 section 134 of 400 of the completegenome.) (nt:o1015; cg site no. 32160; selenocysteine,) (le:4800) (re:7847) (di:direct) AE000244 AE000244 g3868719 Escherichia coli 562 -11532780

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822814	7388	29544	312	103

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822826	7389	29545	705	234

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822827	7390	29546	249	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822835	7391	29547	735	244

Description

6500728923 fdnh:b1475 beta subunit of formate dehydrogenase n:formate dehydrogenase:nitrate-inducible:iron-sulfur subunit:formate dehydrogenase-n beta subunit:fdh-n beta subunit:anaerobic formate dehydrogenase iron-sulfur subunit (gtcfc:1.9:2.2:2.8:12.13) (ec:1.2.1.2) (keggfc:1.9:2.2:12.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b1475 b1475 Escherichia coli 562 -11532781 71264 fdnh (de:dehydrogenase iron-sulfur subunit)) (db:swissprot) FDNH\_ECOLI P24184 ESCHERICHIA COLI 562 -11532781 7000685221 fdnh formate dehydrogenase:n nitrate-inducible beta chain:formate dehydrogenase n iron-sulfur protein (cl:ferredoxin 2(4fe-4s) homology) (ec:1.2.1.2) (db:pir2.dat) JS0629 F64900 Escherichia coli 562 -11532781 223800 fdnh formate dehydrogenase ec 1.2.1.2 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #277(33.2-33.6 min.)) (nt:orf\_id:o277#5; similar to (pir accession number) (le:8265) (re:9149) (di:direct) D90788 D90788 g1742408 Escherichia coli 562 -11532781 223809 fdnh formate dehydrogenase ec 1.2.1.2 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #278(33.3-33.7 min.)) (nt:orf\_id:o277#5; similar to (pir accession number) (le:4641) (re:5525) (di:direct) D90789 D90789 g1742418 Escherichia coli 562 -11532781 300552 fdnh formate dehydrogenase-n:nitrate-inducible (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 134 of 400 of the completegenome.) (nt:o294; 99 pct identical to fdnh\_ecoli sw: p24184; cg) (le:7860) (re:8744) (di:direct) AE000244 AE000244 g1787749 Escherichia coli 562 -11532781 5000690125 fdnh formate dehydrogenase-n:nitrate-inducible (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept) (de:escherichia coli k-12 mg1655 section 134 of 400 of the completegenome.) (nt:o294; 99 pct identical to fdnh\_ecoli sw: p24184; cg) (le:7860) (re:8744) (di:direct) AE000244 AE000244 g1787749 Escherichia coli 562 -11532781

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822855	7392	29548	207	68

# Description

6500728924 fdni:b1476 gamma subunit of formate dehydrogenase n:formate dehydrogenase:nitrate-inducible:cytochrome b556:fdn subunit:formate dehydrogenase-n gamma subunit:fdh-n gamma subunit:anaerobic formate dehydrogenase cytochrome b556 subunit (gtcfc:1.9:2.2:2.8:12.13) (ec:1.2.1.2) (keggfc:1.9:2.2:12.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b1476 b1476 Escherichia coli 562 -11532782 71265 fdni (de:(anaerobic formate dehydrogenase cytochrome b556 subunit)) (db:swissprot) FDNI\_ECOLI P24185 ESCHERICHIA COLI 562 -11532782 7000685222 fdni formate dehydrogenase:n nitrate-inducible gamma chain:cytochrome b556 (cl:formate dehydrogenase gamma chain) (ec:1.2.1.2) (db:pir2.dat) JS0630 G64900 Escherichia coli 562 -11532782 223801 fdni formate dehydrogenase:nitrate-inducible (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #277(33.2-33.6 min.)) (nt:orf\_id:o277#6; similar to (swissprot accession) (le:9142) (re:9795) (di:direct) D90788 D90788 g1742409 Escherichia coli 562 -11532782 223810 fdni formate dehydrogenase:nitrate-inducible (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #278(33.3-33.7 min.)) (nt:orf\_id:o277#6; similar to (swissprot accession) (le:5518) (re:6171) (di:direct) D90789 D90789 g1742419 Escherichia coli 562 -11532782 300553 fdni formate dehydrogenase-n:nitrate-inducible (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 134 of 400 of the completegenome.) (nt:o217; cg site no. 32168; more closely resembles) (le:8737) (re:9390) (di:direct) AE000244 AE000244 g1787750 Escherichia coli 562 -11532782 5000690126 fdni formate dehydrogenase-n:nitrate-inducible (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept) (de:escherichia coli k-12 mg1655 section 134 of 400 of the completegenome.) (nt:o217; cg site no. 32168; more closely resembles) (le:8737) (re:9390) (di:direct) AE000244 AE000244 g1787750 Escherichia coli 562 -11532782

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822856	7393	29549	1173	391

Description

6500728925 hych:hev:h:b2718 formate hydrogenlyase maturation protein:formate hydrogenlyase maturation protein hych (gtcfc:1.9:2.2) (ec:1.18.99.1) (keggfc:1.9:2.2) (rileyfc:1.2.7) (db:gtc-escherichia coli) b2718 b2718 Escherichia coli 562 -11532783 239292 hych:hev:h (de:formate hydrogenlyase maturation protein hych) (db:swissprot) HYCH\_ECOLI P16434 ESCHERICHIA COLI 562 -11532783 164385 hych formate hydrogenlyase maturation protein (cl:formate hydrogenlyase maturation protein) (db:pir2.dat) (mp:58-59 min) S08626 S08626 Escherichia coli 562 -11532783 5000690127 hych (db:genpept-bct1) (de:e.coli hyc operon hyca,b,c,d,e,f,g,h,i genes.) (le:7201) (re:7611) (di:direct) ECHYC X17506 g41687 Escherichia coli 562 -11532783 7500883698 hych formate hydrogenlyase maturation protein (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg site no. 33140; alternate gene name hev:h) (le:15340) (re:15750) (di:complement) ECU29579 U29579 g882611 Escherichia coli 562 -11532783 233178 hych processing of large subunit hyce of (fn:factor; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 246 of 400 of the completegenome.) (nt:f136; 100 pct identical to hych\_ecoli sw: p16434;) (le:573) (re:983) (di:complement) AE000356 AE000356 g1789073 Escherichia coli 562 -11532783 78427 hych:hev:h (de:formate hydrogenlyase maturation protein hych) (db:swissprot) HYCH\_ECOLI P16434 ESCHERICHIA COLI 562 -11532783

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822862	7394	29550	1017	338

Description

6500728926 hycf:hevf:b2720 formate hydrogenlyase subunit 6:fhl subunit 6:hydrogenase-3 component f (gtcfc:1.9:2.2) (ec:1.18.99.1) (keggfc:1.9:2.2) (rileyfc:1.2.7) (db:gtc-escherichia coli) b2720 b2720 Escherichia coli 562 -11532784 239294 hycf:hevf (de:component f)) (db:swissprot) HYCF\_ECOLI P16432 ESCHERICHIA COLI 562 -11532784 164383 hycf formate hydrogenlyase protein 6 (cl:formate hydrogenlyase protein 6:ferredoxin 2(4fe-4s) homology) (db:pir2.dat) (mp:58-59 min) S08624 S08624 Escherichia coli 562 -11532784 5000690128 hycf (db:genpept-bct1) (de:e.coli hyc operon hyca,b,c,d,e,f,g,h,i genes.) (le:5895) (re:6437) (di:direct) ECHYC X17506 g41685 Escherichia coli 562 -11532784 7500883696 hycf formate hydrogenlyase subunit 6 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg site no. 33154; alternate gene name hevf;) (le:16514) (re:17056) (di:complement) ECU29579 U29579 g882613 Escherichia coli 562 -11532784 233176 hycf probable iron-sulfur protein of hydrogenase 3 (fn:putative enzyme; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 246 of 400 of the completegenome.) (nt:f180; 100 pct identical to hycf\_ecoli sw: p16432;) (le:1747) (re:2289) (di:complement) AE000356 AE000356 g1789075 Escherichia coli 562 -11532784 78425 hycf:hevf (de:component f)) (db:swissprot) HYCF\_ECOLI P16432 ESCHERICHIA COLI 562 -11532784

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822873	7395	29551	252	83

Description

GTC ORF with score 125 to: (db:genpept) (de:caenorhabditis elegans cosmid y43f8c, complete sequence.) (nt:similar to abc transporter transmembrane region. ;) (le:74907:79112:80365:81935) (re:75041:79396:80754:82022) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822876	7396	29552	429	142

# Description

6500728927 hyce:heve:b2721 formate hydrogenlyase subunit 5:formate hydrogenlyase subunit 5 precursor:fhl subunit 5:hydrogenase-3 component e (gtcfc:1.9:2.2) (ec:1.18.99.1) (keggfc:1.9:2.2) (rileyfc:1.2.7) (db:gtc-escherichia coli) b2721 b2721 Escherichia coli 562 -11532785 239295 hyce:heve (de:(hydrogenase-3 component e)) (db:swissprot) HYCE\_ECOLI P16431 ESCHERICHIA COLI 562 -11532785 164382 hyce hydrogenase:3 chain 5 precursor:formate hydrogenlyase subunit 5 (ec:1.18.99.1) (db:pir2.dat) (mp:58-59 min) S08623 S08623 Escherichia coli 562 -11532785 5000690129 hyce (db:genpept-bct1) (de:e.coli hyc operon hyca,b,c,d,e,f,g,h,i genes.) (le:4176) (re:5885) (di:direct) ECHYC X17506 g41684 Escherichia coli 562 -11532785 7500883695 hyce formate hydrogenlyase subunit 5 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg site no. 33159; alternate gene name heve;) (le:17066) (re:18775) (di:complement) ECU29579 U29579 g882614 Escherichia coli 562 -11532785 233175 hyce large subunit of hydrogenase 3 part of fhl (fn:enzyme; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 246 of 400 of the completegenome.) (nt:f569; 100 pct identical amino acid sequence and) (le:2299) (re:4008) (di:complement) AE000356 AE000356 g1789076 Escherichia coli 562 -11532785 78424 hyce:heve (de:(hydrogenase-3 component e)) (db:swissprot) HYCE\_ECOLI P16431 ESCHERICHIA COLI 562 -11532785

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822881	7397	29553	537	178

Description

6500728928 hycd:hevd:b2722 formate hydrogenlyase subunit 4:fhl subunit 4:hydrogenase 3 component d (gtcfc:1.9:2.2) (ec:1.18.99.1) (keggfc:1.9:2.2) (rileyfc:1.2.7) (db:gtc-escherichia coli) b2722 b2722 Escherichia coli 562 -11532786 239296 hycd:hevd (de:component d) (db:swissprot) HYCD\_ECOLI P16430 ESCHERICHIA COLI 562 -11532786 164381 hycd probable hydrogenase 3 protein 4 (db:pir2.dat) (mp:58-59 min) S08622 S08622 Escherichia coli 562 -11532786 5000690130 hycd (db:genpept-bct1) (de:e.coli hyc operon hyca,b,c,d,e,f,g,h,i genes.) (le:3235) (re:4158) (di:direct) ECHYC X17506 g41683 Escherichia coli 562 -11532786 7500883694 hycd formate hydrogenlyase subunit 4 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg site no. 33162; alternate gene name hevd;) (le:18793) (re:19716) (di:complement) ECU29579 U29579 g882615 Escherichia coli 562 -11532786 233174 hycd membrane-spanning protein of hydrogenase 3 part (fn:enzyme; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 246 of 400 of the completegenome.) (nt:f307; 100 pct identical to hycd\_ecoli sw: p16430;) (le:4026) (re:4949) (di:complement) AE000356 AE000356 g1789077 Escherichia coli 562 -11532786 78423 hycd:hevd (de:component d) (db:swissprot) HYCD\_ECOLI P16430 ESCHERICHIA COLI 562 -11532786

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822890	7398	29554	207	69

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822892	7399	29555	1110	369

Description

6500728929 hycb:hevb:b2724 formate hydrogenlyase subunit 2:fhl subunit 2:hydrogenase-3 component b (gtcfc:1.9:2.2) (ec:1.18.99.1) (keggfc:1.9:2.2) (rileyfc:1.2.7) (db:gtc-escherichia coli) b2724 b2724 Escherichia coli 562 -11532787 78421 hycb:hevb (de:component b)) (db:swissprot) HYCB\_ECOLI P16428 ESCHERICHIA COLI 562 -11532787 7000685579 hycb formate hydrogenlyase chain 2:probable hydrogenase 3 protein 2 (cl:nrfc protein:ferredoxin 2(4fe-4s) homology) (db:pir2.dat) (mp:58 min) H65052 H65052 Escherichia coli 562 -11532787 7500883692 hycb formate hydrogenlyase subunit 2 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:gtg start; cg site no. 33169; alternate gene name) (le:21542) (re:22153) (di:complement) ECU29579 U29579 g882617 Escherichia coli 562 -11532787 239298 hycb probable small subunit of hydrogenase-3 (fn:putative enzyme; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 246 of 400 of the completegenome.) (nt:f203; 99 pct identical to hycb\_ecoli sw: p16428;) (le:6775) (re:7386) (di:complement) AE000356 AE000356 g1789079 Escherichia coli 562 -11532787 5000690131 (de:(ecoli\_2653) (pn:probable small subunit of hydrogenase-3, iron-sulfur protein:part of formate hydrogenlyase:fhl complex) (gn:hycb) (gtcfc:1.9:2.2) (ec:1.18.99.1) (hycb\_ecoli) (keggfc:1.9:2.2) (rileyfc:1.2.7) (db:gtc-escheric) ECOLI\_2653 ECOLI\_2653 Escherichia coli 562 10123794

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822893	7400	29556	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822897	7401	29557	1476	491
<u>Description</u>				
6500728930 hybc:b2994 hydrogenase-2 large subunit:hydrogenase-2 large chain:nife hydrogenase:membrane-bound hydrogenase 2 large subunit:hyd2 (gtcfc:1.9:2.6:2.8:11.1) (ec:1.18.99.1) (keggfc:1.9:2.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2994 b2994 Escherichia coli 562 -11532788 137393 hybc hydrogenase:2 large chain:hybc protein (cl:hydrogenase (nife) large chain) (ec:1.18.99.1) (db:pir2.dat) C55516 C55516 Escherichia coli 562 -11532788 239207 hybc hydrogenase-2 large subunit (db:genpept-bct1) (de:escherichia coli tg1 hyb operon, hydrogenase-2 large subunit (hybc)gene and hyba, hybb, hybd, hybe, hybf, and hybg genes, completecds.) (le:2280) (re:3983) (di:direct) ECU09177 U09177 g544485 Escherichia coli 562 -11532788 7500885361 hybc hydrogenase-2 large subunit (db:genpept-bct1) (ec:1.18.99.1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f567; cg site no. 33418) (le:95677) (re:97380) (di:complement) ECU28377 U28377 g882523 Escherichia coli 562 -11532788 238548 hybc probable large subunit:hydrogenase-2 (fn:putative enzyme; energy metabolism, carbon:) (db:genpept-bct2) (ec:1.18.99.1) (de:escherichia coli k-12 mg1655 section 272 of 400 of the completegenome.) (nt:f567; 100 pct identical to mbhm_ecoli sw: p37181;) (le:2716) (re:4419) (di:complement) AE000382 AE000382 g1789368 Escherichia coli 562 -11532788 83106 hybc (ec:1.18.99.1) (de:bound hydrogenase 2 large subunit) (hyd2)) (db:swissprot) MBHM_ECOLI P37181 ESCHERICHIA COLI 562 -11532788 5000690132 (de:(ecoli_2916) (pn:probable large subunit, hydrogenase-2) (gn:hybc) (gtcfc:1.9:2.2) (ec:1.18.99.1) (mbhm_ecoli) (keggfc:1.9:2.2) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI_2916 ECOLI_2916 Escherichia coli 562 10025325				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822899	7402	29558	765	254

# Description

6500728931 hyba:b2996 hydrogenase-2 small subunit:hydrogenase-2 small chain precursor:nife hydrogenase:membrane-bound hydrogenase 2 small subunit:hyd2 (gtcfc:1.9:2.6:2.8:11.1) (ec:1.18.99.1) (keggfc:1.9:2.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2996 b2996 Escherichia coli 562 -11532789 83117 hyba (de:hydrogenase-2 operon protein hyba precursor) (db:swissprot) HYBA\_ECOLI P37179 ESCHERICHIA COLI 562 -11532789 7000685794 hyba hydrogenase:2 small chain (cl:ferredoxin 2(4fe-4s) homology) (ec:1.18.99.1) (db:pir2.dat) B65086 B65086 Escherichia coli 562 -11532789 239209 hyba (db:genpept-bct1) (de:escherichia coli tg1 hyb operon, hydrogenase-2 large subunit (hybc)gene and hyba, hybb, hybd, hybe, hybf, and hybg genes, completecds.) (nt:putative hydrogenase-2 small subunit) (le:129) (re:1115) (di:direct) ECU09177 U09177 g544483 Escherichia coli 562 -11532789 7500885363 hyba hydrogenase-2 small subunit (db:genpept-bct1) (ec:1.18.99.1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:cg site no. 33407) (le:98542) (re:99528) (di:complement) ECU28377 U28377 g882525 Escherichia coli 562 -11532789 238546 hyba hydrogenase-2 small subunit (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (ec:1.18.99.1) (de:escherichia coli k-12 mg1655 section 272 of 400 of the completegenome.) (nt:f328; 100 pct identical to mbht\_ecoli sw: p37179;) (le:5584) (re:6570) (di:complement) AE000382 AE000382 g1789370 Escherichia coli 562 -11532789 5000690133 (de:(ecoli\_2918) (pn:hydrogenase-2 small subunit) (gn:hyba) (gtcfc:1.9:2.2) (ec:1.18.99.1) (mbht\_ecoli) (keggfc:1.9:2.2) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI\_2918 ECOLI\_2918 Escherichia coli 562 10025336

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822900	7403	29559	384	127

Description

6500728932 ttta:b3061 tartrate dehydratase:l-tartrate dehydratase alpha subunit:l-ttd alpha (gtcfc:1.9:2.2) (ec:4.2.1.32) (keggfc:1.9) (rileyfc:1.2.7) (db:gtc-escherichia coli) b3061 b3061 Escherichia coli 562 -11532790 7000688897 ttta l + -tartrate dehydratase::iron-dependent:alpha chain (cl:iron-dependent tartrate dehydratase alpha chain:iron-dependent tartrate dehydratase alpha chain homology) (ec:4.2.1.32) (db:pir1.dat) (mp:67 min) QQECRT C65094 Escherichia coli 562 -11532790 7500953346 ttta tartrate dehydratase (db:genpept-bct1) (ec:4.2.1.32) (de:escherichia coli k-12 genome; approximately 68 minutes.) (le:11258) (re:12169) (di:direct) ECU28379 U28379 g882584 Escherichia coli 562 -11532790 239266 ttta l-tartrate dehydratase:subunit a (fn:enzyme; energy metabolism, carbon:) (db:genpept-bct2) (ec:4.2.1.32) (de:escherichia coli k-12 mg1655 section 278 of 400 of the completegenome.) (nt:o303; 99 pct identical amino acid sequence and) (le:134) (re:1045) (di:direct) AE000388 AE000388 g1789442 Escherichia coli 562 -11532790 5000690134 (de:(ecoli\_2984) (pn:l-tartrate dehydratase) (gn:ttta) (gtcfc:1.9) (ec:4.2.1.32) (ttta\_ecoli) (keggfc:1.9) (rileyfc:1.2.7) (db:gtc-escherichia coli)) ECOLI\_2984 ECOLI\_2984 Escherichia coli 562 10123964

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822903	7404	29560	1221	407

Description

6500728933 tttdb:b3062 tartrate dehydratase:l-tartrate dehydratase beta subunit:l-ttd beta (gtcfc:1.9:2.2) (ec:4.2.1.32) (keggfc:1.9) (rileyfc:1.2.7) (db:gtc-escherichia coli) b3062 b3062 Escherichia coli 562 -11532791 7000688898 tttdb l + -tartrate dehydratase::iron-dependent:beta chain (cl:iron-dependent tartrate dehydratase beta chain:iron-dependent tartrate dehydratase beta chain homology) (ec:4.2.1.32) (db:pir1.dat) (mp:67 min) QQECRZ D65094 Escherichia coli 562 -11532791 7500953347 tttdb tartrate dehydratase (db:genpept-bct1) (ec:4.2.1.32) (de:escherichia coli k-12 genome; approximately 68 minutes.) (le:12166) (re:12771) (di:direct) ECU28379 U28379 g882585 Escherichia coli 562 -11532791 239267 tttdb l-tartrate dehydratase:subunit b (fn:enzyme; energy metabolism, carbon:) (db:genpept-bct2) (ec:4.2.1.32) (de:escherichia coli k-12 mg1655 section 278 of 400 of the completegenome.) (nt:o201; 96 pct identical amino acid sequence and) (le:1042) (re:1647) (di:direct) AE000388 AE000388 g1789443 Escherichia coli 562 -11532791 5000690135 (de:(ecoli\_2985) (pn:l-tartrate dehydratase) (gn:tttdb) (gtcfc:1.9) (ec:4.2.1.32) (tttdb\_ecoli) (keggfc:1.9) (rileyfc:1.2.7) (db:gtc-escherichia coli)) ECOLI\_2985 ECOLI\_2985 Escherichia coli 562 10123965

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501822905	7405	29561	372	123

Description

6500728934 def:fms:b3287 n-formylmethionylaminoacyl-trna  
ormylase:n-formylmethionylaminoacyl-trna deformylase / polypeptide  
deformylase:pdf:formylmethionine deformylase (gtcfc:10.6:5.4)  
(keggfc:1.9:5.4:10.1) (rileyfc:3.1.8) (db:gtc-escherichia coli) b3287 b3287  
Escherichia coli 562 -11532792 164863 def:fms  
n-formylmethionylaminoacyl-trna deformylase (cl:polypeptide deformylase)  
(ec:3.5.1.27) (db:pir2.dat) S23107 S23107 Escherichia coli 562 -11532792  
232894 def deformylase (db:genpept-bct1) (de:escherichia coli def, fmt and  
orf374 gene.) (le:1315) (re:1824) (di:direct) ECDEFF X77800 g471304  
Escherichia coli 562 -11532792 232901 fms (db:genpept-bct1) (de:e.coli fmt  
gene for l-methionyl-trnametf n-formyltransferase.) (le:54) (re:563)  
(di:direct) ECFMT X63666 g41474 Escherichia coli 562 -11532792 236520 fms  
n-formylmethionylaminoacyl-trna deformylase (db:genpept-bct1) (ec:3.5.1.27)  
(de:e.coli fms, fmt, fmu, fmv, smf, smg and trka genes.) (nt:peptide  
deformylase) (le:1426) (re:1935) (di:direct) ECFMUJ X77091 g443989  
Escherichia coli 562 -11532792 304567 fms n-formylmethionylaminoacyl-trna  
deformylase (db:genpept-bct1) (ec:3.5.1.27) (de:escherichia coli k-12  
chromosomal region from 67.4 to 76.0 minutes.) (le:214437) (re:214946)  
(di:direct) ECOUW67 U18997 g606221 Escherichia coli 562 -11532792 232657  
def peptide deformylase (fn:enzyme; proteins - translation and)  
(db:genpept-bct2) (ec:3.5.1.31) (de:escherichia coli k-12 mg1655 section 297  
of 400 of the completegenome.) (nt:o169; 100 pct identical amino acid  
sequence and) (le:1760) (re:2269) (di:direct) AE000407 AE000407 g1789682  
Escherichia coli 562 -11532792 5000690136 (de:(ecoli\_3205) (pn:peptide  
ormylase) (gn:def) (gtcfc:1.9:5.4:10.7) (ec:3.5.1.31) (def\_ecoli)  
(keggfc:1.9:5.4:10.1) (rileyfc:3.1.8) (db:gtc-escherichia coli)) ECOLI\_3205  
ECOLI\_3205 Escherichia coli 562 10087493

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822915	7406	29562	1002	333

Description

6500728935 gph:b3385 hypothetical 27.4 kd protein in trps-dod integenic region:phosphoglycolate phosphatase (gtcfc:1.9) (ec:3.1.3.18) (keggfc:1.9) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3385 b3385 Escherichia coli 562 -11532793 236618 gph (ec:3.1.3.18) (de:phosphoglycolate phosphatase, (pgp)) (db:swissprot) GPH\_ECOLI P32662 ESCHERICHIA COLI 562 -11532793 163481 gph hypothetical 27.4k protein trps-dod integenic region (db:pir2.dat) S55288 S55288 Escherichia coli 562 -11532793 5000690137 (db:genpept-bct1) (de:e.coli dam operon.) (nt:orf for 27kd protein.) (le:6542) (re:7300) (di:direct) ECDAMOPRA Z19601 g41223 Escherichia coli 562 -11532793 7500882662 yhfe (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:27 kd protein in ecdamopra) (le:294379) (re:295137) (di:complement) ECOUW67 U18997 g606319 Escherichia coli 562 -11532793 232639 gph phosphoglycolate phosphatase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 304 of 400 of the completegenome.) (nt:f252; 27 kd protein in ecdamopra; 100 pct) (le:2643) (re:3401) (di:complement) AE000414 AE000414 g1789787 Escherichia coli 562 -11532793 74359 gph (ec:3.1.3.18) (de:phosphoglycolate phosphatase,) (db:swissprot) GPH\_ECOLI P32662 ESCHERICHIA COLI 562 -11532793

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822924	7407	29563	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822929	7408	29564	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822932	7409	29565	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822936	7410	29566	438	145
<u>Description</u>				

GTC ORF with score 280 to: (sr:baker's yeast strain=s288c (ab972))  
(db:genpept-pln1) (de:saccharomyces cerevisiae chromosome xii cosmid 9470.)  
(nt:ylr168c; possibly involved in intramitochondrial) (le:1742) (re:2434)  
(di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822953	7411	29567	348	115
<u>Description</u>				

6500728936 fdoid:b3892 formate dehydrogenase:cytochrome b556:fdo  
subunit:formate dehydrogenase-o gamma subunit:fdh-z gamma subunit:aerobic  
formate dehydrogenase cytochrome b556 subunit (gtcfc:1.9:2.2:2.8)  
(ec:1.2.1.2) (keggfc:1.9:2.2) (rileyfc:1.2.6) (db:gtc-escherichia coli)  
b3892 b3892 Escherichia coli 562 -11532794 71268 fdoid (de:dehydrogenase  
cytochrome b556 subunit)) (db:swissprot) FDOI\_ECOLI P32174 ESCHERICHIA COLI  
562 -11532794 163083 fdoid formate dehydrogenase:o aerobic gamma  
chain:cytochrome b556 (cl:formate dehydrogenase gamma chain) (ec:1.2.1.2)  
(db:pir2.dat) S40836 S40836 Escherichia coli 562 -11532794 7500881383 fdoid  
formate dehydrogenase-o gamma subunit (sr:escherichia coli (sub\_strain  
mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli  
chromosomal region from 87.2 to 89.2 minutes.) (nt:similar to e. coli fdh-n  
gamma subunit) (le:42864) (re:43499) (di:complement) ECOUW87 L19201 g304996  
Escherichia coli 562 -11532794 237110 fdoid formate dehydrogenase:cytochrome  
b556 fdo (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.)  
(nt:f211; 100 pct identical to fdoid\_ecoli sw:) (le:10784) (re:11419)  
(di:complement) AE000464 AE000464 g1790325 Escherichia coli 562 -11532794  
5000690138 fdoid formate dehydrogenase:cytochrome b556 fdo (fn:enzyme;  
energy metabolism, carbon: anaerobic) (db:genpept) (de:escherichia coli k-12  
mg1655 section 354 of 400 of the completegenome.) (nt:f211; 100 pct  
identical to fdoid\_ecoli sw:) (le:10784) (re:11419) (di:complement) AE000464  
AE000464 g1790325 Escherichia coli 562 -11532794

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822962	7412	29568	2532	844
<u>Description</u>				
6500728937 fdoh:b3893 formate dehydrogenase-o:iron-sulfur subunit:formate dehydrogenase-o beta subunit:fdh-z beta subunit:aerobic formate dehydrogenase iron-sulfur subunit (gtcfc:1.9:2.2:2.8) (ec:1.2.1.2) (keggfc:1.9:2.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b3893 b3893 Escherichia coli 562 -11532795 71267 fdoh (de:iron-sulfur subunit)) (db:swissprot) FDOH_ECOLI P32175 ESCHERICHIA COLI 562 -11532795 163082 fdoh formate dehydrogenase:o aerobic beta chain:formate dehydrogenase o iron-sulfur protein (cl:ferredoxin 2(4fe-4s) homology) (ec:1.2.1.2) (db:pir2.dat) S40837 S40837 Escherichia coli 562 -11532795 7500881382 fdoh formate dehydrogenase-o beta subunit (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:matches ps00198: 4fe4s_ferredoxin; similar to e.) (le:43496) (re:44398) (di:complement) ECOUW87 L19201 g304997 Escherichia coli 562 -11532795 237111 fdoh formate dehydrogenase-o:iron-sulfur subunit (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:f300; 100 pct identical to fdoh_ecoli sw:) (le:11416) (re:12318) (di:complement) AE000464 AE000464 g1790326 Escherichia coli 562 -11532795 5000690139 fdoh formate dehydrogenase-o:iron-sulfur subunit (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:f300; 100 pct identical to fdoh_ecoli sw:) (le:11416) (re:12318) (di:complement) AE000464 AE000464 g1790326 Escherichia coli 562 -11532795				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822970	7413	29569	750	250
<u>Description</u>				
6500728938 fdog:b3894 formate dehydrogenase-o:alpha subunit:formate dehydrogenase-o alpha subunit:fdh-z alpha subunit:aerobic formate dehydrogenase major subunit (gtcfc:1.9:2.2:2.8) (ec:1.2.1.2) (keggfc:1.9:2.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b3894 b3894 Escherichia coli 562 -11532796 7500974869 fdog formate dehydrogenase-o:alpha subunit (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (ec:1.2.1.2) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:selenocysteine) (le:12331) (re:15381) (di:complement) AE000464 AE000464 g3868720 Escherichia coli 562 -11532796 7502851818 fdog formate dehydrogenase-o:alpha subunit (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept) (ec:1.2.1.2) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:f1016; 98 pct identical to fdog_ecoli sw:) (le:12331) (re:15381) (di:complement) AE000464 AE000464 g3868720 Escherichia coli 562 -11532796				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822976	7414	29570	213	70
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822979	7415	29571	546	181
<u>Description</u>				

6500728939 acea:icl:b4015 isocitrate lyase:isocitrase:isocitratase:icl  
(gtcfc:1.9:2.3) (ec:4.1.3.1) (keggfc:1.9) (rileyfc:1.3.1)  
(db:gtc-escherichia coli) b4015 b4015 Escherichia coli 562 -11532797 228036  
acea:icl (ec:4.1.3.1) (de:isocitrate lyase, (isocitrase) (isocitratase)  
(icl)) (db:swissprot) ACEA\_ECOLI P05313 ESCHERICHIA COLI 562 -11532797  
125523 acea isocitrate lyase::isocitrase:isocitratase:isocitritase  
(cl:isocitrate lyase) (ec:4.1.3.1) (db:pirl.dat) (mp:91 min) WZECIC S05692  
Escherichia coli 562 -11532797 5000690141 (db:genpept-bct1) (de:e. coli  
genes aceb and acea for for malate synthase (ec 4.1.3.2)and isocitrate lyase  
(ec 4.1.3.1).) (nt:isocitrate lyase) (le:2212) (re:3516) (di:direct) ECACEB  
X12431 g40888 Escherichia coli 562 -11532797 237221 acea isocitrate lyase  
(fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:4.1.3.1)  
(de:escherichia coli k-12 mg1655 section 364 of 400 of the completegenome.)  
(nt:o434; 100 pct identical to acea\_ecoli sw: p05313;) (le:9240) (re:10544)  
(di:direct) AE000474 AE000474 g1790445 Escherichia coli 562 -11532797  
7500876306 acea isocitrate lyase (sr:escherichia coli (sub\_strain mg1655,  
strain k-12) (library: lambda) (db:genpept-bct2) (ec:4.1.3.1) (de:e. coli  
chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 1052)  
(le:82351) (re:83655) (di:direct) ECOUW89 U00006 g396350 Escherichia coli  
562 -11532797 58056 acea:icl (ec:4.1.3.1) (de:isocitrate lyase,  
(isocitrase) (isocitratase) (icl)) (db:swissprot) ACEA\_ECOLI P05313  
ESCHERICHIA COLI 562 -11532797

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822980	7416	29572	1077	359

Description

6500728940 fdhf:b4079 formate dehydrogenase:formate-hydrogen-lyase-linked:selenocysteine-containing polypeptide:formate dehydrogenase-h alpha subunit (gtcfc:1.9:2.2:2.8) (ec:1.2.1.2) (keggfc:1.9:2.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b4079 b4079 Escherichia coli 562 -11532798 7500974870 fdhf selenopolypeptide subunit of formate (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (ec:1.2.1.2) (de:escherichia coli k-12 mg1655 section 371 of 400 of the completegenome.) (nt:selenocysteine) (le:5777) (re:7924) (di:complement) AE000481 AE000481 g3868721 Escherichia coli 562 -11532798 7502851819 fdhf selenopolypeptide subunit of formate (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept) (ec:1.2.1.2) (de:escherichia coli k-12 mg1655 section 371 of 400 of the completegenome.) (nt:f715; 99 pct identical amino acid sequence and) (le:5777) (re:7924) (di:complement) AE000481 AE000481 g3868721 Escherichia coli 562 -11532798

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822990	7417	29573	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822991	7418	29574	621	206

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822994	7419	29575	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501822999	7420	29576	861	286

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823016	7421	29577	771	256

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823021	7422	29578	516	171

Description

6500728941 flII:fla\_aIII:flac:b1941 flagellum-specific atp synthase  
(gtcfc:2.1:11.3) (ec:3.6.1.34) (keggfc:2.1) (rileyfc:3.3.3)  
(db:gtc-escherichia coli) b1941 b1941 Escherichia coli 562 -11532799 71996  
flII:fla:flac::aIII (ec:3.6.1.34) (de:flagellum-specific atp synthase,)  
(db:swissprot) FLII\_ECOLI P52612 ESCHERICHIA COLI 562 -11532799 7000685290  
flII h+-transporting atp synthase:flagellum-specific (cl:h+-transporting atp  
synthase alpha chain:h+-transporting atp synthase alpha chain homology)  
(ec:3.6.1.34) (db:pir2.dat) B64958 B64958 Escherichia coli 562 -11532799  
224449 flII:fla\_aIII:flac flagellum-specific atp synthase ec 3.6.1.34 .  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #343(43.3-43.6  
min.)) (nt:orf\_id:o343#4; similar to (swissprot accession) (le:5934)  
(re:7307) (di:direct) D90834 D90834 g1736607 Escherichia coli 562 -11532799  
301089 flII flagellum-specific atp synthase (fn:enzyme; surface structures)  
(db:genpept-bct2) (ec:3.6.1.34) (de:escherichia coli k-12 mg1655 section 176  
of 400 of the completegenome.) (nt:o457; 97 pct identical to flII\_ecoli sw:  
p52612) (le:6047) (re:7420) (di:direct) AE000286 AE000286 g1788251  
Escherichia coli 562 -11532799 5000690143 (de:(ecoli\_1895)  
(pn:flagellum-specific atp synthase) (gn:flII) (gtcfc:2.1) (ec:3.6.1.34)  
(flII\_ecoli) (keggfc:2.1) (rileyfc:3.3.3) (db:gtc-escherichia coli))  
ECOLI\_1895 ECOLI\_1895 Escherichia coli 562 10119920

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823026	7423	29579	948	315

Description

6500728942 nuon:b2276 nadh dehydrogenase i chain n:nadh-ubiquinone oxidoreductase chain 14:nuo14 (gtcfc:2.1:2.8:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2276 b2276 Escherichia coli 562 -11532800 87209 nuon (ec:1.6.5.3) (de:oxidoreductase chain 14) (nuo14)) (db:swissprot) NUON\_ECOLI P33608 ESCHERICHIA COLI 562 -11532800 7000686016 nuon nadh dehydrogenase ubiquinone:i chain n (cl:nadh dehydrogenase (ubiquinone) chain 2) (ec:1.6.5.3) (db:pir2.dat) B64999 B64999 Escherichia coli 562 -11532800 224790 nuon nadh dehydrogenase i chain n ec 1.6.5.3 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #401(51.3-51.6 min.)) (nt:similar to (swissprot accession number p33608)) (le:12136) (re:13413) (di:complement) D90858 D90858 g1799634 Escherichia coli 562 -11532800 224791 nuon nadh dehydrogenase i chain n ec 1.6.5.3 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #403(51.5-51.9 min.)) (nt:similar to (swissprot accession number p33608)) (le:1466) (re:2743) (di:complement) D90859 D90859 g1799636 Escherichia coli 562 -11532800 7500887004 nuon nadh dehydrogenase i chain n (fn:enzyme; energy metabolism, carbon: aerobic) (db:genpept-bct2) (ec:1.6.5.3) (de:escherichia coli k-12 mg1655 section 207 of 400 of the completegenome.) (nt:f425; 96 pct identical to nuon\_ecoli sw: p33608) (le:6119) (re:7396) (di:complement) AE000317 AE000317 g1788612 Escherichia coli 562 -11532800 5000690144 (de:(ecoli\_2225) (pn:nadh dehydrogenase i chain n) (gn:nuon) (gtcfc:2.1:9.12) (ec:1.6.5.3) (nuon\_ecoli) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI\_2225 ECOLI\_2225 Escherichia coli 562 10120075

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823029	7424	29580	414	137

#### Description

6500728943 nuom:b2277 nadh dehydrogenase i chain m:nadh-ubiquinone oxidoreductase chain 13:nuo13 (gtcfc:2.1:2.8:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2277 b2277 Escherichia coli 562 -11532801 87207 nuom (ec:1.6.5.3) (de:oxidoreductase chain 13) (nuo13)) (db:swissprot) NUOM\_ECOLI P31978 ESCHERICHIA COLI 562 -11532801 7000686015 nuom nadh dehydrogenase ubiquinone:chain 4:nadh dehydrogenase i chain m (cl:nadh dehydrogenase (ubiquinone) chain 4) (ec:1.6.5.3) (db:pir2.dat) C64999 C64999 Escherichia coli 562 -11532801 224792 nadh dehydrogenase ubiquinone ec 1.6.5.3 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #403(51.5-51.9 min.)) (nt:similar to (pir accession number a48643)) (le:2929) (re:4458) (di:complement) D90859 D90859 g1799637 Escherichia coli 562 -11532801 7500887003 nuom nadh dehydrogenase i chain m (fn:enzyme; energy metabolism, carbon: aerobic) (db:genpept-bct2) (ec:1.6.5.3) (de:escherichia coli k-12 mg1655 section 207 of 400 of the completegenome.) (nt:f509; 99 pct identical to nuom\_ecoli sw: p31978) (le:7583) (re:9112) (di:complement) AE000317 AE000317 g1788613 Escherichia coli 562 -11532801 5000690145 (de:(ecoli\_2226) (pn:nadh dehydrogenase i chain m) (gn:nuom) (gtcfc:2.1:9.12) (ec:1.6.5.3) (nuom\_ecoli) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI\_2226 ECOLI\_2226 Escherichia coli 562 10120076

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823042	7425	29581	369	122

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823046	7426	29582	357	119

#### Description

GTC ORF with score 160 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome i cosmid c31g5.) (nt:spac31g5.15, anomaly: splicing may be incorrectly) (le:24696:24950:25237:25745) (re:24893:25177:25702:26790) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823074	7427	29583	303	100

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823076	7428	29584	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823088	7429	29585	1287	428

Description

6500728944 nuol:b2278 nadh dehydrogenase i chain 1:nadh-ubiquinone oxidoreductase chain 12:nuo12 (gtcfc:2.1:2.8:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2278 b2278 Escherichia coli 562 -11532802 87204 nuol (ec:1.6.5.3) (de:oxidoreductase chain 12) (nuo12)) (db:swissprot) NUOL\_ECOLI P33607 ESCHERICHIA COLI 562 -11532802 7000686014 nuol nadh dehydrogenase ubiquinone:i chain 1 (ec:1.6.5.3) (db:pir2.dat) D64999 D64999 Escherichia coli 562 -11532802 224793 nadh dehydrogenase i chain nuol (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #403(51.5-51.9 min.)) (nt:similar to (pir accession number s38321)) (le:4622) (re:6463) (di:complement) D90859 D90859 g1799638 Escherichia coli 562 -11532802 7500887002 nuol nadh dehydrogenase i chain 1 (fn:enzyme; energy metabolism, carbon: aerobic) (db:genpept-bct2) (ec:1.6.5.3) (de:escherichia coli k-12 mg1655 section 207 of 400 of the completegenome.) (nt:f613; 97 pct identical to nuol\_ecoli sw: p33607) (le:9276) (re:11117) (di:complement) AE000317 AE000317 g1788614 Escherichia coli 562 -11532802 5000690146 (de:(ecoli\_2227) (pn:nadh dehydrogenase i chain 1) (gn:nuol) (gtcfc:2.1:9.12) (ec:1.6.5.3) (nuol\_ecoli) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI\_2227 ECOLI\_2227 Escherichia coli 562 10120077

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823095	7430	29586	984	327

Description

GTC ORF with score 149 to: (sr:epstein-barr virus (b95-8 isolate) dna, clones pdf322 and pdk286) (db:genpept-vr1) (de:epstein-barr virus (b95-8 isolate) u2-ir2 domain encoding nuclearprotein ebna2, complete cds.) (nt:nuclear protein ebna2) (le:1498) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823102	7431	29587	627	208
<u>Description</u>				

6500728945 nuok:b2279 nadh dehydrogenase i chain k:nadh-ubiquinone oxidoreductase chain 11:nuo11 (gtcfc:2.1:2.8:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2279 b2279 Escherichia coli 562 -11532803 87202 nuok (ec:1.6.5.3) (de:oxidoreductase chain 11) (nuo11)) (db:swissprot) NUOK\_ECOLI P33606 ESCHERICHIA COLI 562 -11532803 7000686012 nuok nuok protein (cl:nadh dehydrogenase (ubiquinone) chain 4l) (db:pir2.dat) E64999 E64999 Escherichia coli 562 -11532803 7500887001 nuok nadh dehydrogenase i chain k (fn:enzyme; energy metabolism, carbon: aerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 207 of 400 of the completegenome.) (nt:f100; this 100 aa orf is 84 pct identical (1 gap)) (le:11114) (re:11416) (di:complement) AE000317 AE000317 g1788615 Escherichia coli 562 -11532803 5000690147 (de:(ecoli\_2228) (pn:nadh dehydrogenase i chain k) (gn:nuok) (gtcfc:2.1:9.12) (ec:1.6.5.3) (nuok\_ecoli) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI\_2228 ECOLI\_2228 Escherichia coli 562 10123625

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823108	7432	29588	1014	337
<u>Description</u>				

6500728946 nuoj:b2280 nadh dehydrogenase i chain j:nadh-ubiquinone oxidoreductase chain 10:nuo10 (gtcfc:2.1:2.8:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2280 b2280 Escherichia coli 562 -11532804 87200 nuoj (ec:1.6.5.3) (de:oxidoreductase chain 10) (nuo10)) (db:swissprot) NUOJ\_ECOLI P33605 ESCHERICHIA COLI 562 -11532804 7000686011 nuoj nadh dehydrogenase ubiquinone:i chain j (cl:nadh dehydrogenase (ubiquinone) chain 6) (ec:1.6.5.3) (db:pir2.dat) (mp:49.5 min) F64999 F64999 Escherichia coli 562 -11532804 224795 nuoj nadh dehydrogenase ubiquinone ec 1.6.5.3 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #403(51.5-51.9 min.)) (nt:similar to (pir accession number s38319)) (le:6759) (re:7313) (di:complement) D90859 D90859 g1799640 Escherichia coli 562 -11532804 7500887000 nuoj nadh dehydrogenase i chain j (fn:enzyme; energy metabolism, carbon: aerobic) (db:genpept-bct2) (ec:1.6.5.3) (de:escherichia coli k-12 mg1655 section 207 of 400 of the completegenome.) (nt:f184; 98 pct identical to nuoj\_ecoli sw: p33605) (le:11413) (re:11967) (di:complement) AE000317 AE000317 g1788616 Escherichia coli 562 -11532804 5000690148 (de:(ecoli\_2229) (pn:nadh dehydrogenase i chain j) (gn:nuoj) (gtcfc:2.1:9.12) (ec:1.6.5.3) (nuoj\_ecoli) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI\_2229 ECOLI\_2229 Escherichia coli 562 10120079

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823112	7433	29589	573	190

#### Description

6500728947 nuoi:b2281 nadh dehydrogenase i chain i:nadh-ubiquinone oxidoreductase chain 9:nuo9 (gtcfc:2.1:2.8:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2281 b2281 Escherichia coli 562 -11532805 87198 nuoi (ec:1.6.5.3) (de:oxidoreductase chain 9) (nuo9)) (db:swissprot) NUOI\_ECOLI P33604 ESCHERICHIA COLI 562 -11532805 7000686010 nuoi nadh dehydrogenase ubiquinone:chain i (ec:1.6.5.3) (db:pir2.dat) (mp:49.5 min) G64999 G64999 Escherichia coli 562 -11532805 7500886999 nuoi nadh dehydrogenase i chain i (fn:enzyme; energy metabolism, carbon: aerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 207 of 400 of the completegenome.) (nt:f180; 90 pct identical (1 gap) to 180 residues of) (le:11979) (re:12521) (di:complement) AE000317 AE000317 g1788617 Escherichia coli 562 -11532805 5000690149 (de:(ecoli\_2230) (pn:nadh dehydrogenase i chain i) (gn:nuoi) (gtcfc:2.1:9.12) (ec:1.6.5.3) (nuoi\_ecoli) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI\_2230 ECOLI\_2230 Escherichia coli 562 10123626

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823124	7434	29590	477	158

#### Description

6500728948 nuoh:b2282 nadh dehydrogenase i chain h:nadh-ubiquinone oxidoreductase chain 8:nuo8 (gtcfc:2.1:2.8:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2282 b2282 Escherichia coli 562 -11532806 87196 nuoh (ec:1.6.5.3) (de:oxidoreductase chain 8) (nuo8)) (db:swissprot) NUOH\_ECOLI P33603 ESCHERICHIA COLI 562 -11532806 7000686009 nuoh:nuob nadh dehydrogenase ubiquinone:i chain h (cl:nadh dehydrogenase (ubiquinone) chain 1) (ec:1.6.5.3) (db:pir2.dat) (mp:49.5 min) H64999 H64999 Escherichia coli 562 -11532806 224797 nuoh nadh dehydrogenase i chain h ec 1.6.5.3 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #403(51.5-51.9 min.)) (nt:similar to (swissprot accession number p33603)) (le:7882) (re:8859) (di:complement) D90859 D90859 g1799642 Escherichia coli 562 -11532806 7500886996 nuoh nadh dehydrogenase i chain h (fn:enzyme; energy metabolism, carbon: aerobic) (db:genpept-bct2) (ec:1.6.5.3) (de:escherichia coli k-12 mg1655 section 207 of 400 of the completegenome.) (nt:f325; 99 pct identical to nuoh\_ecoli sw: p33603) (le:12536) (re:13513) (di:complement) AE000317 AE000317 g1788618 Escherichia coli 562 -11532806 5000690150 (de:(ecoli\_2231) (pn:nadh dehydrogenase i chain h) (gn:nuoh) (gtcfc:2.1:9.12) (ec:1.6.5.3) (nuoh\_ecoli) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI\_2231 ECOLI\_2231 Escherichia coli 562 10120081



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823136	7435	29591	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823137	7436	29592	384	127

Description

6500728949 nuog:b2283 (gtcfc:2.1:2.8:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2283 b2283 Escherichia coli 562 -11532807 7000691869 nuog nadh dehydrogenase:i chain g (ec:1.6.99.3) (db:pir2.dat) A65000 A65000 Escherichia coli 562 -11532807 7500960392 nuog nadh dehydrogenase i chain g (fn:enzyme; energy metabolism, carbon: aerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 207 of 400 of the completengenome.) (nt:f910; this 910 aa orf is 97 pct identical (2 gaps)) (le:13510) (re:16242) (di:complement) AE000317 AE000317 g1788619 Escherichia coli 562 -11532807 5000690151 (de:(ecoli\_2232) (pn:nadh dehydrogenase i chain g) (gn:nuog) (gtcfc:2.1:9.12) (ec:1.6.5.3) (nuog\_ecoli) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI\_2232 ECOLI\_2232 Escherichia coli 562 10123627

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823173	7437	29593	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823194	7438	29594	732	243

Description

6500728950 nuof:b2284 nadh dehydrogenase i chain f:nadh-ubiquinone  
oxidoreductase chain 6:nuo6 (gtcfc:2.1:2.8:9.12) (ec:1.6.5.3)  
(keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2284 b2284  
Escherichia coli 562 -11532808 87192 nuof (ec:1.6.5.3) (de:oxidoreductase  
chain 6) (nuo6)) (db:swissprot) NUOF\_ECOLI P31979 ESCHERICHIA COLI 562  
-11532808 7000686008 nuof nadh dehydrogenase ubiquinone:i chain f:nadh  
dehydrogenase ubiquinone i nadh-binding chain (cl:nadh dehydrogenase  
(ubiquinone) chain f) (ec:1.6.5.3) (db:pir2.dat) B65000 B65000 Escherichia  
coli 562 -11532808 224800 nuof nadh dehydrogenase i chain f ec 1.6.5.3  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #403(51.5-51.9  
min.)) (nt:similar to (swissprot accession number p31979)) (le:11635)  
(re:12972) (di:complement) D90859 D90859 g1799645 Escherichia coli 562  
-11532808 224805 nuof nadh dehydrogenase i chain f ec 1.6.5.3  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #404(51.7-52.1  
min.)) (nt:similar to (swissprot accession number p31979)) (le:2760)  
(re:4097) (di:complement) D90860 D90860 g1799651 Escherichia coli 562  
-11532808 7500886993 nuof nadh dehydrogenase i chain f (fn:enzyme; energy  
metabolism, carbon: aerobic) (db:genpept-bct2) (ec:1.6.5.3) (de:escherichia  
coli k-12 mg1655 section 207 of 400 of the completegenome.) (nt:f445; 99 pct  
identical to nuof\_ecoli sw: p31979) (le:16289) (re:17626) (di:complement)  
AE000317 AE000317 g1788620 Escherichia coli 562 -11532808 5000690152  
(de:(ecoli\_2233) (pn:nadh dehydrogenase i chain f) (gn:nuof)  
(gtcfc:2.1:9.12) (ec:1.6.5.3) (nuof\_ecoli) (keggfc:2.1:9.13) (rileyfc:1.2.6)  
(db:gtc-escherichia coli)) ECOLI\_2233 ECOLI\_2233 Escherichia coli 562  
10120084

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501823195	7439	29595	375	124

# Description

6500728951 nuoe:b2285 nadh dehydrogenase i chain e:nadh-ubiquinone oxidoreductase chain 5:nuo5 (gtcfc:2.1:2.8:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2285 b2285 Escherichia coli 562 -11532809 87190 nuoe (ec:1.6.5.3) (de:oxidoreductase chain 5) (nuo5)) (db:swissprot) NUOE\_ECOLI P33601 ESCHERICHIA COLI 562 -11532809 7000686007 nuoe nadh dehydrogenase ubiquinone:i chain e:complex 1 dehydrogenase:chain e:nadh dehydrogenase i:chain e:type 1 dehydrogenase:chain e:ubiquinone reductase:chain k (cl:nadh dehydrogenase (ubiquinone) i chain e) (ec:1.6.5.3) (db:pir2.dat) (mp:49 min) C65000 C65000 Escherichia coli 562 -11532809 224801 nuoe nadh dehydrogenase ubiquinone ec 1.6.5.3 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #403(51.5-51.9 min.)) (nt:similar to (pir accession number s38314)) (le:12969) (re:13469) (di:complement) D90859 D90859 g1799646 Escherichia coli 562 -11532809 224806 nuoe nadh dehydrogenase ubiquinone ec 1.6.5.3 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #404(51.7-52.1 min.)) (nt:similar to (pir accession number s38314)) (le:4094) (re:4594) (di:complement) D90860 D90860 g1799652 Escherichia coli 562 -11532809 7500886992 nuoe nadh dehydrogenase (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli nadh dehydrogenase (nuod), (nuoe), (nuof), (nuog)gene, complete cds.) (nt:putative) (le:1272) (re:1772) (di:direct) ECONUOD L25055 g431019 Escherichia coli 562 -11532809 235256 nuoe nadh dehydrogenase i chain e (fn:enzyme; energy metabolism, carbon: aerobic) (db:genpept-bct2) (ec:1.6.5.3) (de:escherichia coli k-12 mg1655 section 207 of 400 of the completegenome.) (nt:f166; 99 pct identical to nuoe\_ecoli sw: p33601) (le:17623) (re:18123) (di:complement) AE000317 AE000317 g1788621 Escherichia coli 562 -11532809 5000690153 (de:(ecoli\_2234) (pn:nadh dehydrogenase i chain e) (gn:nuoe) (gtcfc:2.1:9.12) (ec:1.6.5.3) (nuoe\_ecoli) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI\_2234 ECOLI\_2234 Escherichia coli 562 10120085

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823202	7440	29596	375	124

Description

6500728952 nadh dehydrog...:b2286:c chain d (gtcfc:2.1:2.8:9.12)  
(ec:1.6.5.3) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli)  
b2286 b2286 Escherichia coli 562 -11532810 7000691870 nuoc:nuod nadh  
dehydrogenase ubiquinone:i:chain c-d (ec:1.6.5.3) (db:pir2.dat) (mp:49.5  
min) D65000 D65000 Escherichia coli 562 -11532810 7500960393 nuoc nadh  
dehydrogenase i chain c:d (fn:enzyme; energy metabolism, carbon: aerobic)  
(db:genpept-bct2) (ec:1.6.5.3) (de:escherichia coli k-12 mg1655 section 207  
of 400 of the completegenome.) (nt:f600; residues 1-174 are 100 pct  
identical) (le:18126) (re:19928) (di:complement) AE000317 AE000317 g1788622  
Escherichia coli 562 -11532810 5000690154 (de:(ecoli\_2235) (pn:nadh  
dehydrogenase i chain d) (gn:nuod:nuoc) (gtcfc:2.1:9.12) (ec:1.6.5.3)  
(nuod\_ecoli) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli))  
ECOLI\_2235 ECOLI\_2235 Escherichia coli 562 10123628

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823203	7441	29597	807	269

Description

6500728953 nuob:b2287 nadh dehydrogenase i chain b:nadh-ubiquinone  
oxidoreductase chain 2:nuo2 (gtcfc:2.1:2.8:9.12) (ec:1.6.5.3)  
(keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2287 b2287  
Escherichia coli 562 -11532811 87186 nuob (ec:1.6.5.3) (de:oxidoreductase  
chain 2) (nuo2)) (db:swissprot) NUOB\_ECOLI P33598 ESCHERICHIA COLI 562  
-11532811 7000686006 nuob nadh dehydrogenase ubiquinone:i chain b (cl:psbg  
protein) (ec:1.6.5.3) (db:pir1.dat) (mp:49.5 min) E65000 E65000 Escherichia  
coli 562 -11532811 7500886990 nuob nadh dehydrogenase i chain b (fn:enzyme;  
energy metabolism, carbon: aerobic) (db:genpept-bct2) (ec:1.6.5.3)  
(de:escherichia coli k-12 mg1655 section 208 of 400 of the completegenome.)  
(nt:f220; 99 pct identical to nuob\_ecoli sw: p33598) (le:77) (re:739)  
(di:complement) AE000318 AE000318 g1788624 Escherichia coli 562 -11532811  
5000690155 (de:(ecoli\_2236) (pn:nadh dehydrogenase i chain b) (gn:nuob)  
(gtcfc:2.1:9.12) (ec:1.6.5.3) (nuob\_ecoli) (keggfc:2.1:9.13) (rileyfc:1.2.6)  
(db:gtc-escherichia coli)) ECOLI\_2236 ECOLI\_2236 Escherichia coli 562  
10123629

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823207	7442	29598	453	150

Description

6500728954 nuoa:b2288 nadh dehydrogenase i chain a:nadh-ubiquinone oxidoreductase chain 1:nuo1 (gtcfc:2.1:2.8:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2288 b2288 Escherichia coli 562 -11532812 87185 nuoa (ec:1.6.5.3) (de:oxidoreductase chain 1) (nuo1)) (db:swissprot) NUOA\_ECOLI P33597 ESCHERICHIA COLI 562 -11532812 7000686005 nuoa nadh dehydrogenase ubiquinone:chain a:complex 1 dehydrogenase:chain a:nadh dehydrogenase i:chain a:type 1 dehydrogenase:chain a:ubiquinone reductase:chain a (cl:nadh dehydrogenase (ubiquinone) chain 3) (ec:1.6.5.3) (db:pir2.dat) (mp:49 min) F65000 F65000 Escherichia coli 562 -11532812 224810 nuoa nadh dehydrogenase i chain a ec 1.6.5.3 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #404(51.7-52.1 min.)) (nt:similar to (swissprot accession number p33597)) (le:7172) (re:7615) (di:complement) D90860 D90860 g1799656 Escherichia coli 562 -11532812 7500886989 nuoa nadh dehydrogenase i chain a (fn:enzyme; energy metabolism, carbon: aerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 208 of 400 of the completegenome.) (nt:fl47; 92 pct identical to nuoa\_ecoli sw: p33597) (le:755) (re:1198) (di:complement) AE000318 AE000318 g1788625 Escherichia coli 562 -11532812 5000690156 (de:(ecoli\_2237) (pn:nadh dehydrogenase i chain a) (gn:nuoa) (gtcfc:2.1:9.12) (ec:1.6.5.3) (nuoa\_ecoli) (keggfc:2.1:9.13) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI\_2237 ECOLI\_2237 Escherichia coli 562 10120090

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823217	7443	29599	1662	553

Description

GTC ORF with score 206 to: (or:Gallus gallus) (sr:chicken (lambda nm1149-gizzard and okayama-berg plasmid-oviduc) (db:genpept-vrt) (de:chicken smooth muscle caldesmon mrna, complete cds.) (nt:smooth muscle caldesmon) (le:235) (re:2505) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823221	7444	29600	1116	371

Description

6500728955 ppk:b2501 polyphosphate kinase (gtcfc:2.1:13.10) (ec:2.7.4.1) (keggfc:2.1) (rileyfc:1.1.4) (db:gtc-escherichia coli) b2501 b2501  
 Escherichia coli 562 -11532813 164348 ppk polyphosphate kinase (ec:2.7.4.1) (db:pir2.dat) (mp:54 min) A44306 A44306 Escherichia coli 562 -11532813  
 225077 ppk polyphosphate kinase ec 2.7.4.1 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #425(56.2-56.5 min.)) (nt:similar to (pir accession number a44306)) (le:10965) (re:13031) (di:direct) D90878  
 D90878 g1805561 Escherichia coli 562 -11532813 7500960416 ppk polyphosphate kinase (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:2.7.4.1) (de:escherichia coli k-12 mg1655 section 226 of 400 of the completegenome.) (nt:o688; 100 pct identical to ppk\_ecoli sw: p28688 but) (le:7087) (re:9153) (di:direct) AE000336 AE000336 g1788847 Escherichia coli 562 -11532813 5000690157 (de:(ecoli\_2441) (pn:polyphosphate kinase) (gn:ppk) (gtcfc:2.1) (ec:2.7.4.1) (ppk\_ecoli) (keggfc:2.1) (rileyfc:1.1.4) (db:gtc-escherichia coli)) ECOLI\_2441 ECOLI\_2441 Escherichia coli 562 10087284

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823226	7445	29601	891	296

Description

GTC ORF with score 100 to: (fn:phosphorylation; shuttling) (sr:rattus norvegicus liver cdna to mrna) (db:genpept-rod) (de:rattus norvegicus nucleolar phosphoprotein of 140kd, nopp140 mrna,complete cds.) (le:804) (re:2915) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823242	7446	29602	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823248	7447	29603	1758	585

# Description

6500728956 atpc:uncc:papg:b3731 atp synthase f1 epsilon subunit:atp synthase epsilon chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (rileyfc:1.2.8) (db:gtc-escherichia coli) b3731 b3731 Escherichia coli 562 -11532814 125145 atpc:uncc h+-transporting atp synthase:epsilon chain:hydrogen ion-transporting atpase epsilon chain (cl:h+-transporting atp synthase epsilon chain) (ec:3.6.1.34) (db:pir1.dat) (mp:84 min) PWCE B90106 Escherichia coli 562 -11532814 236271 h+ atpase f1 epsilon subunit (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli h+ atpase alpha, beta, gamma, delta and epsilon, and integral membrane proton channel a, b, and c subunit genes, complete cds.) (le:6645) (re:7064) (di:direct) ECOHATP M25464 g146326 Escherichia coli 562 -11532814 236968 uncc (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli atp (unc) operon containing nine genes coding for atpsynthase subunits.) (nt:atp synthase epsilon subunit (atp-9)) (le:7103) (re:7522) (di:direct) ECOUNC J01594 g148140 Escherichia coli 562 -11532814 237697 atpc::cg site no. 31 atp synthase f1 epsilon subunit (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:alternate gene names uncc, papg) (le:104945) (re:105364) (di:complement) ECOUW82 L10328 g290580 Escherichia coli 562 -11532814 240354 (db:genpept-bct1) (de:e. coli genes papb and papg, coding for atpase subunits beta and epsilon, respectively.) (nt:reading frame papg) (le:1404) (re:1823) (di:direct) ECPAP2 V00311 g42278 Escherichia coli 562 -11532814 7500953319 (db:genpept-bct1) (de:e. coli origin of replication oric and genes gid, unc, ecourf-1 and glms.) (nt:uncc protein) (le:10065) (re:10484) (di:direct) ECUNC X01631 g43266 Escherichia coli 562 -11532814 234626 atpc membrane-bound atp synthase:f1 sector (fn:enzyme; atp-proton motive force) (db:genpept-bct2) (ec:3.6.1.34) (de:escherichia coli k-12 mg1655 section 340 of 400 of the complete genome.) (nt:f139; 100 pct identical to atpe\_ecoli sw:p00832;) (le:4006) (re:4425) (di:complement) AE000450 AE000450 g1790169 Escherichia coli 562 -11532814 5000690158 (de:(ecoli\_3649) (pn:membrane-bound atp synthase, f1 sector, epsilon-subunit) (gn:atpc) (gtcfc:2.1) (ec:3.6.1.34) (atpe\_ecoli) (keggfc:2.1) (rileyfc:1.2.8) (db:gtc-escherichia coli)) ECOLI\_3649 ECOLI\_3649 Escherichia coli 562 10066276

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501823255	7448	29604	543	180

# Description

6500728957 atpd:uncd:papb:b3732 atp synthase f1 beta subunit:atp synthase beta chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (rileyfc:1.2.8) (db:gtc-escherichia coli) b3732 b3732 Escherichia coli 562 -11532815 125114 atpd:uncd h+-transporting atp synthase:beta chain:atpase f 1 subunit beta chain:hydrogen ion-transporting atpase beta chain (cl:h+-transporting atp synthase alpha chain:h+-transporting atp synthase alpha chain homology) (ec:3.6.1.34) (db:pir1.dat) (mp:84 min) PWECB A93742 Escherichia coli 562 -11532815 234625 (db:genpept-bct1) (de:e. coli genes from the atp (unc) operon. genes gamma, beta (uncd)and epsilon (uncc) code for subunits of the atp-synthesizing system. uncc codes for the epsilon subunit of f1 and uncd codes for the beta subunit of f1.) (nt:reading f... ECATPY V00267 g41038 Escherichia coli 562 -11532815 236270 h+ atpase f1 beta subunit (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli h+ atpase alpha, beta, gamma, delta and epsilon, and integral membrane proton channel a, b, and c subunit genes, complete cds.) (le:5242) (re:6624) (di:direct) ECOHATP M25464 g146325 Escherichia coli 562 -11532815 236969 uncd (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli atp (unc) operon containing nine genes coding for atp synthase subunits.) (nt:atp synthase beta subunit (atp-8)) (le:5700) (re:7082) (di:direct) ECOUNC J01594 g148139 Escherichia coli 562 -11532815 237696 atpd::cg site no. 30 atp synthase f1 beta subunit (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:alternate gene names uncd, papb) (le:105385) (re:106767) (di:complement) ECOUW82 L10328 g290581 Escherichia coli 562 -11532815 240353 (db:genpept-bct1) (de:e. coli genes papb and papg, coding for atpase subunits beta and epsilon, respectively.) (nt:reading frame papb) (le:1) (re:1383) (di:direct) ECPAP2 V00311 g42277 Escherichia coli 562 -11532815 7500953317 (db:genpept-bct1) (de:e. coli origin of replication oric and genes gid, unc, ecourf-1 and glms.) (nt:uncd protein) (le:8662) (re:10044) (di:direct) ECUNC X01631 g899257 Escherichia coli 562 -11532815 232441 atpd membrane-bound atp synthase:f1 sector (fn:enzyme; atp-proton motive force) (db:genpept-bct2) (ec:3.6.1.34) (de:escherichia coli k-12 mg1655 section 340 of 400 of the complete genome.) (nt:f460; 100 pct identical to atpb\_ecoli sw: p00824;) (le:4446) (re:5828) (di:complement) AE000450 AE000450 g1790170 Escherichia coli 562 -11532815 5000690159 (de:(ecoli\_3650) (pn:membrane-bound atp synthase, f1 sector, beta-subunit) (gn:atpd) (gtcfc:2.1) (ec:3.6.1.34) (atpb\_ecoli) (keggfc:2.1) (rileyfc:1.2.8) (db:gtc-escherichia coli)) ECOLI\_3650 ECOLI\_3650 Escherichia coli 562 10066272



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823257	7449	29605	198	65

Description

Hypothetical protein

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823259	7450	29606	378	125

Description

GTC ORF with score 302 to: (sr:baker's yeast) (db:genpept-pln2) (de:skt5  
(skt5)=protoplast regeneration and killer toxin resistancegene  
(saccharomyces cerevisiae, genomic mutant, 2177 nt).) (nt:protoplast  
regeneration and killer toxin resistance) ...

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823273	7451	29607	483	160

#### Description

6500728958 atpg:uncg:papc:b3733 atp synthase f1 gamma subunit:atp synthase gamma chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (rileyfc:1.2.8) (db:gtc-escherichia coli) b3733 b3733 Escherichia coli 562 -11532816 7500877550 atpg:uncg:papc (ec:3.6.1.34) (de:atp synthase gamma chain,) (db:swissprot) ATPG\_ECOLI P00837 ESCHERICHIA COLI 562 -11532816 125159 atpg:uncg h+-transporting atp synthase:gamma chain (cl:h+-transporting atp synthase gamma chain) (ec:3.6.1.34) (db:pir1.dat) (mp:84 min) PWECC A01038 Escherichia coli 562 -11532816 234624 (db:genpept-bct1) (de:e. coli genes from the atp (unc) operon. genes gamma, beta (uncd) and epsilon (uncc) code for subunits of the atp-synthesizing system. uncc codes for the epsilon subunit of f1 and uncd codes for the beta subunit of f1.) (nt:reading f... ECATPY V00267 g41037 Escherichia coli 562 -11532816 236970 h+ atpase f1 gamma subunit (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli h+ atpase alpha, beta, gamma, delta and epsilon, and integral membrane proton channel a, b, and c subunit genes, complete cds.) (le:4352) (re:5215) (di:direct) ECOHATP M25464 g146324 Escherichia coli 562 -11532816 240352 atpg::cg site no. 27 atp synthase f1 gamma subunit (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:alternate gene names uncg, papc) (le:106794) (re:107657) (di:complement) ECOUW82 L10328 g290582 Escherichia coli 562 -11532816 5000690160 (db:genpept-bct1) (de:e. coli origin of replication oric and genes gid, unc, ecourf-1 and glms.) (nt:uncg protein) (le:7772) (re:8635) (di:direct) ECUNC X01631 g43265 Escherichia coli 562 -11532816 232440 atpg membrane-bound atp synthase:f1 sector (fn:enzyme; atp-proton motive force) (db:genpept-bct2) (ec:3.6.1.34) (de:escherichia coli k-12 mg1655 section 340 of 400 of the complete genome.) (nt:f287; 100 pct identical to atpg\_ecoli sw: p00837;) (le:5855) (re:6718) (di:complement) AE000450 AE000450 g1790171 Escherichia coli 562 -11532816 61061 atpg:uncg:papc (ec:3.6.1.34) (de:atp synthase gamma chain,) (db:swissprot) ATPG\_ECOLI P00837 ESCHERICHIA COLI 562 -11532816

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823278	7452	29608	186	61

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823288	7453	29609	198	65

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823294	7454	29610	417	139
<u>Description</u>				
6500728959 atpa:unca:papa:b3734 atp synthase f1 alpha subunit:atp synthase alpha chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (rileyfc:1.2.8) (db:gtc-escherichia coli) b3734 b3734 Escherichia coli 562 -11532817 60800 atpa:unca:papa (ec:3.6.1.34) (de:atp synthase alpha chain,) (db:swissprot) ATPA_ECOLI P00822 ESCHERICHIA COLI 562 -11532817 7000684667 atpa:unca h+-transporting atp synthase:alpha chain:hydrogen ion-transporting atpase alpha chain (cl:h+-transporting atp synthase alpha chain:h+-transporting atp synthase alpha chain homology) (ec:3.6.1.34) (db:pir1.dat) (mp:84 min) PWECA G65176 Escherichia coli 562 -11532817 7500877459 atpa::cg site no. 33 atp synthase f1 alpha subunit (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:alternate gene names unca, papa) (le:107708) (re:109249) (di:complement) ECOUW82 L10328 g290583 Escherichia coli 562 -11532817 236971 atpa membrane-bound atp synthase:f1 sector (fn:enzyme; atp-proton motive force) (db:genpept-bct2) (ec:3.6.1.34) (de:escherichia coli k-12 mg1655 section 340 of 400 of the completegenome.) (nt:f513; 100 pct identical to atpa_ecoli sw: p00822;) (le:6769) (re:8310) (di:complement) AE000450 AE000450 g1790172 Escherichia coli 562 -11532817 5000690161 (de:(ecoli_3652) (pn:membrane-bound atp synthase, f1 sector, alpha-subunit) (gn:atpa) (gtcfc:2.1) (ec:3.6.1.34) (atpa_ecoli) (keggfc:2.1) (rileyfc:1.2.8) (db:gtc-escherichia coli)) ECOLI_3652 ECOLI_3652 Escherichia coli 562 10003520				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501823308	7455	29611	729	242

# Description

6500728960 atph:unch:pape:b3735 atp synthase f1 delta subunit:atp synthase delta chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (rileyfc:1.2.8) (db:gtc-escherichia coli) b3735 b3735 Escherichia coli 562 -11532818 304553 atph:unch:pape (ec:3.6.1.34) (de:atp synthase delta chain,) (db:swissprot) ATPD\_ECOLI P00831 ESCHERICHIA COLI 562 -11532818 125137 atph:unch h+-transporting atp synthase:delta chain:hydrogen ion-transporting atpase delta chain (cl:h+-transporting atp synthase delta chain) (ec:3.6.1.34) (db:pir1.dat) (mp:84 min) PWEC D A93732 Escherichia coli 562 -11532818 232438 (db:genpept-bct1) (de:e. coli atp (or unc) operon including promoter and five genes for subunits of atp synthetase and membrane proteins.) (nt:reading frame gene 5 (delta)) (le:2226) (re:2759) (di:direct) ECATPX V00264 g41028 Escherichia coli 562 -11532818 234622 atph (db:genpept-bct1) (de:e. coli genes atpb, atpe, atpf, atph and part of atpa. these genes code for the subunits a, c, b, delta and alpha (respectively) of the f0 subunit of atpase.) (le:1803) (re:2336) (di:direct) ECATPXB V00266 g41034 Escherichia coli 562 -11532818 236267 h+ atpase f0 delta subunit (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli h+ atpase alpha, beta, gamma, delta and epsilon, and integral membrane proton channel a, b, and c subunit genes, complete cds.) (le:2214) (re:2747) (di:direct) ECOHATP M25464 g146322 Escherichia coli 562 -11532818 236972 unch (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli atp (unc) operon containing nine genes coding for atp synthase subunits.) (nt:atp synthase delta subunit (atp-5)) (le:2672) (re:3205) (di:direct) ECOUNC J01594 g148136 Escherichia coli 562 -11532818 240350 atph::cg site no. 26 atp synthase f1 delta subunit (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:alternate gene names unch, pape) (le:109262) (re:109795) (di:complement) ECOUW82 L10328 g290584 Escherichia coli 562 -11532818 5000690162 (db:genpept-bct1) (de:e. coli origin of replication oric and genes gid, unc, ecourf-1 and glms.) (nt:unch protein) (le:5634) (re:6167) (di:direct) ECUNC X01631 g43263 Escherichia coli 562 -11532818 232432 atph membrane-bound atp synthase:f1 sector (fn:enzyme; atp-proton motive force) (db:genpept-bct2) (ec:3.6.1.34) (de:escherichia coli k-12 mg1655 section 340 of 400 of the complete genome.) (nt:f177; 100 pct identical to atpd\_ecoli sw: p00831;) (le:8323) (re:8856) (di:complement) AE000450 AE000450 g1790173 Escherichia coli 562 -11532818 60933 atph:unch:pape (ec:3.6.1.34) (de:atp synthase delta chain,) (db:swissprot) ATPD\_ECOLI P00831 ESCHERICHIA COLI 562 -11532818

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823321	7456	29612	633	210

# Description

6500728961 atpf:uncf:papf:b3736 atp synthase f0 subunit b:atp synthase b chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (rileyfc:1.2.8) (db:gtc-escherichia coli) b3736 b3736 Escherichia coli 562 -11532819 304552 atpf:uncf:papf (ec:3.6.1.34) (de:atp synthase b chain,) (db:swissprot) ATPF\_ECOLI P00859 ESCHERICHIA COLI 562 -11532819 125239 atpf:uncf h+-transporting atp synthase:chain b:hydrogen ion-transporting atp synthase chain b:proton-translocating atpase chain b (cl:h+-transporting atp synthase chain i) (ec:3.6.1.34) (db:pir1.dat) (mp:84 min) LWECEB D93732 Escherichia coli 562 -11532819 232437 (db:genpept-bct1) (de:e. coli atp (or unc) operon including promoter and five genes for subunits of atp synthetase and membrane proteins.) (nt:reading frame gene 4 (b)) (le:1741) (re:2211) (di:direct) ECATPX V00264 g581045 Escherichia coli 562 -11532819 234621 atpf (db:genpept-bct1) (de:e. coli genes atpb, atpe, atpf, atph and part of atpa. these genes code for the subunits a, c, b, delta and alpha (respectively) of the f0 subunit of atpase.) (le:1318) (re:1788) (di:direct) ECATPXB V00266 g581046 Escherichia coli 562 -11532819 236266 integral membrane proton channel f0 subunit b (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli h+ atpase alpha, beta, gamma, delta and epsilon, and integral membrane proton channel a, b, and c subunit genes, complete cds.) (le:1729) (re:2199) (di:direct) ECOHATP M25464 g146321 Escherichia coli 562 -11532819 236973 uncf (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli atp (unc) operon containing nine genes coding for atp synthase subunits.) (nt:atp synthase b subunit (atp-4; gtg start codon)) (le:2187) (re:2657) (di:direct) ECOUNC J01594 g148135 Escherichia coli 562 -11532819 240349 atpf::cg site no. 28 atp synthase f0 subunit b (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:alternate gene name uncf) (le:109810) (re:110280) (di:complement) ECOUW82 L10328 g290585 Escherichia coli 562 -11532819 5000690163 (db:genpept-bct1) (de:e. coli origin of replication oric and genes gid, unc, ecourf-1 and glms.) (nt:uncf protein) (le:5149) (re:5619) (di:direct) ECUNC X01631 g581249 Escherichia coli 562 -11532819 232431 atpf membrane-bound atp synthase:f0 sector:subunit (fn:enzyme; atp-proton motive force) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 340 of 400 of the complete genome.) (nt:f156; alternate gene name uncf; cg site no. 28) (le:8871) (re:9341) (di:complement) AE000450 AE000450 g1790174 Escherichia coli 562 -11532819 61023 atpf:uncf:papf (ec:3.6.1.34) (de:atp synthase b chain,) (db:swissprot) ATPF\_ECOLI P00859 ESCHERICHIA COLI 562 -11532819

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823336	7457	29613	762	253

# Description

6500728962 atpe:unce:paph:b3737 atp synthase f0 subunit c:dccd-binding protein:atp synthase c chain:lipid-binding protein:dicyclohexylcarbodiimide-binding protein (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (rileyfc:1.2.8) (db:gtc-escherichia coli) b3737 b3737 Escherichia coli 562 -11532820 304551 atpe:unce:paph (ec:3.6.1.34) (de:(dicyclohexylcarbodiimide-binding protein)) (db:swissprot) ATPL\_ECOLI P00844 ESCHERICHIA COLI 562 -11532820 125192 atpe:unce h+-transporting atp synthase:lipid-binding protein:dccd-binding protein:hydrogen ion-transporting atpase chain c (cl:h+-transporting atp synthase lipid-binding protein) (ec:3.6.1.34) (db:pir1.dat) (mp:84 min) LWECA B93732 Escherichia coli 562 -11532820 232436 (db:genpept-bct1) (de:e. coli atp (or unc) operon including promoter and five genes for subunits of atp synthetase and membrane proteins.) (nt:reading frame gene 3 (proteolipid, c)) (le:1440) (re:1679) (di:direct) ECATPX V00264 g41026 Escherichia coli 562 -11532820 234128 atpe (db:genpept-bct1) (de:e. coli genes atpb, atpe, atpf, atph and part of atpa. these genes code for the subunits a, c, b, delta and alpha (respectively) of the f0 subunit of atpase.) (le:1017) (re:1256) (di:direct) ECATPXB V00266 g41032 Escherichia coli 562 -11532820 234620 (sr:e.coli (strain ky7625) dna, clone pmcr533) (db:genpept-bct1) (de:e.coli dicyclohexylcarbodiimide-binding protein gene, complete cds.) (nt:dicyclohexylcarbodiimide-binding protein) (le:1) (re:240) (di:direct) ECODCCDP M12214 g145714 Escherichia coli 562 -11532820 236265 integral membrane proton channel f0 subunit c (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli h+ atpase alpha, beta, gamma, delta and epsilon, and integral membrane proton channel a, b, and c subunit genes, complete cds.) (le:1428) (re:1667) (di:direct) ECOHATP M25464 g146320 Escherichia coli 562 -11532820 236974 unce (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli atp (unc) operon containing nine genes coding for atp synthase subunits.) (nt:atp synthase c subunit (atp-3)) (le:1886) (re:2125) (di:direct) ECOUNC J01594 g148134 Escherichia coli 562 -11532820 240348 atpe::cg site no. 29 atp synthase f0 subunit c:dccd-binding protein (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:alternate gene names unce, paph) (le:110342) (re:110581) (di:complement) ECOUW82 L10328 g290586 Escherichia coli 562 -11532820 240357 (db:genpept-bct1) (de:e. coli origin of replication oric and genes gid, unc, ecourf-1 and glms.) (nt:unce protein) (le:4848) (re:5087) (di:direct) ECUNC X01631 g43261 Escherichia coli 562 -11532820 5000690164 (db:genpept-bct1) (de:e. coli gene unce fragment encoding f1-f0-atpase c-subunit.) (nt:c-subunit) (le:<1) (re:240) (di:direct) ECUNCE V01506 g43270 Escherichia coli 562 -11532820 232430 atpe membrane-bound atp synthase:f0 sector:subunit (fn:enzyme; atp-proton motive force) (db:genpept-bct2) (ec:3.6.1.34) (de:escherichia coli k-12 mg1655 section 340 of 400 of the complete genome.) (nt:f79; 100 pct identical to atpl\_ecoli sw: p00844;) (le:9403) (re:9642) (di:complement) AE000450 AE000450 g1790175 Escherichia coli 562 -11532820 61128 atpe:unce:paph (ec:3.6.1.34)

coli 562 -11532820 61128 atpe:unce:paph (ec:3.6.1.34)

(de:(dicyclohexylcarbodiimide-binding protein)) (db:swissprot) ATPL - ECOLI

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
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7501823352	7458	29614	1251	417
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Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
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7501823358	7459	29615	198	65
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Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823367	7460	29616	1419	472

Description

6500728963 atpb:uncb:papd:b3738 atp synthase f0 subunit a:atp synthase a chain:protein 6 (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (rileyfc:1.2.8) (db:gtc-escherichia coli) b3738 b3738 Escherichia coli 562 -11532821 304549 atpb:uncb:papd (ec:3.6.1.34) (de:atp synthase a chain, (protein 6)) (db:swissprot) ATP6\_ECOLI P00855 ESCHERICHIA COLI 562 -11532821 125216 atpb:uncb h+-transporting atp synthase:protein 6:hydrogen ion-transporting atp synthase chain a (cl:h+-transporting atp synthase protein 6) (ec:3.6.1.34) (db:pir1.dat) (mp:84 min) LWEC6 C93732 Escherichia coli 562 -11532821 232434 (db:genpept-bct1) (de:e. coli atp (or unc) operon including promoter and five genes for subunits of atp synthetase and membrane proteins.) (nt:reading frame gene 2 (a)) (le:578) (re:1393) (di:direct) ECATPX V00264 g41025 Escherichia coli 562 -11532821 236264 atpb (db:genpept-bct1) (de:e. coli genes atpb, atpe, atpf, atph and part of atpa. these genes code for the subunits a, c, b, delta and alpha (respectively) of the f0 subunit of atpase.) (nt:alternate atpb cds) (le:155) (re:970) (di:direct) ECATPXB V00266 g669111 Escherichia coli 562 -11532821 236975 uncb (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli atp (unc) operon containing nine genes coding for atp synthase subunits.) (nt:atp synthase a subunit (atp-2)) (le:1024) (re:1839) (di:direct) ECOUNC J01594 g148133 Escherichia coli 562 -11532821 240347 atpb::cg site no. 32 atp synthase f0 subunit a (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:alternate gene names uncb, papd) (le:110628) (re:111443) (di:complement) ECOUW82 L10328 g290587 Escherichia coli 562 -11532821 5000690165 (db:genpept-bct1) (de:e. coli origin of replication oric and genes gid, unc, ecourf-1 and glms.) (nt:uncb protein) (le:3986) (re:4801) (di:direct) ECUNC X01631 g43260 Escherichia coli 562 -11532821 232429 atpb membrane-bound atp synthase:f0 sector:subunit (fn:enzyme; atp-proton motive force) (db:genpept-bct2) (ec:3.6.1.34) (de:escherichia coli k-12 mg1655 section 340 of 400 of the complete genome.) (nt:f271; 100 pct identical to atp6\_ecoli sw: p00855;) (le:9689) (re:10504) (di:complement) AE000450 AE000450 g1790176 Escherichia coli 562 -11532821 60670 atpb:uncb:papd (ec:3.6.1.34) (de:atp synthase a chain, (protein 6)) (db:swissprot) ATP6\_ECOLI P00855 ESCHERICHIA COLI 562 -11532821

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823384	7461	29617	246	81

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823387	7462	29618	993	330

Description

6500728964 atpi:b3739 atp synthase subunit (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (rileyfc:1.2.8) (db:gtc-escherichia coli) b3739 b3739  
Escherichia coli 562 -11532822 131647 atpi:unci unci protein:atp synthase subunit atpi (cl:unci protein) (db:pir1.dat) (mp:84 min) BVECUI D30389  
Escherichia coli 562 -11532822 232428 (db:genpept-bct1) (de:e. coli atp operon promoter region.) (nt:atpj gene product (aa 1-128)) (le:654) (re:1046) (di:direct) ECATPP X01383 g581043 Escherichia coli 562 -11532822 236263 (db:genpept-bct1) (de:e. coli atp (or unc) operon including promoter and five genes for subunits of atp synthetase and membrane proteins.) (nt:reading frame gene 1 (a)) (le:177) (re:569) (di:direct) ECATPX V00264 g581044 Escherichia coli 562 -11532822 236976 unci (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli atp (unc) operon containing nine genes coding for atpsynthase subunits.) (nt:atp synthase unci polypeptide (atp-1; gtg start) (le:623) (re:1015) (di:direct) ECOUNC J01594 g148132 Escherichia coli 562 -11532822 240346 atpi::cg site no. 1... atp synthase subunit? (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:alternate gene name unci) (le:111452) (re:111844) (di:complement) ECOUW82 L10328 g290588 Escherichia coli 562 -11532822 7500953671 (db:genpept-bct1) (de:e. coli origin of replication oric and genes gid, unc, ecourf-1 and glms.) (nt:unci protein) (le:3585) (re:3977) (di:direct) ECUNC X01631 g581248 Escherichia coli 562 -11532822 232425 atpi membrane-bound atp synthase:dispensable (fn:enzyme; atp-proton motive force) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 340 of 400 of the complete genome.) (nt:f130; alternate gene name unci; cg site no. 18511) (le:10513) (re:10905) (di:complement) AE000450 AE000450 g1790177 Escherichia coli 562 -11532822 5000690166 (de:(ecoli\_3657) (pn:membrane-bound atp synthase, dispensable protein) (gn:atpi) (gtcfc:2.1) (ec:3.6.1.34) (atpz\_ecoli) (keggfc:2.1) (rileyfc:1.2.8) (db:gtc-escherichia coli)) ECOLI\_3657 ECOLI\_3657 Escherichia coli 562 10068169

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823391	7463	29619	879	292
<u>Description</u>				
6500728965 ppa:b4226 pyrophosphate phospho:inorganic pyrophosphatase:pyrophosphate phospho-hydrolase:ppase (gtcfc:2.1:2.3) (ec:3.6.1.1) (keggfc:2.1) (rileyfc:1.3.1) (db:gtc-escherichia coli) b4226 b4226 Escherichia coli 562 -11532823 125069 ppa inorganic pyrophosphatase::pyrophosphate phosphohydrolase (cl:inorganic pyrophosphatase) (ec:3.6.1.1) (db:pir1.dat) (mp:100 min) PWEA A27648 Escherichia coli 562 -11532823 237432 ppa inorganic pyrophosphatase (db:genpept-bct1) (ec:3.6.1.1) (de:escherichia coli inorganic pyrophosphatase (ppa) gene, completecds.) (le:292) (re:822) (di:direct) ECOPPA M23550 g450373 Escherichia coli 562 -11532823 7500953316 ppa (fn:inorganic pyrophosphatase) (db:genpept-bct1) (ec:3.6.1.1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:139954) (re:140484) (di:complement) ECOUW93 U14003 g537068 Escherichia coli 562 -11532823 235541 ppa inorganic pyrophosphatase (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (ec:3.6.1.1) (de:escherichia coli k-12 mg1655 section 384 of 400 of the completegenome.) (nt:f176; 100 pct identical amino acid sequence and) (le:809) (re:1339) (di:complement) AE000494 AE000494 g1790673 Escherichia coli 562 -11532823 5000690167 (de:(ecoli_4109) (pn:inorganic pyrophosphatase) (gn:ppa) (gtcfc:2.1) (ec:3.6.1.1) (ipyr_ecoli) (keggfc:2.1) (rileyfc:1.3.1) (db:gtc-escherichia coli)) ECOLI_4109 ECOLI_4109 Escherichia coli 562 10066269				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823410	7464	29620	519	172
<u>Description</u>				
6500728966 gntr:b3438 gtnukr operon regulator (gtcfc:2.1) (keggfc:14.2) (rileyfc:1.2.5) (db:gtc-escherichia coli) b3438 b3438 Escherichia coli 562 -11532824 7000690901 gntr gtnukr operon regulator (cl:gntr protein) (db:pir2.dat) A65140 A65140 Escherichia coli 562 -11532824 7500959758 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f313) (le:358522) (re:359463) (di:complement) ECOUW67 U18997 g606373 Escherichia coli 562 -11532824 236672 gntr regulator of gluconate gnt operon (fn:regulator; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 310 of 400 of the completegenome.) (nt:f313; 100 pct identical amino acid sequence and) (le:4175) (re:5116) (di:complement) AE000420 AE000420 g1789846 Escherichia coli 562 -11532824				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823418	7465	29621	453	150

Description

6500728967 mpha:b0347 hypothetical protein:3-:3-hydroxy-phenylpropionate hydroxylase (gtcfc:1.10) (ec:1.14.13.-)  
 (keggfc:2.2:3.4:3.5:3.7:5.11:5.13:5.14:9.13:9.14) (rileyfc:5.7.0)  
 (db:gtc-escherichia coli) b0347 b0347 Escherichia coli 562 -11532825 239964 mpha (ec:1.14.13.-) (de:3-(3-hydroxy-phenyl)propionate hydroxylase,)  
 (db:swissprot) MHPA\_ECOLI P77397 ESCHERICHIA COLI 562 -11532825 7000685840 mpha probable monooxygenase:mpha (ec:1.14.13.-) (db:pir2.dat) C64762 C64762 Escherichia coli 562 -11532825 5000691526 mpha 3-3-hydroxy-phenyl propionate hydroxylase (db:genpept-bct1) (de:e.coli mhp cluster for 3-hydroxy-phenylpropionic acid degradation.) (nt:putative) (le:1043) (re:2707) (di:direct) ECMHP Y09555 g1702881 Escherichia coli 562 -11532825 7500885607 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:similar to putative oxygenase of s. fradiae) (le:76406) (re:78070) (di:direct) ECU73857 U73857 g1657543 Escherichia coli 562 -11532825 233384 mpha 3-3-hydroxyphenyl propionate hydroxylase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 32 of 400 of the completegenome.) (nt:o554; this 554 aa orf is 23 pct identical (8 gaps)) (le:69) (re:1733) (di:direct) AE000142 AE000142 g1786543 Escherichia coli 562 -11532825 120050 mpha (ec:1.14.13.-) (de:3-(3-hydroxy-phenyl)propionate hydroxylase,) (db:swissprot) MHPA\_ECOLI P77397 ESCHERICHIA COLI 562 -11532825

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823421	7466	29622	870	289

Description

GTC ORF with score 169 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c09d4.) (nt:weak similarity to bacillus and pseudomonas) (le:19132:20065:20385:20902) (re:19176:20211:20597:20935) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823432	7467	29623	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823438	7468	29624	1971	657

# Description

6500728968 torc:b0996 cytochrome c-type protein torc (gtcfc:2.8:12.13) (ec:1.6.6.9) (keggfc:2.2:12.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b0996 b0996 Escherichia coli 562 -11532826 101828 torc (de:cytochrome c-type protein torc) (db:swissprot) TORC\_ECOLI P33226 ESCHERICHIA COLI 562 -11532826 7000686814 torc cytochrome c-type protein torc (cl:membrane-bound cytochrome torc:nirt homology) (db:pir1.dat) S34221 B64841 Escherichia coli 562 -11532826 223318 torc cytochrome c-type protein torc (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept-bct1) (de:escherichia coli genomic dna. (22.5 - 22.9 min).) (le:12579) (re:13751) (di:direct) D90736 D90736 g1651488 Escherichia coli 562 -11532826 223323 torc cytochrome c-type protein torc (sr:escherichia coli(strain:k12) dna, clone:kohara clone #227) (db:genpept-bct1) (de:escherichia coli genomic dna. (22.7 - 23.0 min).) (le:3581) (re:4753) (di:direct) D90737 D90737 g1651494 Escherichia coli 562 -11532826 7500893272 torc trimethylamine n-oxide reductase:cytochrome (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 91 of 400 of the completegenome.) (nt:o390; 99 pct identical to torc\_ecoli sw: p33226) (le:6857) (re:8029) (di:direct) AE000201 AE000201 g1787230 Escherichia coli 562 -11532826 5000690168 torc cytochrome c-type protein torc. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #227) (db:genpept) (de:escherichia coli genomic dna. (22.8 - 23.1 min).) (nt:orf\_id:o227#3; similar to swissprot accession) (le:3581) (re:4753) (di:direct) D90737 D90737 g1651494 Escherichia coli 562 -11532826 7502851820 torc cytochrome c-type protein torc. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept) (de:escherichia coli genomic dna. (22.6 - 23.0 min).) (nt:orf\_id:o227#3; similar to swissprot accession) (le:12579) (re:13751) (di:direct) D90736 D90736 g1651488 Escherichia coli 562 -11532826

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823444	7469	29625	405	134

Description

6500728969 tora:b0997 trimethylamine-n-oxide reductase precursor:tmao reductase:trimethylamine oxidase (gtcfc:2.2:2.8:12.13) (ec:1.6.6.9) (keggfc:2.2:12.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b0997 b0997 Escherichia coli 562 -11532827 101827 tora (ec:1.6.6.9) (de:reductase) (trimethylamine oxidase)) (db:swissprot) TORA\_ECOLI P33225 ESCHERICHIA COLI 562 -11532827 7000686813 tora trimethylamine-n-oxide reductase:precursor (cl:trimethylamine-n-oxide reductase) (ec:1.6.6.9) (db:pir2.dat) C64841 C64841 Escherichia coli 562 -11532827 223319 tora trimethylamine-n-oxide reductase precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept-bct1) (de:escherichia coli genomic dna. (22.5 - 22.9 min).) (le:13751) (re:16297) (di:direct) D90736 D90736 g1651489 Escherichia coli 562 -11532827 223324 tora trimethylamine-n-oxide reductase precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #227) (db:genpept-bct1) (de:escherichia coli genomic dna. (22.7 - 23.0 min).) (le:4753) (re:7299) (di:direct) D90737 D90737 g1651495 Escherichia coli 562 -11532827 7500893271 tora trimethylamine n-oxide reductase subunit (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (ec:1.6.6.9) (de:escherichia coli k-12 mg1655 section 91 of 400 of the completegenome.) (nt:o848; 98 pct identical to tora\_ecoli sw: p33225) (le:8029) (re:10575) (di:direct) AE000201 AE000201 g1787231 Escherichia coli 562 -11532827 5000690169 tora trimethylamine-n-oxide reductase precursor ec (sr:escherichia coli(strain:k12) dna, clone:kohara clone #227) (db:genpept) (de:escherichia coli genomic dna. (22.8 - 23.1 min).) (nt:orf\_id:o227#4; similar to swissprot accession) (le:4753) (re:7299) (di:direct) D90737 D90737 g1651495 Escherichia coli 562 -11532827 7502851821 tora trimethylamine-n-oxide reductase precursor ec (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept) (de:escherichia coli genomic dna. (22.6 - 23.0 min).) (nt:orf\_id:o227#4; similar to swissprot accession) (le:13751) (re:16297) (di:direct) D90736 D90736 g1651489 Escherichia coli 562 -11532827

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823445	7470	29626	777	258

Description

6500728970 kate:b1732 catalase hpii:hydroxyperoxidase ii  
 (gtcfc:2.2:5.14:12.12) (ec:1.11.1.6) (keggfc:2.2:5.14) (rileyfc:4.7.0)  
 (db:gtc-escherichia coli) b1732 b1732 Escherichia coli 562 -11532828  
 7500974860 kate catalase:hydroperoxidase hpii iii (fn:enzyme;  
 detoxification) (db:genpept-bct2) (ec:1.11.1.6) (de:escherichia coli k-12  
 mg1655 section 158 of 400 of the completegenome.) (nt:o753; 99 pct identical  
 to cate\_ecoli sw: p21179; cg) (le:3774) (re:6035) (di:direct) AE000268  
 AE000268 g1788027 Escherichia coli 562 -11532828 5000690170  
 (de:(ecoli\_1689) (pn:catalase; hydroperoxidase hpii:iii) (gn:kate)  
 (gtcfc:2.2:5.14) (ec:1.11.1.6) (cate\_ecoli) (keggfc:2.2:5.14)  
 (rileyfc:4.7.0) (db:gtc-escherichia coli)) ECOLI\_1689 ECOLI\_1689 Escherichia  
 coli 562 10123441

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823471	7471	29627	543	180

# Description

6500728971 glya:b2551 serine hydroxymethyltransferase:serine methylase:shmt  
(gtcfc:2.2:5.3:5.9:6.5:9.3:9.6) (ec:2.1.2.1)  
(keggfc:2.2:5.3:5.9:6.5:9.3:9.8) (rileyfc:1.4.3) (db:gtc-escherichia coli)  
(gtcfc:energy metabolism-methane metabolism:l-amino acid  
metabolism-glycine--serine and threonine metabolism:l-amino acid  
metabolism... b2551 b2551 Escherichia coli 562 -11532829 234548 glya  
(ec:2.1.2.1) (de:(shmt)) (db:swissprot) GLYA\_ECOLI P00477 ESCHERICHIA COLI  
562 -11532829 123289 glya glycine hydroxymethyltransferase::serine  
methylase (cl:glycine hydroxymethyltransferase) (ec:2.1.2.1) (db:pir1.dat)  
(mp:55 min) XYECS A00559 Escherichia coli 562 -11532829 225148 glya serine  
hydroxymethyltransferase ec 2.1.2.1 (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #432(57.5-57.9 min.)) (nt:similar to (swissprot accession  
number p00477)) (le:12283) (re:13536) (di:complement) D90885 D90885 g1799975  
Escherichia coli 562 -11532829 5000690171 (db:genpept-bct1) (de:e. coli  
gene glya coding for serine hydroxymethyltransferase(shmt), responsible for  
the conversion of serine to glycine and5,10-methylenetetrahydrofolate.)  
(nt:reading frame glya) (le:181) (re:1434) (di:direct) ECGLYA V00283 g41603  
Escherichia coli 562 -11532829 7500882595 glya serine  
hydroxymethyltransferase (sr:escherichia coli k12 dna) (db:genpept-bct1)  
(ec:2.1.2.1) (de:e.coli glya gene coding for serine  
hydroxymethyltransferase,complete cds.) (le:358) (re:1611) (di:direct)  
ECOGLYA J01620 g146218 Escherichia coli 562 -11532829 233025 glya serine  
hydroxymethyltransferase (fn:enzyme; amino acid biosynthesis: glycine)  
(db:genpept-bct2) (ec:2.1.2.1) (de:escherichia coli k-12 mg1655 section 231  
of 400 of the completegenome.) (nt:f417; 100 pct identical to glya\_ecoli sw:  
p00477) (le:4869) (re:6122) (di:complement) AE000341 AE000341 g1788902  
Escherichia coli 562 -11532829 74195 glya (ec:2.1.2.1) (de:(shmt))  
(db:swissprot) GLYA\_ECOLI P00477 ESCHERICHIA COLI 562 -11532829

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823472	7472	29628	264	87
<u>Description</u>				

6500728972 ubih:visb:b2907 ubih protein  
 (gtcfc:2.2:3.4:3.5:3.7:5.11:5.13:5.14:9.12:9.13) (ec:1.14.13.-)  
 (keggfc:2.2:3.4:3.5:3.7:5.11:5.13:5.14:9.13:9.14) (rileyfc:1.7.11)  
 (db:gtc-escherichia coli) b2907 b2907 Escherichia coli 562 -11532830  
 7000689007 ubih:ubih::visb ubih protein::visb protein (cl:ubih protein)  
 (ec:1.14.13.-) (db:pir2.dat) (mp:63 min) C65075 C65075 Escherichia coli 562  
 -11532830 7500953723 ubih (db:genpept-bct1) (de:escherichia coli k-12  
 genome; approximately 65 to 68 minutes.) (nt:orf\_f392) (le:6731) (re:7909)  
 (di:complement) ECU28377 U28377 g882437 Escherichia coli 562 -11532830  
 239121 ubih 2-octaprenyl-6-methoxyphenol-- (fn:enzyme; biosynthesis of  
 cofactors, carriers:) (db:genpept-bct2) (ec:1.14.13.-) (de:escherichia coli  
 k-12 mg1655 section 264 of 400 of the completegenome.) (nt:f392; 99 pct  
 identical to ubih\_ecoli sw: p25534) (le:3270) (re:4448) (di:complement)  
 AE000374 AE000374 g1789274 Escherichia coli 562 -11532830 5000690172  
 (de:(ecoli\_2830) (pn:2-octaprenyl-6-methoxyphenol--)) (gn:ubih)  
 (gtcfc:2.2:3.4:3.5:3.6:3.7:5.11:5.14:9.12) (ec:1.14.13.-) (ubih\_ecoli)  
 (keggfc:2.2:3.4:3.5:3.6:3.7:5.11:5.14:9.13) (rileyfc:1.7.11)  
 (db:gtc-escherichia coli)) ECOLI\_2830 ECOLI\_2830 Escherichia coli 562  
 10123905

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823477	7473	29629	210	69
<u>Description</u>				

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823488	7474	29630	639	212

Description

6500728973 metf:b3941 5:10 methylenetetrahydrofolate reductase:5:10-methylenetetrahydrofolate reductase (gtcfc:10.7:2.3:9.6) (ec:1.7.99.5) (keggfc:2.2:9.8) (rileyfc:1.3.1) (db:gtc-escherichia coli) (gtcfc:metabolism of macromolecules-protein translation and modification:energy metabolism-glyoxylate cycle:metabolism of cofactors and vitamins-biotin metabo... b3941 b3941 Escherichia coli 562 -11532831 237158 metf (ec:1.7.99.5) (de:5,10-methylenetetrahydrofolate reductase,) (db:swissprot) METF\_ECOLI P00394 ESCHERICHIA COLI 562 -11532831 122914 metf 5:10-methylenetetrahydrofolate reductase fadh2 (cl:5,10-methylenetetrahydrofolate reductase (fadh2)) (ec:1.7.99.5) (db:pir1.dat) (mp:89 min) RDECMH A00462 Escherichia coli 562 -11532831 5000690666 (db:genpept-bct1) (de:e. coli gene metf coding 5-10 methylene tetrahydrofolate reductase.) (nt:reading frame metf) (le:109) (re:999) (di:direct) ECMETF V01502 g42000 Escherichia coli 562 -11532831 7500885533 metf 5:10 methylenetetrahydrofolate reductase (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 511) (le:94249) (re:95139) (di:direct) ECOUW87 L19201 g305044 Escherichia coli 562 -11532831 233379 metf 5:10-methylenetetrahydrofolate reductase (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (ec:1.7.99.5) (de:escherichia coli k-12 mg1655 section 358 of 400 of the completegenome.) (nt:o296; 100 pct identical amino acid sequence and) (le:4167) (re:5057) (di:direct) AE000468 AE000468 g1790377 Escherichia coli 562 -11532831 83549 metf (ec:1.7.99.5) (de:5,10-methylenetetrahydrofolate reductase,) (db:swissprot) METF\_ECOLI P00394 ESCHERICHIA COLI 562 -11532831

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823496	7475	29631	426	141

#### Description

6500728974 katg:b3942 catalase hydroperoxidase i:catalase  
 hpi:hydroperoxidase i (gtcfc:2.2:5.14:12.12) (ec:1.11.1.6) (keggfc:2.2:5.14)  
 (rileyfc:4.7.0) (db:gtc-escherichia coli) b3942 b3942 Escherichia coli 562  
 -11532832 62934 katg (ec:1.11.1.6) (de:catalase hpi, (hydroperoxidase i))  
 (db:swissprot) CATA\_ECOLI P13029 ESCHERICHIA COLI 562 -11532832 7000684754  
 katg catalase:hpi:catalase-peroxidase:hydroperoxidase i (cl:catalase hpi)  
 (ec:1.11.1.6) (db:pir1.dat) (mp:89.2 min) CSECHP A65201 Escherichia coli 562  
 -11532832 7500878201 katg catalase:hydroperoxidase hpi i (fn:enzyme;  
 detoxification) (db:genpept-bct2) (ec:1.11.1.6) (de:escherichia coli k-12  
 mg1655 section 358 of 400 of the completegenome.) (nt:o726; 99 pct identical  
 amino acid sequence and) (le:5386) (re:7566) (di:direct) AE000468 AE000468  
 g1790378 Escherichia coli 562 -11532832 5000690173 (de:(ecoli\_3840)  
 (pn:catalase; hydroperoxidase hpi:i) (gn:katg) (gtcfc:2.2:5.14)  
 (ec:1.11.1.6) (cata\_ecoli) (keggfc:2.2:5.14) (rileyfc:4.7.0)  
 (db:gtc-escherichia coli)) ECOLI\_3840 ECOLI\_3840 Escherichia coli 562  
 10005608

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823500	7476	29632	687	228

#### Description

6500728975 pfla:act:b0902 pyruvate formate-lyase 1 activating enzyme  
 (gtcfc:2.2) (ec:1.97.1.4) (keggfc:14.1) (rileyfc:1.2.7) (db:gtc-escherichia  
 coli) b0902 b0902 Escherichia coli 562 -11532833 163077 pfla:act pyruvate  
 formate-lyase activating enzyme::lyase 1-specific:formate  
 c-acetyltransferase 1-activating enzyme:pyruvate formate-lyase i  
 activase:formate c-acetyltransferase 1-activating enzyme:pyruvate  
 formate-lyase i activase (cl:pyruvate formate-lyase activating enzyme)  
 (sr:strain k-12, , strain k-12) (sr:strain k-12, ) (ec:1.97.1.4)  
 (db:pir1.dat) (mp:20.5) S01789 S01789 Escherichia coli 562 -11532833  
 7500960443 (db:genpept-bct1) (de:e. coli pfl gene for pyruvate  
 formate-lyase (ec 2.3.1.54).) (nt:pyruvate formate-lyase activating enzyme  
 (aa) (le:2575) (re:3315) (di:direct) ECPFL X08035 g42371 Escherichia coli  
 562 -11532833 237794 pfla pyruvate formate lyase activating enzyme 1  
 (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2)  
 (ec:1.97.1.4) (de:escherichia coli k-12 mg1655 section 82 of 400 of the  
 completegenome.) (nt:f246; 100 pct identical to pfla\_ecoli sw: p09374)  
 (le:4656) (re:5396) (di:complement) AE000192 AE000192 g1787130 Escherichia  
 coli 562 -11532833 7502851822 act pyruvate formate-lyase 1 activating  
 enzyme ec (sr:escherichia coli(strain:k12) dna, clone:kohara clone #216)  
 (db:genpept) (de:escherichia coli genomic dna. (20.4 - 20.8 min).)  
 (nt:orf\_id:o216#6; similar to swissprot accession) (le:6033) (re:6773)  
 (di:complement) D90728 D90728 g4062478 Escherichia coli 562 -11532833

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823511	7477	29633	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823517	7478	29634	1260	419

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823521	7479	29635	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823524	7480	29636	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823539	7481	29637	459	152

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823558	7482	29638	477	159

Description

6500728976 hycg:hevg:b2719 formate hydrogenlyase subunit 7:fhl subunit 7:hydrogenase-3 component g (gtcfc:2.2) (keggfc:14.2) (rileyfc:1.2.7) (db:gtc-escherichia coli) b2719 b2719 Escherichia coli 562 -11532834 78426 hycg:hevg (de:component g) (db:swissprot) HYCG\_ECOLI P16433 ESCHERICHIA COLI 562 -11532834 164384 hycg formate hydrogenlyase subunit 7 (cl:psbg protein) (db:pir2.dat) (mp:58-59 min) S08625 S08625 Escherichia coli 562 -11532834 7500883697 hycg formate hydrogenlyase subunit 7 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg site no. 33151; alternate gene name hevg) (le:15747) (re:16514) (di:complement) ECU29579 U29579 g882612 Escherichia coli 562 -11532834 239293 hycg hydrogenase activity (fn:phenotype; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 246 of 400 of the completgenome.) (nt:f255; 99 pct identical to hycg\_ecoli sw: p16433; cg) (le:980) (re:1747) (di:complement) AE000356 AE000356 g1789074 Escherichia coli 562 -11532834

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823564	7483	29639	435	145

Description

6500728977 hycc:hevc:b2723 formate hydrogenlyase subunit 3:fhl subunit 3:hydrogenase-3 component c (gtcfc:2.2) (keggfc:14.2) (rileyfc:1.2.7) (db:gtc-escherichia coli) b2723 b2723 Escherichia coli 562 -11532835 78422 hycc:hevc (de:component c) (db:swissprot) HYCC\_ECOLI P16429 ESCHERICHIA COLI 562 -11532835 7000685580 hycc formate hydrogenlyase chain 3:probable hydrogenase 3 protein 3 (cl:formate hydrogenlyase chain 3) (db:pir2.dat) (mp:58 min) G65052 G65052 Escherichia coli 562 -11532835 7500883693 hycc membrane-spanning protein of hydrogenase 3 part (fn:enzyme; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 246 of 400 of the completgenome.) (nt:f608; 99 pct identical to hycc\_ecoli sw: p16429; cg) (le:4952) (re:6778) (di:complement) AE000356 AE000356 g2367154 Escherichia coli 562 -11532835

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823567	7484	29640	423	141

Description

6500728978 hyca:heva:b2725 formate hydrogenlyase regulatory protein:formate hydrogenlyase regulatory protein hyca (gtcfc:2.2) (keggfc:14.2) (rileyfc:1.2.7) (db:gtc-escherichia coli) b2725 b2725 Escherichia coli 562 -11532836 239299 hyca:heva (de:formate hydrogenlyase regulatory protein hyca) (db:swissprot) HYCA\_ECOLI P16427 ESCHERICHIA COLI 562 -11532836 164378 hyca formate hydrogenlyase regulatory protein:probable hydrogenase 3 protein 1 (db:pir2.dat) (mp:58-59 min) S08619 S08619 Escherichia coli 562 -11532836 7500883691 hyca (db:genpept-bct1) (de:e.coli hyc operon hyca,b,c,d,e,f,g,h,i genes.) (le:212) (re:673) (di:direct) ECHYC X17506 g41680 Escherichia coli 562 -11532836 7502851823 hyca formate hydrogenlyase regulatory protein (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg site no. 33143; alternate gene name heva;) (le:22278) (re:22739) (di:complement) ECU29579 U29579 g882618 Escherichia coli 562 -11532836 233171 hyca transcriptional repression of hyc and hyp (fn:regulator; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 246 of 400 of the completegenome.) (nt:f153; 100 pct identical to hyca\_ecoli sw: p16427;) (le:7511) (re:7972) (di:complement) AE000356 AE000356 g1789080 Escherichia coli 562 -11532836 78420 hyca:heva (de:formate hydrogenlyase regulatory protein hyca) (db:swissprot) HYCA\_ECOLI P16427 ESCHERICHIA COLI 562 -11532836

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823568	7485	29641	792	263

Description

6500728979 hypb:b2727 hydrogenase isoenzymes formation protein hypb (gtcfc:2.2) (keggfc:14.2) (rileyfc:1.2.7) (db:gtc-escherichia coli) b2727 b2727 Escherichia coli 562 -11532837 78465 hypb (de:hydrogenase isoenzymes formation protein hypb) (db:swissprot) HYPB\_ECOLI P24190 ESCHERICHIA COLI 562 -11532837 7000685594 hypb hydrogenase isoenzymes formation protein hypb (cl:hydrogenase expression/formation protein hypb) (db:pir2.dat) C65053 C65053 Escherichia coli 562 -11532837 7500883725 hypb (fn:required for formation of all 3 hydrogenase) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg site no. 33110; orf\_o290) (le:23305) (re:24177) (di:direct) ECU29579 U29579 g882620 Escherichia coli 562 -11532837 239301 hypb guanine-nucleotide binding protein:functions as (fn:phenotype; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 246 of 400 of the completegenome.) (nt:o290; 99 pct identical amino acid sequence and) (le:8538) (re:9410) (di:direct) AE000356 AE000356 g1789082 Escherichia coli 562 -11532837

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823579	7486	29642	246	81

Description

6500728980 fhla:b2731 transcriptional activator of the formate hydrogenlyase system:formate hydrogenlyase transcriptional activator (gtcfc:10.2:2.2) (keggfc:14.2) (rileyfc:1.2.7) (db:gtc-escherichia coli) b2731 b2731 Escherichia coli 562 -11532838 239305 fhla (de:formate hydrogenlyase transcriptional activator) (db:swissprot) FHLA\_ECOLI P19323 ESCHERICHIA COLI 562 -11532838 164734 fhla transcription activator fhla:formate hydrogen lyase system transcriptional activator (cl:transcription activator fhla:rna polymerase sigma factor interaction domain homology) (db:pir2.dat) S12079 S12079 Escherichia coli 562 -11532838 7500881437 (db:genpept-bct1) (de:e.coli fhla gene for the transcriptional activator of the formatehydrogenlyase.) (nt:fhla gene product (aa 1-692)) (le:73) (re:2151) (di:direct) ECFHLAT X52227 g41437 Escherichia coli 562 -11532838 7502851824 fhla transcriptional activator of the formate (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg site no. 18370; orf\_o692) (le:26642) (re:28720) (di:direct) ECU29579 U29579 g882624 Escherichia coli 562 -11532838 232858 fhla formate hydrogen-lyase transcriptional activator (fn:regulator; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 247 of 400 of the completgenome.) (nt:o692; 100 pct identical to fhla\_ecoli sw: p19323;) (le:67) (re:2145) (di:direct) AE000357 AE000357 g1789087 Escherichia coli 562 -11532838 71549 fhla (de:formate hydrogenlyase transcriptional activator) (db:swissprot) FHLA\_ECOLI P19323 ESCHERICHIA COLI 562 -11532838

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823584	7487	29643	1056	351

Description

GTC ORF with score 200 to: (sr:streptomyces thermoviolaceus (strain:opc-520) dna) (db:genpept-bct2) (ec:3.2.1.30) (de:streptomyces thermoviolaceus naga gene forbета-n-acetylglucosaminidase, complete cds.) (le:400) (re:2298) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823586	7488	29644	726	241

Description

GTC ORF with score 512 to: (sr:streptomyces thermoviolaceus (strain:opc-520) dna) (db:genpept-bct2) (ec:3.2.1.30) (de:streptomyces thermoviolaceus naga gene forbета-n-acetylglucosaminidase, complete cds.) (le:400) (re:2298) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823602	7489	29645	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823605	7490	29646	297	98

Description

6500728981 pflc:b3952 probable pyruvate formate-lyase 2 activating enzyme (gtcfc:2.2) (ec:1.97.1.4) (keggfc:14.1) (rileyfc:1.2.7) (db:gtc-escherichia coli) b3952 b3952 Escherichia coli 562 -11532839 89198 pflc (ec:1.97.1.4) (de:probable pyruvate formate-lyase 2 activating enzyme,) (db:swissprot) PFLC\_ECOLI P32675 ESCHERICHIA COLI 562 -11532839 7000686122 pflc probable pyruvate formate-lyase 2 activating enzyme (ec:1.97.1.4) (db:pir2.dat) C65202 C65202 Escherichia coli 562 -11532839 7500887893 pflc probable pyruvate formate lyase activating (fn:putative enzyme; energy metabolism, carbon:) (db:genpept-bct2) (ec:1.97.1.4) (de:escherichia coli k-12 mg1655 section 359 of 400 of the completegenome.) (nt:o292; 100 pct identical to pflc\_ecoli sw: p32675) (le:4026) (re:4904) (di:direct) AE000469 AE000469 g1790389 Escherichia coli 562 -11532839

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823611	7491	29647	378	125

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823617	7492	29648	1113	371

Description

6500728982 hyd:b4003 sensor protein hyd (gtcfc:2.2:12.13) (ec:2.7.3.-) (keggfc:12.1) (rileyfc:1.2.7) (db:gtc-escherichia coli) b4003 b4003 Escherichia coli 562 -11532840 78430 hyd (ec:2.7.3.-) (de:sensor protein hyd,) (db:swissprot) HYDH\_ECOLI P14377 ESCHERICHIA COLI 562 -11532840 7000685582 hyd hyd protein (db:pir2.dat) F65207 F65207 Escherichia coli 562 -11532840 237213 hyd sensor kinase for hyd:hydrogenase 3 activity (fn:enzyme; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 363 of 400 of the completegenome.) (nt:o465) (le:12288) (re:13685) (di:direct) AE000473 AE000473 g1790436 Escherichia coli 562 -11532840 7500883709 hyd (fn:member of two-component regulatory system) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:67167) (re:68564) (di:direct) ECOUW89 U00006 g396342 Escherichia coli 562 -11532840

Description

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823630	7494	29650	237	79

Description

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823631	7495	29651	891	296

#### Description

6500728984 cynt:b0339 cyanate permease:carbonic anhydrase (gtcfc:2.3:2.6) (ec:4.2.1.1) (keggfc:2.5) (rileyfc:1.3.1) (db:gtc-escherichia coli) b0339 b0339 Escherichia coli 562 -11532842 67525 cynt (ec:4.2.1.1) (de:carbonic anhydrase,) (db:swissprot) CYNT\_ECOLI P17582 ESCHERICHIA COLI 562 -11532842 7000684962 cynt carbonate dehydratase::carbonic anhydrase (cl:escherichia coli carbonate dehydratase) (ec:4.2.1.1) (db:pir1.dat) (mp:8 min) QRECTC C64761 Escherichia coli 562 -11532842 7500879860 cynt cyanate anhydrase (db:genpept-bct1) (ec:4.2.1.1) (de:escherichia coli chromosome minutes 6-8.) (le:66594) (re:67253) (di:direct) ECU73857 U73857 g1657535 Escherichia coli 562 -11532842 239956 cynt carbonic anhydrase (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (ec:4.2.1.1) (de:escherichia coli k-12 mg1655 section 31 of 400 of the completegenome.) (nt:o219; 97 pct identical (1 gap) to cynt\_ecoli) (le:1207) (re:1866) (di:direct) AE000141 AE000141 g1786534 Escherichia coli 562 -11532842 5000690189 (de:(ecoli\_323) (pn:carbonic anhydrase) (gn:cynt) (gtcfc:2.6) (ec:4.2.1.1) (cynt\_ecoli) (keggfc:2.5) (rileyfc:1.3.1) (db:gtc-escherichia coli)) ECOLI\_323 ECOLI\_323 Escherichia coli 562 10122783

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823639	7496	29652	255	84

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823652	7497	29653	333	110

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823665	7498	29654	261	86

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823671	7499	29655	339	112

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823681	7500	29656	468	155
<u>Description</u>				
6500728985 cysn:cnt:b0340 cyanate lyase:cyanate hydrolase:cyanase (gtcfc:2.3:2.6) (ec:4.3.99.1) (keggfc:2.5) (rileyfc:1.3.1) (db:gtc-escherichia coli) b0340 b0340 Escherichia coli 562 -11532843 67094 cysn:cnt (ec:4.3.99.1) (de:cyanate lyase, (cyanate hydrolase) (cyanase)) (db:swissprot) CYNS_ECOLI P00816 ESCHERICHIA COLI 562 -11532843 125066 cysn cyanate lyase::cyanase:cyanate aminohydrolase:cyanate c-n-lyase:cyanate hydrolase (cl:cyanate lyase) (ec:4.3.99.1) (db:pir1.dat) (mp:8 min) YNEC A91850 Escherichia coli 562 -11532843 234085 cysn cyanase (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli cyanate permease (cynt), cyanase (cysn) and protein of unknown function (cynx) genes, complete cds.) (le:808) (re:1278) (di:direct) ECOCYNOPRN M23219 g145643 Escherichia coli 562 -11532843 239957 (sr:e.coli (strain k12) dna, clones psj105) (db:genpept-bct1) (de:e.coli cysn gene encoding cyanase, complete cds.) (nt:cyanase protein (cysn)) (le:151) (re:621) (di:direct) ECOCYNSA M17891 g145648 Escherichia coli 562 -11532843 7500879858 cysn cyanate lyase (db:genpept-bct1) (ec:4.3.99.1) (de:escherichia coli chromosome minutes 6-8.) (le:67284) (re:67754) (di:direct) ECU73857 U73857 g1657536 Escherichia coli 562 -11532843 234082 cysn cyanate aminohydrolase:cyanase (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (ec:4.3.99.1) (de:escherichia coli k-12 mg1655 section 31 of 400 of the complete genome.) (nt:ol56; 100 pct identical to cyan_ecoli sw: p00816;) (le:1897) (re:2367) (di:direct) AE000141 AE000141 g1786535 Escherichia coli 562 -11532843 5000690190 (de:(ecoli_324) (pn:cyanate aminohydrolase, cyanase) (gn:cysn) (gtcfc:2.6) (ec:4.3.99.1) (cyan_ecoli) (keggfc:2.5) (rileyfc:1.3.1) (db:gtc-escherichia coli)) ECOLI_324 ECOLI_324 Escherichia coli 562 10009708				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823683	7501	29657	237	78

# Description

6500728986 appy:b0564 appy protein:m5 polypeptide (gtcfc:2.3) (keggfc:14.2) (rileyfc:1.3.1) (db:gtc-escherichia coli) b0564 b0564 Escherichia coli 562 -11532844 240073 appy (de:appy protein (m5 polypeptide)) (db:swissprot) APPY\_ECOLI P05052 ESCHERICHIA COLI 562 -11532844 131177 appy transcription regulator appy:m5 polypeptide (cl:m5 polypeptide) (db:pir1.dat) (mp:13 min) BVECM5 A94498 Escherichia coli 562 -11532844 5000690174 (db:genpept-bct1) (de:e. coli gene for m5 polypeptide.) (nt:m5 polypeptide (aa 1 - 249)) (le:1) (re:750) (di:direct) ECM5 Y00138 g41948 Escherichia coli 562 -11532844 7500877002 appy appy (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (le:24312) (re:25061) (di:direct) ECU82598 U82598 g1778477 Escherichia coli 562 -11532844 233338 appy regulatory protein affecting appa and other (fn:regulator; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 51 of 400 of the completegenome.) (nt:o249; 100 pct identical to gb: ecm5\_1 accession:) (le:6570) (re:7319) (di:direct) AE000161 AE000161 g1786776 Escherichia coli 562 -11532844 59884 appy (de:appy protein (m5 polypeptide)) (db:swissprot) APPY\_ECOLI P05052 ESCHERICHIA COLI 562 -11532844

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501823685	7502	29658	666	221

# Description

6500728987 lrp:alsb:livr:b0889 leucine-responsive regulatory protein (gtcfc:2.3) (keggfc:14.2) (rileyfc:1.3.1) (db:gtc-escherichia coli) b0889 b0889 Escherichia coli 562 -11532845 131516 lrp:alsb:livr transcription regulator lrp:leucine-responsive (cl:regulatory protein asnc) (db:pir1.dat) RGECLR JH0412 Escherichia coli 562 -11532845 7500885158 lrp leucine-responsive regulatory protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #214) (db:genpept-bct1) (de:escherichia coli genomic dna.(19.9 - 20.2 min).) (le:8475) (re:8969) (di:direct) D90726 D90726 g1651411 Escherichia coli 562 -11532845 223250 lrp leucine-responsive regulatory protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #215) (db:genpept-bct1) (de:escherichia coli genomic dna.(20.0 - 20.3 min).) (le:1778) (re:2272) (di:direct) D90727 D90727 g1651417 Escherichia coli 562 -11532845 223255 lrp (fn:leucine-responsive regulatory protein) (db:genpept-bct1) (de:enterobacter aerogenes leucine-responsive regulatory protein (lrp)gene, complete cds.) (le:1) (re:495) (di:direct) EAU02272 U02272 g407914 Enterobacter aerogenes 548 -11532845 235018 lrp::alsb leucine responsive regulatory protein (sr:escherichia coli (strain k12) dna, clone #213) (db:genpept-bct1) (de:e. coli lrp (alsb) gene encoding leucine responsive regulatoryprotein.) (le:462) (re:956) (di:direct) ECOLRP D11105 g216586 Escherichia coli 562 -11532845 235019 (sr:e.coli (strain k12) dna) (db:genpept-bct1) (de:e.coli leucine-responsive-regulatory protein (lrp) gene, completedcds.) (nt:leucine-responsive-regulatory protein (lrp)) (le:1) (re:495) (di:direct) ECOLRRPA M35869 g146665 Escherichia coli 562 -11532845 227890 lrp regulator for leucine or lrp regulon and (fn:regulator; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 81 of 400 of the completgenome.) (nt:o164; 100 pct identical to lrp\_ecoli sw: p19494) (le:303) (re:797) (di:direct) AE000191 AE000191 g1787116 Escherichia coli 562 -11532845 5000690175 alsb leucine-responsive regulatory protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #214) (db:genpept) (de:escherichia coli genomic dna. (19.9 - 20.3 min).) (nt:orf\_id:o215#2; similar to swissprot accession) (le:8475) (re:8969) (di:direct) D90726 D90726 g1651411 Escherichia coli 562 -11532845 7502851825 alsb leucine-responsive regulatory protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #215) (db:genpept) (de:escherichia coli genomic dna. (20.1 - 20.4 min).) (nt:orf\_id:o215#2; similar to swissprot accession) (le:1778) (re:2272) (di:direct) D90727 D90727 g1651417 Escherichia coli 562 -11532845 82479 lrp:alsb:livr (sr:,aerobacter aerogenes) (de:leucine-responsive regulatory protein) (db:swissprot) LRP\_ECOLI P19494 ESCHERICHIA COLI 562 -11532845 7502851826 lrp:alsb:livr (sr:,aerobacter aerogenes) (de:leucine-responsive regulatory protein) (db:swissprot) LRP\_ECOLI P19494 ENTEROBACTER AEROGENES 548 -11532845 82480 lrp:alsb:livr (sr:,aerobacter aerogenes) (de:leucine-responsive regulatory protein) (db:swissprot) LRP\_ECOLI P19494 ESCHERICHIA COLI 562 -11532845 7502851827 lrp:alsb:livr (sr:,aerobacter aerogenes) (de:leucine-responsive regulatory protein) (db:swissprot) LRP\_ECOLI P19494 ENTEROBACTER AEROGENES 548 -11532845

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823687	7503	29659	306	101

Description

6500728988 appa:b0980 periplasmic phosphoanhydride phosphohydrolase precursor:ph 2.5 acid phosphatase:ap6-phytase (gtcfc:11.1:2.3:8.2:9.13:12.13) (keggfc:8.2:9.2:9.12:12.1) (rileyfc:1.3.1) (db:gtc-escherichia coli) b0980 b0980 Escherichia coli 562 -11532846 90702 appa (ec:3.1.3.2:3.1.3.26) (de:(ph 2.5 acid phosphatase) (ap) (6-phytase),) (db:swissprot) PPA\_ECOLI P07102 ESCHERICHIA COLI 562 -11532846 162660 appa acid phosphatase:precursor:phosphoanhydride phosphohydrolase:periplasmic:phytase 6 (ec:3.1.3.2) (db:pir2.dat) (mp:25 min) B36733 B36733 Escherichia coli 562 -11532846 223312 appa periplasmic phosphoanhydride phosphohydrolase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #225) (db:genpept-bct1) (de:escherichia coli genomic dna. (22.2 - 22.6 min).) (le:6540) (re:7838) (di:direct) D90735 D90735 g1651481 Escherichia coli 562 -11532846 7500888335 appa periplasmic phosphoanhydride phosphohydrolase (sr:escherichia coli dna) (db:genpept-bct1) (de:e. coli periplasmic phosphoanhydride phosphohydrolase (appa) gene,complete cds.) (le:188) (re:1486) (di:direct) ECOAPPAA M58708 g145285 Escherichia coli 562 -11532846 233809 appa phosphoanhydride phosphorylase:ph 2.5 acid (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (ec:3.1.3.2:3.1.3.26) (de:escherichia coli k-12 mg1655 section 90 of 400 of the completegenome.) (nt:o432; 100 pct identical to ppa\_ecoli sw: p07102) (le:123) (re:1421) (di:direct) AE000200 AE000200 g1787215 Escherichia coli 562 -11532846 5000690576 appa acid phosphatase ec 3.1.3.2 precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #225) (db:genpept) (de:escherichia coli genomic dna. (22.3 - 22.7 min).) (nt:orf\_id:o225#7; similar to pir accession number) (le:6536) (re:7834) (di:direct) D90735 D90735 g1651481 Escherichia coli 562 -11532846

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823697	7504	29660	456	151

Description

GTC ORF with score 93 to: (sr:herpes simplex virus type 2 (isolate:hg52) dna, clone:f, p and g) (db:genpept-vrl) (de:herpes simplex virus type 2 genomic dna for 0.74-0.84 region,complete cds.) (nt:rl2 orf) (le:8251:10156:<11242) (re:9974:10834:11316) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823702	7505	29661	1293	430

Description

6500728989 pntb:b1602 pyridine nucleotide transhydrogenase subunit-beta:nadp  
transhydrogenase subunit beta:pyridine nucleotide transhydrogenase subunit  
beta:nicotinamide nucleotide transhydrogenase subunit beta (gtcfc:2.3:9.4)  
(ec:1.6.1.1) (keggfc:9.4) (rileyfc:1.3.1) (db:gtc-escherichia coli) b1602  
b1602 Escherichia coli 562 -11532847 300722 pntb (ec:1.6.1.1)  
(de:transhydrogenase subunit beta)) (db:swissprot) PNTB\_ECOLI P07002  
ESCHERICHIA COLI 562 -11532847 122773 pntb nad p + transhydrogenase  
b-specific:beta chain:pyridine nucleotide transhydrogenase beta chain  
(cl:nad(p)+ transhydrogenase (b-specific) beta chain:nad(p)+  
transhydrogenase (b-specific) beta chain homology) (ec:1.6.1.1)  
(db:pir1.dat) (mp:35 min) DEECXB S24381 Escherichia coli 562 -11532847  
224014 pntb nad p + transhydrogenase b-specific ec (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #311(35.7-36.1 min.)).)  
(nt:orf\_id:o312#1; similar to (pir accession number) (le:17626) (re:19014)  
(di:complement) D90802 D90802 g1742636 Escherichia coli 562 -11532847  
224019 pntb nad p + transhydrogenase b-specific ec (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #312(36.0-36.3 min.)).)  
(nt:orf\_id:o312#1; similar to (pir accession number) (le:2678) (re:4066)  
(di:complement) D90803 D90803 g1742642 Escherichia coli 562 -11532847  
5000690176 pntb pyridine nucleotide transhydrogenase (db:genpept-bct1)  
(ec:1.6.1.1) (de:e.coli pnta and pntb genes for pyridine  
nucleotidetranhydrogenase.) (nt:beta subunit) (le:2070) (re:3458)  
(di:direct) ECPNT X66086 g42457 Escherichia coli 562 -11532847 237856 pntb  
pyridine nucleotide transhydrogenase:beta (fn:enzyme; central intermediary  
metabolism: pool,) (db:genpept-bct2) (ec:1.6.1.1) (de:escherichia coli k-12  
mg1655 section 145 of 400 of the completegenome.) (nt:f462; 100 pct  
identical to pntb\_ecoli sw: p07002;) (le:9815) (re:11203) (di:complement)  
AE000255 AE000255 g1787886 Escherichia coli 562 -11532847 90185 pntb  
(ec:1.6.1.1) (de:transhydrogenase subunit beta)) (db:swissprot) PNTB\_ECOLI  
P07002 ESCHERICHIA COLI 562 -11532847

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823715	7506	29662	264	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823718	7507	29663	810	269

Description

GTC ORF with score 123 to: (fn:induces actin polymerization and redistribution) (sr:human) (db:genpept-pri2) (de:homo sapiens wasp interacting protein (wip) mrna, partial cds.) (nt:similar to prpl-2, encoded by genbank accession) (le:109) (re:1620) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823719	7508	29664	738	245

Description

6500728990 pnta:b1603 pyridine nucleotide transhydrogenase subunit-alpha:nadp transhydrogenase subunit alpha:pyridine nucleotide transhydrogenase subunit alpha:nicotinamide nucleotide transhydrogenase subunit alpha (gtcfc:2.3:9.4) (ec:1.6.1.1) (keggfc:9.4) (rileyfc:1.3.1) (db:gtc-escherichia coli) b1603 b1603 Escherichia coli 562 -11532848 300725 pnta (ec:1.6.1.1) (de:transhydrogenase subunit alpha)) (db:swissprot) PNTA\_ECOLI P07001 ESCHERICHIA COLI 562 -11532848 122772 pnta nad p + transhydrogenase b-specific:alpha chain:pyridine nucleotide transhydrogenase alpha chain (cl:nad(p)+ transhydrogenase (b-specific) alpha chain:alanine dehydrogenase homology:nad(p)+ transhydrogenase (b-specific) alpha chain homology) (ec:1.6.1.1) (db:pir1.dat) (mp:35 min) DEECXA S24380 Escherichia coli 562 -11532848 224020 pnta nad p + transhydrogenase b-specific ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #312(36.0-36.3 min.)) (nt:orf\_id:o312#2; similar to (pir accession number) (le:4077) (re:5609) (di:complement) D90803 D90803 g1742643 Escherichia coli 562 -11532848 224030 pnta nad p + transhydrogenase b-specific ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #313(36.1-36.4 min.)) (nt:orf\_id:o312#2; similar to (pir accession number) (le:191) (re:1723) (di:complement) D90804 D90804 g1742654 Escherichia coli 562 -11532848 5000690177 pnta pyridine nucleotide transhydrogenase (db:genpept-bct1) (ec:1.6.1.1) (de:e.coli pnta and pntb genes for pyridine nucleotidetranhydrogenase.) (nt:alpha subunit) (le:527) (re:2059) (di:direct) ECPNT X66086 g42456 Escherichia coli 562 -11532848 237855 pnta pyridine nucleotide transhydrogenase:alpha (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (ec:1.6.1.1) (de:escherichia coli k-12 mg1655 section 145 of 400 of the completegenome.) (nt:f510; 100 pct identical to pnta\_ecoli sw: p07001;) (le:11214) (re:12746) (di:complement) AE000255 AE000255 g1787887 Escherichia coli 562 -11532848 90183 pnta (ec:1.6.1.1) (de:transhydrogenase subunit alpha)) (db:swissprot) PNTA\_ECOLI P07001 ESCHERICHIA COLI 562 -11532848

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823725	7509	29665	675	224

# Description

6500728991 hdha:hsdh:b1619 7-alpha-hydroxysteroid dehydrogenase:7-alpha-hsdh (gtcfc:2.3) (ec:1.1.1.159) (keggfc:14.1) (rileyfc:1.3.1) (db:gtc-escherichia coli) b1619 b1619 Escherichia coli 562 -11532849 76415 hdha:hsdh (ec:1.1.1.159) (de:7-alpha-hydroxysteroid dehydrogenase, (7-alpha-hsdh)) (db:swissprot) HDHA\_ECOLI P25529 ESCHERICHIA COLI 562 -11532849 136097 hdha:hsdh 7alpha-hydroxysteroid dehydrogenase (cl:ribitol dehydrogenase:short-chain alcohol dehydrogenase homology) (ec:1.1.1.159) (db:pir2.dat) A38527 A38527 Escherichia coli 562 -11532849 224048 hdha:hsdh 7-a-hydroxysteroid dehydrogenase ec 1.1.1.159 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #314(36.3-36.7 min.)) (nt:orf\_id:o314#5; similar to (swissprot accession) (le:11957) (re:12724) (di:complement) D90805 D90805 g1742673 Escherichia coli 562 -11532849 224055 hdha:hsdh 7-a-hydroxysteroid dehydrogenase ec 1.1.1.159 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #315(36.6-36.9 min.)) (nt:orf\_id:o314#5; similar to (swissprot accession) (le:269) (re:1036) (di:complement) D90806 D90806 g1742681 Escherichia coli 562 -11532849 300768 hdha:hsdh 7-a-hydroxysteroid dehydrogenase ec 1.1.1.159 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #317(36.6-36.9 min.)) (nt:orf\_id:o314#5; similar to (swissprot accession) (le:370) (re:1137) (di:complement) D90808 D90808 g1742713 Escherichia coli 562 -11532849 300743 hsdh 7alpha-hydroxysteroid dehydrogenase (sr:escherichia coli (strain:hb101) dna) (db:genpept-bct1) (ec:1.1.1.159) (de:escherichia coli hsdh gene encoding 7alpha-hydroxysteroiddehydrogenase.) (le:750) (re:1517) (di:direct) ECOHSDH D10497 g912437 Escherichia coli 562 -11532849 234691 hdha nad-dependent 7alpha-hydroxysteroid (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (ec:1.1.1.159) (de:escherichia coli k-12 mg1655 section 147 of 400 of the completegenome.) (nt:f255; 100 pct identical to hdha\_ecoli sw: p25529;) (le:8850) (re:9617) (di:complement) AE000257 AE000257 g1787905 Escherichia coli 562 -11532849 224085 hdha:hsdh 7-a-hydroxysteroid dehydrogenase ec 1.1.1.159 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #317(36.6-36.9 min.)) (nt:orf\_id:o314#5; similar to (swissprot accession) (le:370) (re:1137) (di:complement) D90808 D90808 g1742713 Escherichia coli 562 -11532849 5000690178 (de:(ecoli\_1578) (pn:nad-dependent 7alpha-hydroxysteroid dehydrogenase, dehydroxylation of bile acids) (gn:hdha) (gtcfc:2.3) (ec:1.1.1.159) (hdha\_ecoli) (keggfc:11.1) (rileyfc:1.3.1) (db:gtc-escherichia coli)) ECOLI\_1578 ECOLI\_1578 Escherichia coli 562 10018778



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823730	7510	29666	426	141

Description

6500728992 glpq:b2239 glycerophosphoryl diester phosphodiesterase  
periplasmic precursor:glycerophosphodiester phosphodiesterase  
(gtcfc:2.3:8.1:8.4:11.1) (ec:3.1.4.46) (keggfc:8.1:8.4) (rileyfc:1.3.1)  
(db:gtc-escherichia coli) b2239 b2239 Escherichia coli 562 -11532850  
7500882515 glpq (ec:3.1.4.46) (de:(ec 3.1.4.46) (glycerophosphodiester  
phosphodiesterase)) (db:swissprot) GLPQ\_ECOLI P09394 ESCHERICHIA COLI 562  
-11532850 163135 glpq glycerophosphodiester  
phosphodiesterase:precursor:periplasmic (ec:3.1.4.46) (db:pir2.dat) S15945  
S15945 Escherichia coli 562 -11532850 224745 glpq glycerophosphodiester  
phosphodiesterase ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara  
lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#377(50.5-50.9 min.)) (nt:similar to (pir accession number s15945))  
(le:10219) (re:11295) (di:complement) D90855 D90855 g1799586 Escherichia  
coli 562 -11532850 5000690563 glpq glycerophosphocholine phosphodiesterase  
(db:genpept-bct1) (ec:3.1.4.2) (de:e. coli glpq gene for glycerophosphoryl  
diester phosphodiesterase(periplasmic).) (le:31) (re:1107) (di:direct)  
ECGLPQ X56907 g41581 Escherichia coli 562 -11532850 233008 glpq  
glycerophosphodiester phosphodiesterase (fn:enzyme; central intermediary  
metabolism: pool,) (db:genpept-bct2) (de:escherichia coli k-12 mgl655  
section 204 of 400 of the completegenome.) (nt:f358; 100 pct identical to  
glpq\_ecoli sw: p09394) (le:386) (re:1462) (di:complement) AE000314 AE000314  
g1788572 Escherichia coli 562 -11532850 74046 glpq (ec:3.1.4.46) (de:(ec  
3.1.4.46) (glycerophosphodiester phosphodiesterase)) (db:swissprot)  
GLPQ\_ECOLI P09394 ESCHERICHIA COLI 562 -11532850

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823765	7511	29667	1020	339

#### Description

6500728993 gcva:b2808 regulatory protein for glycine cleavage pathway:glycine cleavage system transcriptional activator (gtcfc:2.3:10.2) (keggfc:14.2) (rileyfc:1.3.1) (db:gtc-escherichia coli) b2808 b2808 Escherichia coli 562 -11532851 234468 gcva (de:activator)) (db:swissprot) GCVA\_ECOLI P32064 ESCHERICHIA COLI 562 -11532851 163136 gcva glycine cleavage system transcription activator (db:pir2.dat) I41065 I41065 Escherichia coli 562 -11532851 5000690179 gcva glycine cleavage activator protein (db:genpept-bct1) (de:e.coli gene for glycine cleavage activator protein and orf 2 and 3.) (le:43) (re:960) (di:direct) ECGCVA X73413 g312766 Escherichia coli 562 -11532851 239382 gcva (fn:regulatory protein for glycine cleavage enzyme) (db:genpept-bct1) (de:escherichia coli k12 glycine cleavage activator protein (gcva)gene, complete cds.) (le:304) (re:1221) (di:direct) ECOGCVA U01030 g523331 Escherichia coli 562 -11532851 7500882301 gcva (fn:regulatory protein for glycine cleavage) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:cg site no. 28676) (le:23205) (re:24122) (di:complement) ECU29581 U29581 g882703 Escherichia coli 562 -11532851 232978 gcva positive regulator of gcv operon (fn:regulator; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 254 of 400 of the completegenome.) (nt:f305; 100 pct identical to gcva\_ecoli sw: p32064;) (le:7719) (re:8636) (di:complement) AE000364 AE000364 g1789173 Escherichia coli 562 -11532851 73473 gcva (de:glycine cleavage system transcriptional activator) (db:swissprot) GCVA\_ECOLI P32064 ESCHERICHIA COLI 562 -11532851

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823779	7512	29668	339	112

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823788	7513	29669	270	89

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823806	7514	29670	696	231

Description

6500728994 gcvp:b2903 glycine dehydrogenase:decarboxylating:glycine decarboxylase:glycine cleavage system p-protein (gtcfc:2.3:5.3) (ec:1.4.4.2) (keggfc:5.3) (rileyfc:1.3.1) (db:gtc-escherichia coli) b2903 b2903 Escherichia coli 562 -11532852 163137 gcvp:gcvhp glycine dehydrogenase decarboxylating (ec:1.4.4.2) (db:pir2.dat) S36834 S36834 Escherichia coli 562 -11532852 234472 gcvp glycine dehydrogenase decarboxylating (db:genpept-bct1) (ec:1.4.4.2) (de:e.coli gcv operon dna sequence.) (le:1904) (re:4777) (di:direct) ECGCVOP X73958 g403345 Escherichia coli 562 -11532852 7500882279 gcvhp (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli gcvh gene, 3' end; gcvp gene, complete cds.) (le:203) (re:3076) (di:direct) ECOGCVHP L20872 g304892 Escherichia coli 562 -11532852 232983 gcvp glycine decarboxylase:p protein of glycine (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (ec:1.4.4.2) (de:escherichia coli k-12 mg1655 section 263 of 400 of the completegenome.) (nt:99 pct identical to gcsp\_ecoli sw: p33195) (le:9871) (re:12744) (di:complement) AE000373 AE000373 g1789269 Escherichia coli 562 -11532852 73455 gcvp (ec:1.4.4.2) (de:decarboxylase) (glycine cleavage system p-protein)) (db:swissprot) GCSP\_ECOLI P33195 ESCHERICHIA COLI 562 -11532852 5000690439 (de:(ecoli\_2826) (pn:glycine decarboxylase, p protein of glycine cleavage system) (gn:gcvp) (gtcfc:5.3) (ec:1.4.4.2) (gcsp\_ecoli) (keggfc:5.3) (rileyfc:1.3.1) (db:gtc-escherichia coli)) ECOLI\_2826 ECOLI\_2826 Escherichia coli 562 10015989

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823812	7515	29671	198	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823819	7516	29672	909	303

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823828	7517	29673	372	123

Description

6500728995 gcvh:b2904 glycine cleavage system h protein (gtcfc:2.3) (keggfc:14.2) (rileyfc:1.3.1) (db:gtc-escherichia coli) b2904 b2904 Escherichia coli 562 -11532853 130131 gcvh glycine cleavage system:h protein:aminomethyl carrier protein:glycine decarboxylasecomplex protein h (cl:glycine cleavage system protein h:lipoyl/biotin-binding homology) (db:pir1.dat) (mp:63 min) A56623 A56623 Escherichia coli 562 -11532853 234470 gcvh h protein (db:genpept-bct1) (de:e.coli gcv operon dna sequence.) (le:1396) (re:1785) (di:direct) ECGCVOP X73958 g403344 Escherichia coli 562 -11532853 239118 gcvh h-protein (sr:e.coli (k-12) dna) (db:genpept-bct1) (de:e.coli h-protein (gcvh) gene, complete cds.) (nt:h-protein for glycine cleavage enzyme complex) (le:72) (re:461) (di:direct) ECOGCVH M57690 g146122 Escherichia coli 562 -11532853 7500882274 gcvh (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf\_f129) (le:3551) (re:3940) (di:complement) ECU28377 U28377 g882434 Escherichia coli 562 -11532853 232982 gcvh in glycine cleavage complex:carrier of (fn:carrier; central intermediary metabolism: pool,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 264 of 400 of the completegenome.) (nt:100 pct identical to gcsh\_ecoli sw: p23884) (le:90) (re:479) (di:complement) AE000374 AE000374 g1789271 Escherichia coli 562 -11532853 73447 gcvh (de:glycine cleavage system h protein) (db:swissprot) GCSH\_ECOLI P23884 ESCHERICHIA COLI 562 -11532853 5000690180 (de:(ecoli\_2827) (pn:in glycine cleavage complex, carrier of aminomethyl moiety via covalently bound lipoyl cofactor) (gn:gcvh) (gtcfc:2.3) (ec:) (gcsh\_ecoli) (keggfc:11.2) (rileyfc:1.3.1) (db:gtc-escherichia coli)) ECOLI\_2827 ECOLI\_2827 Escherichia coli 562 10015981

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823837	7518	29674	357	118

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823839	7519	29675	828	275

Description

6500728996 gcv:b2905 aminomethyltransferase:glycine cleavage system t protein (gtcfc:2.3:2.6:5.3:9.6) (ec:2.1.2.10) (keggfc:2.5:5.3:9.8) (rileyfc:1.3.1) (db:gtc-escherichia coli) (gtcfc:energy metabolism-glyoxylate cycle:energy metabolism-nitrogen metabolism:l-amino acid metabolism-glycine--serine and threonine metabolism:metabo... b2905 b2905 Escherichia coli 562 -11532854 162721 gcv aminomethyltransferase::glycine cleavage system protein t (cl:aminomethyltransferase) (ec:2.1.2.10) (db:pir2.dat) A56689 A56689 Escherichia coli 562 -11532854 236133 gcv aminomethyltransferase (db:genpept-bct1) (ec:2.1.2.10) (de:e.coli gcv operon dna sequence.) (le:278) (re:1372) (di:direct) ECGCVOP X73958 g403343 Escherichia coli 562 -11532854 239119 gcv (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf\_f364) (le:3964) (re:5058) (di:complement) ECU28377 U28377 g882435 Escherichia coli 562 -11532854 232981 gcv aminomethyltransferase t protein (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (ec:2.1.2.10) (de:escherichia coli k-12 mg1655 section 264 of 400 of the completegenome.) (nt:f364; 100 pct identical to gcst\_ecoli sw: p27248) (le:503) (re:1597) (di:complement) AE000374 AE000374 g1789272 Escherichia coli 562 -11532854 7500959674 gcv t-protein (sr:escherichia coli (strain k-12) dna) (db:genpept-bct2) (de:e. coli t-protein (gcv) gene, complete cds and gcvh gene, 5' end.) (le:574) (re:1668) (di:direct) ECOTPRO M97263 g148040 Escherichia coli 562 -11532854 5000690203 (de:(ecoli\_2828) (pn:t protein:tetrahydrofolate-dependent of glycine cleavage system) (gn:gcv) (gtcfc:2.6:5.3:9.6) (ec:2.1.2.10) (gcst\_ecoli) (keggfc:2.5:5.3:9.8) (rileyfc:1.3.1) (db:gtc-escherichia coli) ECOLI\_2828 ECOLI\_2828 Escherichia coli 562 10015999

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823842	7520	29676	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823846	7521	29677	396	131

Description

6500728997 metk:metx:b2942 s-adenosylmethionine synthetase:methionine  
adenosyltransferase:adomet synthetase (gtcfc:2.3:5.4:6.4) (ec:2.5.1.6)  
(keggfc:5.4:6.4) (rileyfc:1.3.1) (db:gtc-escherichia coli) b2942 b2942  
Escherichia coli 562 -11532855 83565 metk:metx (ec:2.5.1.6)  
(de:adenosyltransferase) (adomet synthetase)) (db:swissprot) METK\_ECOLI  
P04384 ESCHERICHIA COLI 562 -11532855 7000685836 metk methionine  
adenosyltransferase::s-adenosylmethionine synthetase (cl:methionine  
adenosyltransferase) (ec:2.5.1.6) (db:pir1.dat) (mp:64 min) SYEC SM E65079  
Escherichia coli 562 -11532855 7500885547 metk (fn:s-adenosylmethionine  
synthetase) (db:genpept-bct1) (ec:2.5.1.6) (de:escherichia coli k-12 genome;  
approximately 65 to 68 minutes.) (nt:cg site no. 507) (le:41101) (re:42255)  
(di:direct) ECU28377 U28377 g882471 Escherichia coli 562 -11532855 239155  
metk methionine adenosyltransferase 1 adomet (fn:enzyme; central  
intermediary metabolism: pool,) (db:genpept-bct2) (ec:2.5.1.6)  
(de:escherichia coli k-12 mg1655 section 267 of 400 of the completegenome.)  
(nt:o384; 98 pct identical (1 gap) to metx\_ecoli) (le:5024) (re:6178)  
(di:direct) AE000377 AE000377 g1789311 Escherichia coli 562 -11532855  
5000690455 (de:(ecoli\_2864) (pn:methionine adenosyltransferase 1:adomet  
synthetase; methyl and propylamine donor, corepressor of met genes)  
(gn:metk) (gtcfc:5.4:6.4) (ec:2.5.1.6) (metk\_ecoli) (keggfc:5.4:6.4)  
(rileyfc:1.3.1) (db:gtc-escher) ECOLI\_2864 ECOLI\_2864 Escherichia coli 562  
10025779

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823849	7522	29678	1251	416

#### Description

6500728998 glcg:b2977 hypothetical 13.7 kd protein in glcb-hybg intergenic region:glcg protein (gtcfc:2.3) (keggfc:14.2) (rileyfc:1.3.1) (db:gtc-escherichia coli) b2977 b2977 Escherichia coli 562 -11532856 73745 glcg (de:glcg protein) (db:swissprot) GLCG\_ECOLI P45504 ESCHERICHIA COLI 562 -11532856 7000685392 glcg hypothetical 13.7 kd protein in glcb-hybg intergenic region (db:pir2.dat) G65083 G65083 Escherichia coli 562 -11532856 239190 glcg (db:genpept-bct1) (de:escherichia coli glcc gene, glycolate oxidase (glcd, glce, glcf)genes, and glcg gene, complete cds.) (nt:putative) (le:4907) (re:5311) (di:direct) ECOGLCC L43490 g1141715 Escherichia coli 562 -11532856 7500882388 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf\_f134) (le:78219) (re:78623) (di:complement) ECU28377 U28377 g882506 Escherichia coli 562 -11532856 234487 glcg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 270 of 400 of the completegenome.) (nt:f134; 100 pct identical to yghc\_ecoli sw: p45504) (le:9344) (re:9748) (di:complement) AE000380 AE000380 g1789349 Escherichia coli 562 -11532856 5000690181 (de:(ecoli\_2899) (pn:glcg protein) (gn:glcg) (gtcfc:2.3) (ec:) (glcg\_ecoli) (keggfc:11.2) (rileyfc:1.3.1) (db:gtc-escherichia coli)) ECOLI\_2899 ECOLI\_2899 Escherichia coli 562 10016277

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823853	7523	29679	327	108

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823867	7524	29680	807	268

#### Description

5000690182 glycolate oxidase subunits glce and glcf (gtcfc:2.3) (keggfc:14.2) (rileyfc:1.3.1) (db:gtc-escherichia coli) b2978 b2978 Escherichia coli 562 -11532857 7000690896 glycolate oxidase subunits glce and glcf (db:pir2.dat) H65083 H65083 Escherichia coli 562 -11532857 7500959753 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf\_f761) (le:78628) (re:80913) (di:complement) ECU28377 U28377 g882507 Escherichia coli 562 -11532857 239191 glcf glycolate oxidase iron-sulfur subunit (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 270 of 400 of the completegenome.) (nt:f761; frameshift fuses two proteins) (le:9753) (re:12038) (di:complement) AE000380 AE000380 g1789350 Escherichia coli 562 -11532857 6500728999 glycolate oxidase subunits glce and glcf (gtcfc:2.3) (keggfc:14.2) (rileyfc:1.3.1) (db:gtc-escherichia coli) b2978 b2978 Escherichia coli 562 -11532857

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823874	7525	29681	366	121
<u>Description</u>				
6500729000 glcd:gox:b2979 glycolate oxidase subunit glcd (gtcfc:2.3) (keggfc:14.2) (rileyfc:1.3.1) (db:gtc-escherichia coli) b2979 b2979 Escherichia coli 562 -11532858 73742 glcd:gox (de:glycolate oxidase subunit glcd) (db:swissprot) GLCD_ECOLI P52075 ESCHERICHIA COLI 562 -11532858 7000685391 glcd glycolate oxidase subunit glcd (cl:glycolate oxidase chain glcd) (db:pir2.dat) A65084 A65084 Escherichia coli 562 -11532858 239192 glcd glycolate oxidase subunit (fn:glycolate oxidation) (db:genpept-bct1) (de:escherichia coli glcc gene, glycolate oxidase (glcd, glce, glcf)genes, and glcg gene, complete cds.) (le:1117) (re:2616) (di:direct) ECOGLCC L43490 g1141712 Escherichia coli 562 -11532858 7500882387 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f499) (le:80913) (re:82412) (di:complement) ECU28377 U28377 g882508 Escherichia coli 562 -11532858 234484 glcd glycolate oxidase subunit d (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 270 of 400 of the completegenome.) (nt:f499; 100 pct identical to glcd_ecoli sw: p52075) (le:12038) (re:13537) (di:complement) AE000380 AE000380 g1789351 Escherichia coli 562 -11532858 5000690183 (de:(ecoli_2901) (pn:glycolate oxidase subunit glcd) (gn:glcd) (gtcfc:2.3) (ec:) (glcd_ecoli) (keggfc:11.2) (rileyfc:1.3.1) (db:gtc-escherichia coli)) ECOLI_2901 ECOLI_2901 Escherichia coli 562 10016274				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823877	7526	29682	600	199
<u>Description</u>				
6500729001 glcc:b2980 glc operon transcriptional activator (gtcfc:2.3:10.2) (keggfc:14.2) (rileyfc:1.3.1) (db:gtc-escherichia coli) b2980 b2980 Escherichia coli 562 -11532859 73741 glcc (de:glc operon transcriptional activator) (db:swissprot) GLCC_ECOLI P52072 ESCHERICHIA COLI 562 -11532859 7000685390 glcc transcription activator of glc operon (db:pir2.dat) B65084 B65084 Escherichia coli 562 -11532859 7500882386 glcc (fn:activator) (db:genpept-bct1) (de:escherichia coli glcc gene, glycolate oxidase (glcd, glce, glcf)genes, and glcg gene, complete cds.) (nt:regulatory protein) (le:102) (re:866) (di:complement) ECOGLCC L43490 g1141711 Escherichia coli 562 -11532859 234483 glcc transcriptional activator for glc operon (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 271 of 400 of the completegenome.) (nt:o254; 100 pct identical to glcc_ecoli sw: p52072) (le:156) (re:920) (di:direct) AE000381 AE000381 g1789353 Escherichia coli 562 -11532859 5000690184 (de:(ecoli_2902) (pn:glc operon transcriptional activator) (gn:glcc) (gtcfc:2.3) (ec:) (glcc_ecoli) (keggfc:11.2) (rileyfc:1.3.1) (db:gtc-escherichia coli)) ECOLI_2902 ECOLI_2902 Escherichia coli 562 10016273				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823882	7527	29683	327	108

Description

6500729002 gltb:aspb:b3212 glutamate synthase:nadph large chain  
precursor:glutamate synthase alpha subunit:nadph-gogat:glts alpha chain  
(gtcfc:2.3:2.6:5.1) (ec:1.4.1.13) (keggfc:2.5:5.1) (rileyfc:1.3.1)  
(db:gtc-escherichia coli) b3212 b3212 Escherichia coli 562 -11532860 74116  
gltb:aspb (ec:1.4.1.13) (de:(glutamate synthase alpha subunit) (nadph-gogat)  
(glts alpha chain)) (db:swissprot) GLTB\_ECOLI P09831 ESCHERICHIA COLI 562  
-11532860 7000685423 gltb glutamate synthase nadph:large chain precursor  
(cl:glutamate synthase (nadph)) (ec:1.4.1.13) (db:pir2.dat) (mp:69 min)  
F65112 F65112 Escherichia coli 562 -11532860 7500882553 gltb glutamate  
synthase:large subunit (db:genpept-bct1) (ec:2.6.1.53) (de:escherichia coli  
k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 686;  
alternate name aspb) (le:135377) (re:139930) (di:direct) ECOUW67 U18997  
g606151 Escherichia coli 562 -11532860 236450 gltb glutamate synthase:large  
subunit (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2)  
(ec:2.6.1.53:1.4.1.13) (de:escherichia coli k-12 mg1655  
section 290 of 400 of the completegenome.) (nt:o1517; cg site no. 686;  
alternate name aspb; 100) (le:8156) (re:12709) (di:direct) AE000400 AE000400  
g1789605 Escherichia coli 562 -11532860 5000690206 (de:(ecoli\_3135)  
(pn:glutamate synthase, large subunit) (gn:gltb) (gtcfc:2.6:5.1)  
(ec:1.4.1.13) (gltb\_ecoli) (keggfc:2.5:5.1) (rileyfc:1.3.1)  
(db:gtc-escherichia coli)) ECOLI\_3135 ECOLI\_3135 Escherichia coli 562  
10016646

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823884	7528	29684	432	143

#### Description

6500729003 gltd:aspb:b3213 glutamate synthase:nadph small chain:glutamate synthase beta subunit:nadph-gogat:glts beta chain (gtcfc:2.3:2.6:5.1) (ec:1.4.1.13) (keggfc:2.5:5.1) (rileyfc:1.3.1) (db:gtc-escherichia coli) b3213 b3213 Escherichia coli 562 -11532861 7000690893 gltd glutamate synthase nadph:small chain (cl:glutamate synthase small chain) (ec:1.4.1.13) (db:pir2.dat) (mp:69 min) G65112 G65112 Escherichia coli 562 -11532861 7500959750 gltd glutamate synthase:small subunit (db:genpept-bct1) (ec:2.6.1.53) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 17689; alternate name aspb) (le:139943) (re:141361) (di:direct) ECOUW67 U18997 g606152 Escherichia coli 562 -11532861 236451 gltd glutamate synthase:small subunit (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (ec:2.6.1.53:1.4.1.13) (de:escherichia coli k-12 mg1655 section 290 of 400 of the completegenome.) (nt:o472; cg site no. 17689; alternate name aspb; 100) (le:12722) (re:14140) (di:di... AE000400 AE000400 g1789606 Escherichia coli 562 -11532861 5000690207 (de:(ecoli\_3136) (pn:glutamate synthase, small subunit) (gn:gltd) (gtcfc:2.6:5.1) (ec:1.4.1.13) (gltd\_ecoli) (keggfc:2.5:5.1) (rileyfc:1.3.1) (db:gtc-escherichia coli)) ECOLI\_3136 ECOLI\_3136 Escherichia coli 562 10123993

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823935	7529	29685	276	91

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823936	7530	29686	378	125

#### Description

GTC ORF with score 95 to: (sr:caenorhabditis elegans (strain bristol n2) hermaphrodite mixe) (db:genpept-inv) (de:c. elegans cosmid k02d10.) (nt:homology with 4-nitrophenylphosphatase and mouse) (le:4388:5555:6199:7498) (re:5166:5727:6762:7563) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823937	7531	29687	501	166

Description

6500729004 gltf:b3214 protein gltf precursor (gtcfc:2.3) (keggfc:14.2) (rileyfc:1.3.1) (db:gtc-escherichia coli) b3214 b3214 Escherichia coli 562 -11532862 74123 gltf (de:protein gltf precursor) (db:swissprot) GLTF\_ECOLI P28721 ESCHERICHIA COLI 562 -11532862 163110 gltf gltf protein precursor (db:pir2.dat) S25281 S25281 Escherichia coli 562 -11532862 236452 gltf (fn:involved in nitrogen-regulated gene expression) (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli gltbdf operon gltf gene (involved innitrogen-regulated gene expression), complete cds.) (le:549) (re:1313) (di:direct) ECOGLTF M74162 g146214 Escherichia coli 562 -11532862 7500882556 gltf (fn:regulatory protein) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 18259) (le:141921) (re:142685) (di:direct) ECOUW67 U18997 g606153 Escherichia coli 562 -11532862 234545 gltf regulator of gltbdf operon:induction of ntr (fn:regulator; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 291 of 400 of the completegenome.) (nt:o254; cg site no. 18259; 100 pct identical amino) (le:463) (re:1227) (di:direct) AE000401 AE000401 g1789608 Escherichia coli 562 -11532862 5000690185 (de:(ecoli\_3137) (pn:regulator of gltbdf operon, induction of ntr enzymes) (gn:gltf) (gtcfc:2.3) (ec:) (gltf\_ecoli) (keggfc:11.2) (rileyfc:1.3.1) (db:gtc-escherichia coli)) ECOLI\_3137 ECOLI\_3137 Escherichia coli 562 10016653

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501823945	7532	29688	438	145

Description

6500729005 ugpq:b3449 glycerophosphoryl diester  
phosphodiesterase:glycerophosphodiester phosphodiesterase  
(gtcfc:2.3:8.1:8.4) (ec:3.1.4.46) (keggfc:8.1:8.4) (rileyfc:1.3.1)  
(db:gtc-escherichia coli) b3449 b3449 Escherichia coli 562 -11532863  
7500893762 ugpq (ec:3.1.4.46) (de:(glycerophosphodiester  
phosphodiesterase)) (db:swissprot) UGPQ\_ECOLI P10908 ESCHERICHIA COLI 562  
-11532863 124724 ugpq glycerophosphodiester phosphodiesterase  
(cl:glycerophosphodiester phosphodiesterase) (ec:3.1.4.46) (db:pir1.dat)  
(mp:76 min) ESECGD JV0024 Escherichia coli 562 -11532863 240334 ugpq  
glycerophosphocholine phosphodiesterase (sr:escherichia coli (sub\_strain  
mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (ec:3.1.4.2) (de:e.  
coli chromosomal region from 76.0 to 81.5 minutes.) (le:1632) (re:2375)  
(di:complement) ECOUW76 U00039 g466585 Escherichia coli 562 -11532863  
240335 (db:genpept-bct1) (de:escherichia coli ugpq gene for  
glycerophosphoryl diesterphosphodiesterase.) (nt:ugpq protein (aa 1-247))  
(le:9) (re:752) (di:direct) ECUQPQ X14437 g43251 Escherichia coli 562  
-11532863 5000690569 ugpq glycerophosphocholine phosphodiesterase  
(db:genpept-bct1) (ec:3.1.4.2) (de:e. coli ugpq gene for glycerophosphoryl  
diester phosphodiesterase(cytoplasmic) and orfq.) (le:28) (re:771)  
(di:direct) ECUQPQ X56908 g43253 Escherichia coli 562 -11532863 236684  
ugpq glycerophosphodiester phosphodiesterase (fn:enzyme; central  
intermediary metabolism: pool,) (db:genpept-bct2) (ec:3.1.4.46)  
(de:escherichia coli k-12 mg1655 section 311 of 400 of the completegenome.)  
(nt:f247; 100 pct identical to ugpq\_ecoli sw: p10908) (le:2923) (re:3666)  
(di:complement) AE000421 AE000421 g1789858 Escherichia coli 562 -11532863  
103346 ugpq (ec:3.1.4.46) (de:(glycerophosphodiester phosphodiesterase))  
(db:swissprot) UGPQ\_ECOLI P10908 ESCHERICHIA COLI 562 -11532863

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823949	7533	29689	339	112

Description

6500729006 kbl:b3617 2-amino-3-ketobutyrate coenzyme a ligase:akb  
ligase:glycine acetyltransferase (gtcfc:2.3:5.3) (ec:2.3.1.29) (keggfc:5.3)  
(rileyfc:1.3.1) (db:gtc-escherichia coli) b3617 b3617 Escherichia coli 562  
-11532864 80455 kbl (ec:2.3.1.29) (de:(glycine acetyltransferase))  
(db:swissprot) KBL\_ECOLI P07912 ESCHERICHIA COLI 562 -11532864 7000685664  
kbl glycine c-acetyltransferase::2-amino-3-ketobutyrate coa ligase  
(cl:5-aminolevulinate synthase) (ec:2.3.1.29) (db:pir1.dat) (mp:81 min)  
XUECGA C65162 Escherichia coli 562 -11532864 7500884484 kbl glycine  
acetyltransferase (sr:escherichia coli (sub\_strain mg1655, strain k-12)  
(library: lambda) (db:genpept-bct1) (ec:2.3.1.29) (de:e. coli chromosomal  
region from 76.0 to 81.5 minutes.) (nt:cg site no. 18205) (le:205605)  
(re:206801) (di:complement) ECOUW76 U00039 g466755 Escherichia coli 562  
-11532864 236854 kbl 2-amino-3-ketobutyrate coa ligase glycine (fn:enzyme;  
central intermediary metabolism: pool,) (db:genpept-bct2) (ec:2.3.1.29)  
(de:escherichia coli k-12 mg1655 section 329 of 400 of the completegenome.)  
(nt:f398; cg site no. 18205) (le:8783) (re:9979) (di:complement) AE000439  
AE000439 g1790046 Escherichia coli 562 -11532864 5000690448  
(de:(ecoli\_3537) (pn:2-amino-3-ketobutyrate coa ligase:glycine  
acetyltransferase) (gn:kbl) (gtcfc:5.3) (ec:2.3.1.29) (kbl\_ecoli)  
(keggfc:5.3) (rileyfc:1.3.1) (db:gtc-escherichia coli)) ECOLI\_3537  
ECOLI\_3537 Escherichia coli 562 10022703

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823950	7534	29690	327	108
<u>Description</u>				
6500729007 glpk:b3926 glycerol kinase:atp:glycerol 3-phosphotransferase:glycerokinase:gk (gtcfc:2.3:8.1) (ec:2.7.1.30) (keggfc:8.1) (rileyfc:1.3.1) (db:gtc-escherichia coli) b3926 b3926 Escherichia coli 562 -11532865 123536 glpk glycerol kinase (cl:xylulokinase) (ec:2.7.1.30) (db:pir1.dat) (mp:88 min) KIECGL A27339 Escherichia coli 562 -11532865 237143 glpk (sr:e.coli (strain k12; e.c.lin strain 61, cell line jj161) dna, clon) (db:genpept-bct1) (de:e.coli glp-kappa gene encoding glycerol kinase, complete cds.) (nt:atp:glycerol 3-phosphotransferase (ec 2.1.7.30)) (le:37) (re:1545) (di:direct) ECOGLYK M18393 g146220 Escherichia coli 562 -11532865 7500953248 glpk glycerol kinase (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 691) (le:77347) (re:78855) (di:complement) ECOUW87 L19201 g305029 Escherichia coli 562 -11532865 234549 glpk glycerol kinase (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (ec:2.7.1.30) (de:escherichia coli k-12 mg1655 section 357 of 400 of the completeness.) (nt:f502; 100 pct identical to glpk_ecoli sw: p08859;) (le:2840) (re:4348) (di:complement) AE000467 AE000467 g1790361 Escherichia coli 562 -11532865 5000690572 (de:(ecoli_3824) (pn:glycerol kinase) (gn:glpk) (gtcfc:8.1) (ec:2.7.1.30) (glpk_ecoli) (keggfc:8.1) (rileyfc:1.3.1) (db:gtc-escherichia coli)) ECOLI_3824 ECOLI_3824 Escherichia coli 562 10065859				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823990	7535	29691	186	61
<u>Description</u>				
6500729008 glda:b3945 glycerol dehydrogenase (gtcfc:2.3:8.1) (ec:1.1.1.6) (keggfc:8.1) (rileyfc:1.3.1) (db:gtc-escherichia coli) b3945 b3945 Escherichia coli 562 -11532866 7000690895 glda glycerol dehydrogenase (cl:lactaldehyde reductase:lactaldehyde reductase homology) (ec:1.1.1.6) (db:pir2.dat) D65201 D65201 Escherichia coli 562 -11532866 7500959752 glda glycerol dehydrogenase:nad (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (ec:1.1.1.6) (de:escherichia coli k-12 mg1655 section 358 of 400 of the completeness.) (nt:f380; 99 pct identical amino acid sequence and) (le:9483) (re:10625) (di:complement) AE000468 AE000468 g1790381 Escherichia coli 562 -11532866 5000690573 (de:(ecoli_3843) (pn:glycerol dehydrogenase,:nad) (gn:glda) (gtcfc:8.1) (ec:1.1.1.6) (glda_ecoli) (keggfc:8.1) (rileyfc:1.3.1) (db:gtc-escherichia coli)) ECOLI_3843 ECOLI_3843 Escherichia coli 562 10124122				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501823998	7536	29692	234	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824010	7537	29693	228	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824022	7538	29694	1146	381

Description

6500729009 acek:b4016 isocitrate dehydrogenase kinase/phosphatase:ldh kinase/phosphatase (gtcfc:2.3:7.1:9.1:9.3:9.4) (keggfc:4.4:9.1:9.3:9.4) (rileyfc:1.3.1) (db:gtc-escherichia coli) (gtcfc:energy metabolism-glyoxylate cycle:metabolism of complex carbohydrates-di-saccharide metabolism (maltose--cellobiose--trehalose--lactose--sucrose):met... b4016 b4016 Escherichia coli 562 -11532867 7000688866 acek isocitrate dehydrogenase nadp+ kinase, / phosphatase, precursor) (cl:isocitrate dehydrogenase kinase) (ec:2.7.1.116:3.1.3.-) (db:pir1.dat) (mp:91 min) KIECID G65208 Escherichia coli 562 -11532867 237222 acek isocitrate dehydrogenase kinase/phosphatase (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:2.7.1.116) (de:escherichia coli k-12 mg1655 section 364 of 400 of the completengenome.) (nt:o578; 99 pct identical amino acid sequence and) (le:10727) (re:12463) (di:direct) AE000474 AE000474 g1790446 Escherichia coli 562 -11532867 7500953261 acek isocitrate dehydrogenase kinase/phosphatase (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (ec:2.7.1.116) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 17770) (le:83838) (re:85574) (di:direct) ECOUW89 U00006 g396351 Escherichia coli 562 -11532867 5000690539 (de:(ecoli\_3902) (pn:isocitrate dehydrogenase kinase) (gn:acek) (gtcfc:7.1:9.1:9.3:9.4) (ec:2.7.1.116) (acek\_ecoli) (keggfc:4.4:9.1:9.3:9.4) (rileyfc:1.3.1) (db:gtc-escherichia coli)) ECOLI\_3902 ECOLI\_3902 Escherichia coli 562 10124131

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824030	7539	29695	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824036	7540	29696	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824043	7541	29697	300	99

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824052	7542	29698	225	74

Description

6500729010 iclr:b4018 acetate operon repressor (gtcfc:2.3) (keggfc:14.2) (rileyfc:1.3.1) (db:gtc-escherichia coli) b4018 b4018 Escherichia coli 562 -11532868 7000688975 iclr acetate operon repressor (cl:acetate operon repressor) (db:pir1.dat) (mp:91 min) RPECIR A65209 Escherichia coli 562 -11532868 237224 iclr repressor of the acebak operon (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli (clone pgn1009) repressor protein for the acebak operon(iclr) gene, complete cds.) (le:181) (re:1044) (di:direct) ECOICLRA M63914 g146441 Escherichia coli 562 -11532868 234839 iclr repressor of aceba operon (fn:regulator; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 365 of 400 of the completegenome.) (nt:f287; 100 pct identical to 274 amino acids) (le:160) (re:1023) (di:complement) AE000475 AE000475 g1790449 Escherichia coli 562 -11532868 7500953616 iclr (fn:regulatory gene for acebak operon) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 614) (le:88046) (re:88909) (di:complement) ECOUW89 U00006 g396353 Escherichia coli 562 -11532868 5000690186 (de:(ecoli\_3904) (pn:repressor of aceba operon) (gn:iclr) (gtcfc:2.3) (ec:) (iclr\_ecoli) (keggfc:11.2) (rileyfc:1.3.1) (db:gtc-escherichia coli)) ECOI\_3904 ECOI\_3904 Escherichia coli 562 10124133



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824088	7543	29699	1272	424

Description

6500729011 aspa:b4139 aspartate ammonia-lyase:aspartase (gtcfc:2.3:2.6:5.2) (ec:4.3.1.1) (keggfc:2.5:5.2) (rileyfc:1.3.1) (db:gtc-escherichia coli) b4139 b4139 Escherichia coli 562 -11532869 125627 aspa aspartate ammonia-lyase::aspartase (cl:fumarate hydratase) (ec:4.3.1.1) (db:pir1.dat) (mp:94 min) UFECDW S56367 Escherichia coli 562 -11532869 7500953337 aspa aspartase (db:genpept-bct1) (ec:4.3.1.1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 991) (le:57719) (re:59200) (di:complement) ECOUW93 U14003 g536983 Escherichia coli 562 -11532869 237347 aspa aspartate ammonia-lyase aspartase (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (ec:4.3.1.1) (de:escherichia coli k-12 mg1655 section 376 of 400 of the completegenome.) (nt:f493; 100 pct identical to 478 amino acids) (le:8264) (re:9745) (di:complement) AE000486 AE000486 g1790581 Escherichia coli 562 -11532869 5000690214 (de:(ecoli\_4025) (pn:aspartate ammonia-lyase:aspartase) (gn:aspa) (gtcfc:2.6:5.2) (ec:4.3.1.1) (aspa\_ecoli) (keggfc:2.5:5.2) (rileyfc:1.3.1) (db:gtc-escherichia coli)) ECOLI\_4025 ECOLI\_4025 Escherichia coli 562 10066378

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824089	7544	29700	423	140

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824098	7545	29701	837	278

Description

6500729012 aspc:b0928 aspartate aminotransferase:transaminase a:aspat  
(gtcfc:2.4:5.1:5.10:5.15:5.2:5.5) (ec:2.6.1.1)  
(keggfc:2.3:5.1:5.2:5.5:5.10:5.15) (rileyfc:1.4.2) (db:gtc-escherichia coli)  
b0928 b0928 Escherichia coli 562 -11532870 7500876246 aspc (ec:2.6.1.1)  
(de:aspartate aminotransferase, (transaminase a) (aspat)) (db:swissprot)  
AAT\_ECOLI P00509 ESCHERICHIA COLI 562 -11532870 123493 aspc aspartate  
transaminase::aspartate aminotransferase:transaminase a (cl:aspartate  
aminotransferase) (ec:2.6.1.1) (db:pir1.dat) (mp:21 min) XNECD A00598  
Escherichia coli 562 -11532870 223284 aspc aspartate transaminase  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #218)  
(db:genpept-bct1) (de:escherichia coli genomic dna. (20.8 - 21.2 min).)  
(le:16873) (re:18063) (di:complement) D90730 D90730 g1651449 Escherichia  
coli 562 -11532870 223287 aspc aspartate transaminase (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #219) (db:genpept-bct1)  
(de:escherichia coli genomic dna. (21.1 - 21.4 min).) (le:1672) (re:2862)  
(di:complement) D90731 D90731 g1651453 Escherichia coli 562 -11532870  
232422 (db:genpept-bct1) (de:e. coli aspc gene for aspartate  
aminotransferase.) (nt:aspartate aminotransferase (aspc)) (le:138) (re:1328)  
(di:direct) ECASPC X03629 g41011 Escherichia coli 562 -11532870 5000690187  
(db:genpept-bct1) (de:e. coli aspc gene for aspartate aminotransferase.)  
(nt:aspartate aminotransferase (aa 1 - 396)) (le:10) (re:1200) (di:direct)  
ECASPCG X05904 g41013 Escherichia coli 562 -11532870 232421 aspc aspartate  
aminotransferase (fn:enzyme; amino acid biosynthesis: aspartate)  
(db:genpept-bct2) (ec:2.6.1.1) (de:escherichia coli k-12 mg1655 section 85  
of 400 of the completegenome.) (nt:f396; 100 pct identical to aat\_ecoli sw:  
p00509) (le:1565) (re:2755) (di:complement) AE000195 AE000195 g1787159  
Escherichia coli 562 -11532870 7502851828 aspc aspartate transaminase ec  
2.6.1.1 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #218)  
(db:genpept) (de:escherichia coli genomic dna. (20.9 - 21.3 min).)  
(nt:orf\_id:o219#3; similar to pir accession number) (le:16873) (re:18063)  
(di:complement) D90730 D90730 g1651449 Escherichia coli 562 -11532870  
7502851829 aspc aspartate transaminase ec 2.6.1.1 (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #219) (db:genpept) (de:escherichia  
coli genomic dna. (21.2 - 21.5 min).) (nt:orf\_id:o219#3; similar to pir  
accession number) (le:1672) (re:2862) (di:complement) D90731 D90731 g1651453  
Escherichia coli 562 -11532870 57893 aspc (ec:2.6.1.1) (de:aspartate  
aminotransferase, (transaminase a) (aspat)) (db:swissprot) AAT\_ECOLI P00509  
ESCHERICHIA COLI 562 -11532870

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824100	7546	29702	204	67

Description

6500729013 prkb:b3355 phosphoribulokinase:phosphopentokinase:prk (gtcfc:2.4:1.4) (ec:2.7.1.19) (keggfc:2.3) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3355 b3355 Escherichia coli 562 -11532871 80994 prkb (ec:2.7.1.19) (de:probable phosphoribulokinase, (phosphopentokinase) (prk)) (db:swissprot) KPPR\_ECOLI P37307 ESCHERICHIA COLI 562 -11532871 7000685699 prkb phosphoribulokinase (cl:phosphoribulokinase) (ec:2.7.1.19) (db:pir2.dat) F65129 F65129 Escherichia coli 562 -11532871 7500884700 prkb probable phosphoribulokinase (fn:putative enzyme; central intermediary) (db:genpept-bct2) (ec:2.7.1.19) (de:escherichia coli k-12 mg1655 section 301 of 400 of the completegenome.) (nt:o289; n-terminal differs from earlier version; 100) (le:6991) (re:7860) (di:direct) AE000411 AE000411 g2367214 Escherichia coli 562 -11532871

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824101	7547	29703	414	137

Description

6500729014 ybcf:arcc:b0521 hypothetical protein in purk 5 region:carbamate kinase (gtcfc:2.6:5.1:5.10) (ec:2.7.2.2) (keggfc:2.5:5.1:5.10) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0521 b0521 Escherichia coli 562 -11532872 110213 arcc (ec:2.7.2.2) (de:carbamate kinase,) (db:swissprot) ARCC\_ECOLI P37306 ESCHERICHIA COLI 562 -11532872 7000684605 arcc:ybcf carbamate kinase (cl:carbamate kinase) (ec:2.7.2.2) (db:pir2.dat) H64783 H64783 Escherichia coli 562 -11532872 7500877078 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to p. aeruginosa carbamate kinase) (le:129888) (re:130781) (di:direct) ECU82664 U82664 g1773201 Escherichia coli 562 -11532872 240294 arcc putative carbamate kinase ec 2.7.2.2 (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 48 of 400 of the completegenome.) (nt:o297; formerly designated ybcf) (le:3947) (re:4840) (di:direct) AE000158 AE000158 g1786732 Escherichia coli 562 -11532872 5000691642 (de:(ecoli\_504) (pn:hypothetical protein in purk 5"region:fragment) (gn:ybcf) (gtcfc:13.7:14.1) (ec:) (ybcf\_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_504 ECOLI\_504 Escherichia coli 562 10122876

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824102	7548	29704	1008	335

Description

GTC ORF with score 380 to: (fn:apurinic/apyrimidic endonuclease) (sr:fission yeast) (db:genpept-pln2) (de:schizosaccharomyces pombe apn1 apurinic/apyrimidic endonuclease(spapn1) mrna, complete cds.) (nt:apn1 endonuclease) (le:472) (re:1443) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824104	7549	29705	216	71

Description

GTC ORF with score 97 to: (fn:apurinic/apyridimic endonuclease) (sr:fission yeast) (db:genpept-pln2) (de:schizosaccharomyces pombe apn1 apurinic/apyrimidic endonuclease(spapn1) mrna, complete cds.) (nt:apn1 endonuclease) (le:472) (re:1443) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824109	7550	29706	411	136

Description

6500729015 asnb:b0674 asparagine synthetase b:glutamine-hydrolyzing (gtcfc:2.6:5.2) (ec:6.3.5.4) (keggfc:2.5:5.2) (rileyfc:1.4.2) (db:gtc-escherichia coli) b0674 b0674 Escherichia coli 562 -11532873 60371 asnb (ec:6.3.5.4) (de:asparagine synthetase b (glutamine-hydrolyzing),) (db:swissprot) ASNB\_ECOLI P22106 ESCHERICHIA COLI 562 -11532873 126056 asnb asparagine synthase glutamine-hydrolyzing::asparagine synthetase b (cl:asparagine synthase (glutamine-hydrolyzing)) (ec:6.3.5.4) (db:pir1.dat) AJECN A36616 Escherichia coli 562 -11532873 223134 asnb asparagine synthase glutamine-hydrolyzing (sr:escherichia coli(strain:k12) dna, clone:kohara clone #171) (db:genpept-bct1) (de:escherichia coli genomic dna. (14.8 - 15.2 min).) (le:10491) (re:12155) (di:complement) D90706 D90706 g1651277 Escherichia coli 562 -11532873 7500877250 asnb asparagine synthetase b (sr:e.coli (k12) dna) (db:genpept-bct1) (ec:6.3.5.4) (de:e.coli asparagine synthetase b (asnb) gene, complete cds.) (le:1001) (re:2665) (di:direct) ECOASNB J05554 g145393 Escherichia coli 562 -11532873 233870 asnb asparagine synthetase b (fn:enzyme; amino acid biosynthesis: asparagine) (db:genpept-bct2) (ec:6.3.5.4) (de:escherichia coli k-12 mg1655 section 61 of 400 of the completegenome.) (nt:f554; 100 pct identical to asnb\_ecoli sw: p22106) (le:220) (re:1884) (di:complement) AE000171 AE000171 g1786889 Escherichia coli 562 -11532873 5000690191 asnb asparagine synthase glutamine-hydrolyzing ec (sr:escherichia coli(strain:k12) dna, clone:kohara clone #171) (db:genpept) (de:escherichia coli genomic dna. (14.8 - 15.2 min).) (nt:orf\_id:o171#7; similar to pir accession number) (le:10306) (re:11970) (di:complement) D90706 D90706 g1651277 Escherichia coli 562 -11532873

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501824112	7551	29707	285	94

#### Description

6500729016 dada:dadr:b1189 d-amino acid dehydrogenase:d-amino acid dehydrogenase small subunit (gtcfc:2.6:5.13:6.6) (ec:1.4.99.1) (keggfc:2.5:5.13) (rileyfc:1.1.2) (db:gtc-escherichia coli) b1189 b1189 Escherichia coli 562 -11532874 67839 dada:dadr (ec:1.4.99.1) (de:d-amino acid dehydrogenase small subunit,) (db:swissprot) DADA\_ECOLI P29011 ESCHERICHIA COLI 562 -11532874 162903 dada:dadr d-amino-acid dehydrogenase:small chain (ec:1.4.99.1) (db:pir2.dat) B53383 B53383 Escherichia coli 562 -11532874 223405 dada d-amino acid dehydrogenase small subunit (sr:escherichia coli(strain:k12) dna, clone:kohara clone #244) (db:genpept-bct1) (de:escherichia coli genomic dna. (26.4 - 26.7 min).) (le:9317) (re:10615) (di:direct) D90753 D90753 g1651591 Escherichia coli 562 -11532874 234122 dada d-amino acid dehydrogenase subunit (fn:enzyme; degradation of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 107 of 400 of the completegenome.) (nt:o432; 100 pct identical to dada\_ecoli sw: p29011) (le:4498) (re:5796) (di:direct) AE000217 AE000217 g1787438 Escherichia coli 562 -11532874 7500879975 dada d-amino acid dehydrogenase (fn:oxidative deamination of d-amino acids) (sr:escherichia coli (strain k-12) dna) (db:genpept-bct2) (de:e. coli d-amino acid dehydrogenase and alanine racemase (dadoperon) genes, complete coding regions.) (nt:minor subunit) (le:1660) (re:2958) (di:di... ECODADAX L02948 g145703 Escherichia coli 562 -11532874 5000690388 dadr d-amino acid dehydrogenase small subunit ec (sr:escherichia coli(strain:k12) dna, clone:kohara clone #244) (db:genpept) (de:escherichia coli genomic dna. (26.5 - 26.8 min).) (nt:orf\_id:o244#9; similar to swissprot accession) (le:9317) (re:10615) (di:direct) D90753 D90753 g1651591 Escherichia coli 562 -11532874

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501824114	7552	29708	228	75

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824142	7553	29709	213	70

Description

6500729017 narg:narc:bisd:b1224 respiratory nitrate reductase 1 alpha chain  
 (gtcfc:2.6:2.8:12.13) (ec:1.7.99.4) (keggfc:2.5:12.1) (rileyfc:1.2.6)  
 (db:gtc-escherichia coli) b1224 b1224 Escherichia coli 562 -11532875  
 7000688850 narg:narc:bisd nitrate reductase:1 alpha chain:respiratory  
 nitrate reductase alpha chain (cl:nitrate reductase alpha chain)  
 (ec:1.7.99.4) (db:pir1.dat) (mp:27 min) RDECNA E64869 Escherichia coli 562  
 -11532875 7500953210 narg nitrate reductase alpha subunit (db:genpept-bct1)  
 (de:escherichia coli narg, narh, narj genes for nitrate reductase.)  
 (nt:catalytic subunit containint the molybdenum) (le:1) (re:3744)  
 (di:direct) ECNARGHJ X16181 g42086 Escherichia coli 562 -11532875 233454  
 narg nitrate reductase 1:alpha subunit (fn:enzyme; energy metabolism,  
 carbon: anaerobic) (db:genpept-bct2) (ec:1.7.99.4) (de:escherichia coli k-12  
 mg1655 section 111 of 400 of the completegenome.) (nt:ol247; 99 pct  
 identical to narg\_ecoli sw: p09152) (le:288) (re:4031) (di:direct) AE000221  
 AE000221 g1787477 Escherichia coli 562 -11532875 5000690192 bisd  
 respiratory nitrate reductase 1 alpha chain ec (sr:escherichia  
 coli(strain:k12) dna, clone:kohara clone #249) (db:genpept) (de:escherichia  
 coli genomic dna. (27.6 - 27.9 min).) (nt:orf\_id:o249#1; similar to  
 swissprot accession) (le:1203) (re:4946) (di:direct) D90758 D90758 g4062800  
 Escherichia coli 562 -11532875

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501824144	7554	29710	1239	412
Description				
<p>6500729018 narh:b1225 respiratory nitrate reductase 1 beta chain  (gtcf:2.6:2.8:12.13) (ec:1.7.99.4) (keggfc:2.5:12.1) (rileyfc:1.2.6)  (db:gtc-escherichia coli) b1225 b1225 Escherichia coli 562 -11532876 301346  narh (ec:1.7.99.4) (de:respiratory nitrate reductase 1 beta chain,)  (db:swissprot) NARH_ECOLI P11349 ESCHERICHIA COLI 562 -11532876 7000685924  narh nitrate reductase:1 beta chain:respiratory nitrate reductase beta chain  (cl:nitrate reductase beta chain:ferredoxin 2(4fe-4s) homology)  (ec:1.7.99.4) (db:pir1.dat) (mp:27 min) RDECNB F64869 Escherichia coli 562  -11532876 223431 narh nitrate reductase beta chain (sr:escherichia  coli(strain:k12) dna, clone:kohara clone #249) (db:genpept-bct1)  (de:escherichia coli genomic dna(27.5-27.8 min).) (le:4943) (re:6481)  (di:direct) D90758 D90758 g1651621 Escherichia coli 562 -11532876 223439  narh nitrate reductase beta chain (sr:escherichia coli(strain:k12) dna,  clone:kohara clone #250) (db:genpept-bct1) (de:escherichia coli genomic dna  (27.6-28.0 min).) (le:600) (re:2138) (di:direct) D90759 D90759 g1651630  Escherichia coli 562 -11532876 224706 narh respiratory nitrate reductase 1  beta chain ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda  minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  #251(27.7-28.2 min).) (nt:orf_id:o249#2; similar to (swissprot accession)  (le:600) (re:2138) (di:direct) D90852 D90852 g1805505 Escherichia coli 562  -11532876 5000690193 narh nitrate reductase beta subunit (db:genpept-bct1)  (de:escherichia coli narg, narh, narj genes for nitrate reductase.)  (nt:subunit containing 4 iron-sulfur centers) (le:3741) (re:5279)  (di:direct) ECNARGHJ X16181 g42087 Escherichia coli 562 -11532876 233455  narh nitrate reductase 1:beta subunit (fn:enzyme; energy metabolism, carbon:  anaerobic) (db:genpept-bct2) (ec:1.7.99.4) (de:escherichia coli k-12 mg1655  section 111 of 400 of the completengenome.) (nt:o512; 100 pct identical to  narh_ecoli sw: p11349) (le:4028) (re:5566) (di:direct) AE000221 AE000221  g1787478 Escherichia coli 562 -11532876 7502851830 narh respiratory nitrate  reductase 1 beta chain ec (sr:escherichia coli(strain:k12) dna, clone:kohara  clone #249) (db:genpept) (de:escherichia coli genomic dna. (27.6 - 27.9  min).) (nt:orf_id:o250#1; similar to swissprot accession) (le:4943)  (re:6481) (di:direct) D90758 D90758 g1651621 Escherichia coli 562 -11532876  7502851831 narh respiratory nitrate reductase 1 beta chain ec  (sr:escherichia coli(strain:k12) dna, clone:kohara clone #250) (db:genpept)  (de:escherichia coli genomic dna. (27.7 - 28.1 min).) (nt:orf_id:o250#1;  similar to swissprot accession) (le:600) (re:2138) (di:direct) D90759 D90759  g1651630 Escherichia coli 562 -11532876 85239 narh (ec:1.7.99.4)  (de:respiratory nitrate reductase 1 beta chain,) (db:swissprot) NARH_ECOLI  P11349 ESCHERICHIA COLI 562 -11532876</p>				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824157	7555	29711	1038	345

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824174	7556	29712	1470	489

Description

6500729019 narj:b1226 respiratory nitrate reductase 1 delta chain  
(gtcfc:2.6:2.8:12.13) (ec:1.7.99.4) (keggfc:2.5:12.1) (rileyfc:1.2.6)  
(db:gtc-escherichia coli) b1226 b1226 Escherichia coli 562 -11532877 85243  
narj (ec:1.7.99.4) (de:respiratory nitrate reductase 1 delta chain,)  
(db:swissprot) NARJ\_ECOLI P11351 ESCHERICHIA COLI 562 -11532877 131432 narj  
nitrate reductase:1 delta chain (cl:narj protein) (ec:1.7.99.4)  
(db:pir1.dat) (mp:27 min) BVE CJ B27737 Escherichia coli 562 -11532877  
223432 narj narj protein (sr:escherichia coli(strain:k12) dna, clone:kohara  
clone #249) (db:genpept-bct1) (de:escherichia coli genomic dna(27.5-27.8  
min).) (le:6478) (re:7188) (di:direct) D90758 D90758 g1651622 Escherichia  
coli 562 -11532877 223440 narj narj protein (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #250) (db:genpept-bct1)  
(de:escherichia coli genomic dna (27.6-28.0 min).) (le:2135) (re:2845)  
(di:direct) D90759 D90759 g1651631 Escherichia coli 562 -11532877 224707  
narj narj protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara  
lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#251(27.7-28.2 min).) (nt:orf\_id:o249#3; similar to (pir accession number)  
(le:2135) (re:2845) (di:direct) D90852 D90852 g1805506 Escherichia coli 562  
-11532877 301347 (sr:e.coli dna) (db:genpept-bct1) (de:e.coli nar operon  
with two genes encoding nitrate reductasesubunits, complete cds.) (nt:narj  
protein) (le:446) (re:1156) (di:direct) ECONARI M20147 g146920 Escherichia  
coli 562 -11532877 235215 narj nitrate reductase 1:delta subunit:assembly  
(fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2)  
(ec:1.7.99.4) (de:escherichia coli k-12 mg1655 section 111 of 400 of the  
completegenome.) (nt:o236; 100 pct identical to narj\_ecoli sw: p11351)  
(le:5563) (re:6273) (di:direct) AE000221 AE000221 g1787479 Escherichia coli  
562 -11532877 5000690194 narj narj protein. (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #249) (db:genpept) (de:escherichia  
coli genomic dna. (27.6 - 27.9 min).) (nt:orf\_id:o250#2; similar to pir  
accession number) (le:6478) (re:7188) (di:direct) D90758 D90758 g1651622  
Escherichia coli 562 -11532877 7502851832 narj narj protein.  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #250) (db:genpept)  
(de:escherichia coli genomic dna. (27.7 - 28.1 min).) (nt:orf\_id:o250#2;  
similar to pir accession number) (le:2135) (re:2845) (di:direct) D90759  
D90759 g1651631 Escherichia coli 562 -11532877



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824180	7557	29713	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824182	7558	29714	444	147

Description

6500729020 nari:chli:b1227 respiratory nitrate reductase 1 gamma chain:cytochrome b-nr (gtcfc:2.6:2.8:12.13) (ec:1.7.99.4) (keggfc:2.5:12.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b1227 b1227 Escherichia coli 562 -11532878 85241 nari:chli (ec:1.7.99.4) (de:b-nr)) (db:swissprot) NARI\_ECOLI P11350 ESCHERICHIA COLI 562 -11532878 122913 nari:chli nitrate reductase:1 gamma chain:cytochrome b-nr:respiratory nitrate reductase gamma chain (cl:nitrate reductase gamma chain) (ec:1.7.99.4) (db:pir1.dat) (mp:27 min) RDECNG C27737 Escherichia coli 562 -11532878 223433 nari respiratory nitrate reductase 1 gamma chain (sr:escherichia coli(strain:k12) dna, clone:kohara clone #249) (db:genpept-bct1) (de:escherichia coli genomic dna(27.5-27.8 min).) (le:7188) (re:7865) (di:direct) D90758 D90758 g1651623 Escherichia coli 562 -11532878 223441 nari respiratory nitrate reductase 1 gamma chain (sr:escherichia coli(strain:k12) dna, clone:kohara clone #250) (db:genpept-bct1) (de:escherichia coli genomic dna (27.6-28.0 min).) (le:2845) (re:3522) (di:direct) D90759 D90759 g1651632 Escherichia coli 562 -11532878 224708 chli respiratory nitrate reductase 1 gamma chain ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #251(27.7-28.2 min).) (nt:orf\_id:o249#4; similar to (swissprot accession) (le:2845) (re:3522) (di:direct) D90852 D90852 g1805507 Escherichia coli 562 -11532878 301348 (sr:e.coli dna) (db:genpept-bct1) (de:e.coli nar operon with two genes encoding nitrate reductasesubunits, complete cds.) (nt:nari protein, gamma subunit) (le:1156) (re:1833) (di:direct) ECONARI M20147 g146921 Escherichia coli 562 -11532878 235216 nari nitrate reductase 1:cytochrome b nr:gamma (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (ec:1.7.99.4) (de:escherichia coli k-12 mg1655 section 111 of 400 of the completegenome.) (nt:o225; 100 pct identical to nari\_ecoli sw: p11350) (le:6273) (re:6950) (di:direct) AE000221 AE000221 g1787480 Escherichia coli 562 -11532878 5000690195 chli respiratory nitrate reductase 1 gamma chain ec (sr:escherichia coli(strain:k12) dna, clone:kohara clone #249) (db:genpept) (de:escherichia coli genomic dna. (27.6 - 27.9 min).) (nt:orf\_id:o250#3; similar to swissprot accession) (le:7188) (re:7865) (di:direct) D90758 D90758 g1651623 Escherichia coli 562 -11532878 7502851833 chli respiratory nitrate reductase 1 gamma chain ec (sr:escherichia coli(strain:k12) dna, clone:kohara clone #250) (db:genpept) (de:escherichia coli genomic dna. (27.7 - 28.1 min).) (nt:orf\_id:o250#3; similar to swissprot accession) (le:2845) (re:3522) (di:direct) D90759 D90759 g1651632 Escherichia coli 562 -11532878

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824186	7559	29715	813	271

#### Description

6500729021 narv:b1465 respiratory nitrate reductase 2 gamma chain  
 (gtcfc:2.6:2.8) (ec:1.7.99.4) (keggfc:2.5) (rileyfc:1.2.6)  
 (db:gtc-escherichia coli) b1465 b1465 Escherichia coli 562 -11532879 300542  
 narv (ec:1.7.99.4) (de:respiratory nitrate reductase 2 gamma chain,)  
 (db:swissprot) NARV\_ECOLI P19316 ESCHERICHIA COLI 562 -11532879 136998 narv  
 nitrate reductase:2 gamma chain:narv protein (cl:nitrate reductase gamma  
 chain) (ec:1.7.99.4) (db:pir2.dat) S11430 S11430 Escherichia coli 562  
 -11532879 223778 narv narv protein (sr:escherichia coli (strain:k12) dna,  
 clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
 kohara clone #275(32.8-33.2 min.)) (nt:orf\_id:o276#4; similar to (pir  
 accession number) (le:12241) (re:12921) (di:complement) D90786 D90786  
 g1742384 Escherichia coli 562 -11532879 223790 narv narv protein  
 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
 (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #276(33.0-33.3  
 min.)) (nt:orf\_id:o276#4; similar to (pir accession number) (le:6167)  
 (re:6847) (di:complement) D90787 D90787 g1742397 Escherichia coli 562  
 -11532879 5000690196 narv apocytochrome b nr (db:genpept-bct1) (de:e. coli  
 transcription unit narzywv dna for nitrate reductasesubunits.) (le:6218)  
 (re:6898) (di:direct) ECNARZYW X17110 g42111 Escherichia coli 562 -11532879  
 233472 narv cryptic nitrate reductase 2:gamma subunit (fn:enzyme; energy  
 metabolism, carbon: anaerobic) (db:genpept-bct2) (ec:1.7.99.4)  
 (de:escherichia coli k-12 mg1655 section 133 of 400 of the completegenome.)  
 (nt:f226; 100 pct identical to narv\_ecoli sw: p19316;) (le:5472) (re:6152)  
 (di:complement) AE000243 AE000243 g1787738 Escherichia coli 562 -11532879  
 85256 narv (ec:1.7.99.4) (de:respiratory nitrate reductase 2 gamma chain,)  
 (db:swissprot) NARV\_ECOLI P19316 ESCHERICHIA COLI 562 -11532879

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824201	7560	29716	252	83

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824211	7561	29717	186	61

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824219	7562	29718	516	171

Description

6500729022 narw:bl466 respiratory nitrate reductase 2 delta chain  
 (gtcfc:2.6:2.8) (ec:1.7.99.4) (keggfc:2.5) (rileyfc:1.2.6)  
 (db:gtc-escherichia coli) bl466 bl466 Escherichia coli 562 -11532880 300543  
 narw (ec:1.7.99.4) (de:respiratory nitrate reductase 2 delta chain,)  
 (db:swissprot) NARW\_ECOLI P19317 ESCHERICHIA COLI 562 -11532880 154713 narw  
 nitrate reductase:2 delta chain:narw protein (cl:narj protein) (ec:1.7.99.4)  
 (db:pir2.dat) S11429 S11429 Escherichia coli 562 -11532880 223779 narw narw  
 protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda  
 minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
 #275(32.8-33.2 min.)) (nt:orf\_id:o276#5; similar to (pir accession number)  
 (le:12918) (re:13613) (di:complement) D90786 D90786 g1742385 Escherichia  
 coli 562 -11532880 223791 narw narw protein (sr:escherichia coli  
 (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
 (de:e.coli genomic dna, kohara clone #276(33.0-33.3 min.))  
 (nt:orf\_id:o276#5; similar to (pir accession number) (le:6844) (re:7539)  
 (di:complement) D90787 D90787 g1742398 Escherichia coli 562 -11532880  
 5000690197 narw narw product (db:genpept-bct1) (de:e. coli transcription  
 unit narzywv dna for nitrate reductasesubunits.) (le:5526) (re:6221)  
 (di:direct) ECNARZYW X17110 g42110 Escherichia coli 562 -11532880 233471  
 narw cryptic nitrate reductase 2:delta subunit (fn:enzyme; energy  
 metabolism, carbon: anaerobic) (db:genpept-bct2) (ec:1.7.99.4)  
 (de:escherichia coli k-12 mg1655 section 133 of 400 of the completegenome.)  
 (nt:f231; 100 pct identical to narw\_ecoli sw: p19317;) (le:6149) (re:6844)  
 (di:complement) AE000243 AE000243 g1787739 Escherichia coli 562 -11532880  
 85257 narw (ec:1.7.99.4) (de:respiratory nitrate reductase 2 delta chain,)  
 (db:swissprot) NARW\_ECOLI P19317 ESCHERICHIA COLI 562 -11532880

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824227	7563	29719	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824239	7564	29720	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824248	7565	29721	702	233

Description

GTC ORF with score 1008 to: (sr:aspergillus oryzae (strain:jcm02238) dna)  
(db:genpept-pln1) (de:aspergillus oryzae gene for hape, complete cds.)  
(nt:putative compornent of ccaat binding complex: yeast)  
(le:1016:1215:1299:1413) (re:1097:1228:1355:2054) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824249	7566	29722	471	156

Description

6500729023 nary:b1467 respiratory nitrate reductase 2 beta chain  
(gtcfc:2.6:2.8) (ec:1.7.99.4) (keggfc:2.5) (rileyfc:1.2.6)  
(db:gtc-escherichia coli) b1467 b1467 Escherichia coli 562 -11532881 85259  
nary (ec:1.7.99.4) (de:respiratory nitrate reductase 2 beta chain,)  
(db:swissprot) NARY\_ECOLI P19318 ESCHERICHIA COLI 562 -11532881 7000685931  
nary nitrate reductase:2 beta chain (cl:nitrate reductase beta  
chain:ferredoxin 2(4fe-4s) homology) (ec:1.7.99.4) (db:pir2.dat) F64899  
F64899 Escherichia coli 562 -11532881 223780 nary nary protein  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #275(32.8-33.2  
min.)) (nt:orf\_id:o276#6; similar to (pir accession number) (le:13613)  
(re:15157) (di:complement) D90786 D90786 g1742386 Escherichia coli 562  
-11532881 223792 nary nary protein (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #276(33.0-33.3 min.)) (nt:orf\_id:o276#6; similar to (pir  
accession number) (le:7539) (re:9083) (di:complement) D90787 D90787 g1742399  
Escherichia coli 562 -11532881 300544 nary cryptic nitrate reductase 2:beta  
subunit (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2)  
(ec:1.7.99.4) (de:escherichia coli k-12 mg1655 section 133 of 400 of the  
completegenome.) (nt:f514; 99 pct identical to nary\_ecoli sw: p19318; cg)  
(le:6844) (re:8388) (di:complement) AE000243 AE000243 g1787740 Escherichia  
coli 562 -11532881 5000690198 (de:(ecoli\_1427) (pn:cryptic nitrate  
reductase ii, beta subunit) (gn:nary) (gtcfc:2.6) (ec:1.7.99.4) (nary\_ecoli)  
(keggfc:2.5) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI\_1427  
ECOLI\_1427 Escherichia coli 562 10119624

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824258	7567	29723	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824259	7568	29724	681	226
<u>Description</u>				
6500729024 narz:b1468 respiratory nitrate reductase 2 alpha chain (gtcfc:2.6:2.8) (ec:1.7.99.4) (keggfc:2.5) (rileyfc:1.2.6) (db:gtc-escherichia coli) b1468 b1468 Escherichia coli 562 -11532882 7000689042 narz nitrate reductase:2 alpha chain (cl:nitrate reductase alpha chain) (ec:1.7.99.4) (db:pir2.dat) G64899 G64899 Escherichia coli 562 -11532882 7500953898 narz cryptic nitrate reductase 2:alpha subunit (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (ec:1.7.99.4) (de:escherichia coli k-12 mg1655 section 133 of 400 of the completegenome.) (nt:f1246; 99 pct identical to narz_ecoli sw: p19319;) (le:8385) (re:12125) (di:complement) AE000243 AE000243 g1787741 Escherichia coli 562 -11532882 5000690199 (de:(ecoli_1428) (pn:cryptic nitrate reductase ii, alpha subunit) (gn:narz) (gtcfc:2.6) (ec:1.7.99.4) (narz_ecoli) (keggfc:2.5) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI_1428 ECOLI_1428 Escherichia coli 562 10123341				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824263	7569	29725	474	157

Description

6500729025 gdha:b1761 nadp-specific glutamate dehydrogenase:nadp-gdh  
 (gtcfc:2.6:5.1) (ec:1.4.1.4) (keggfc:2.5:5.1) (rileyfc:1.4.1)  
 (db:gtc-escherichia coli) b1761 b1761 Escherichia coli 562 -11532883 234473  
 gdha (ec:1.4.1.4) (de:nadp-specific glutamate dehydrogenase, (nadp-gdh))  
 (db:swissprot) DHE4\_ECOLI P00370 ESCHERICHIA COLI 562 -11532883 122729 gdha  
 glutamate dehydrogenase nadp+:glutamic dehydrogenase:nadp-specific  
 glutamate dehydrogenase (cl:glutamate dehydrogenase (nad(p+))) (ec:1.4.1.4)  
 (db:pir1.dat) (mp:27 min) DEECEN A00382 Escherichia coli 562 -11532883  
 224230 gdha nadp-specific glutamate dehydrogenase ec (sr:escherichia coli  
 (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
 (de:e.coli genomic dna, kohara clone #328(39.4-39.8 min.))  
 (nt:orf\_id:o328#14; similar to (swissprot accession) (le:13885) (re:15228)  
 (di:direct) D90819 D90819 g1742869 Escherichia coli 562 -11532883 300872  
 gdha glutamate dehydrogenase (db:genpept-bct1) (de:e. coli gdha gene for  
 nadp-specific glutamate dehydrogenase(ec1.4.1.4).) (le:73) (re:1416)  
 (di:direct) ECGDHA X00988 g41544 Escherichia coli 562 -11532883 5000690200  
 gdha glutamate dehydrogenase (sr:escherichia coli (strain k-12) (clone:  
 pbgl) dna; and escherichi) (db:genpept-bct1) (de:e.coli gdha gene coding for  
 nadp-specific glutamate dehydrogenase.) (le:193) (re:1536) (di:direct)  
 ECGDHA J01615 g146124 Escherichia coli 562 -11532883 232984 gdha  
 nadp-specific glutamate dehydrogenase (fn:enzyme; amino acid biosynthesis:  
 glutamate) (db:genpept-bct2) (ec:1.4.1.4) (de:escherichia coli k-12 mg1655  
 section 161 of 400 of the completegenome.) (nt:o447; 100 pct identical to  
 dhe4\_ecoli sw: p00370;) (le:148) (re:1491) (di:direct) AE000271 AE000271  
 g1788059 Escherichia coli 562 -11532883 68483 gdha (ec:1.4.1.4)  
 (de:nadp-specific glutamate dehydrogenase, (nadp-gdh)) (db:swissprot)  
 DHE4\_ECOLI P00370 ESCHERICHIA COLI 562 -11532883

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824265	7570	29726	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824266	7571	29727	885	294

Description

6500729026 ansa:b1767 l-asparaginase i:l-asparagine amidohydrolase i  
(gtcfc:2.6:5.2:6.5:6.6) (ec:3.5.1.1) (keggfc:2.5:5.2:6.5) (rileyfc:1.1.2)  
(db:gtc-escherichia coli) b1767 b1767 Escherichia coli 562 -11532884 60345  
ansa (ec:3.5.1.1) (de:l-asparaginase i, (l-asparagine amidohydrolase i))  
(db:swissprot) ASG1\_ECOLI P18840 ESCHERICHIA COLI 562 -11532884 7000684643  
ansa asparaginase:i (cl:asparaginase) (ec:3.5.1.1) (db:pir1.dat) (mp:39 min)  
XDEC1 G64936 Escherichia coli 562 -11532884 224238 ansa l-asparaginase i ec  
3.5.1.1 l-asparagine (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara  
lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#329(39.7-40.0 min.)) (nt:orf\_id:o329#4; similar to (swissprot accession)  
(le:7717) (re:8733) (di:direct) D90820 D90820 g1742878 Escherichia coli 562  
-11532884 300880 ansa cytoplasmic l-asparaginase i (fn:enzyme; degradation  
of small molecules: amino) (db:genpept-bct2) (ec:3.5.1.1) (de:escherichia  
coli k-12 mg1655 section 161 of 400 of the completegenome.) (nt:o338; 100  
pct identical to asg1\_ecoli sw: p18840;) (le:8637) (re:9653) (di:direct)  
AE000271 AE000271 g1788065 Escherichia coli 562 -11532884 5000690201  
(de:(ecoli\_1724) (pn:cytoplasmic l-asparaginase i) (gn:ansa)  
(gtcfc:2.6:5.2:6.5) (ec:3.5.1.1) (asg1\_ecoli) (keggfc:2.5:5.2:6.5)  
(rileyfc:1.1.2) (db:gtc-escherichia coli)) ECOLI\_1724 ECOLI\_1724 Escherichia  
coli 562 10003071

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824282	7572	29728	525	174

Description

6500729027 napa:b2206 probable nitrate reductase:periplasmic nitrate  
reductase precursor (gtcfc:2.6:11.1) (ec:1.7.99.4) (keggfc:2.5)  
(rileyfc:5.8.0) (db:gtc-escherichia coli) b2206 b2206 Escherichia coli 562  
-11532885 85217 napa (ec:1.7.99.4) (de:periplasmic nitrate reductase  
precursor,) (db:swissprot) NAPA\_ECOLI P33937 ESCHERICHIA COLI 562 -11532885  
7000685913 napa probable nitrate reductase (cl:formate dehydrogenase)  
(ec:1.7.99.4) (db:pir2.dat) D64990 D64990 Escherichia coli 562 -11532885  
7500886286 napa probable nitrate reductase 3 (fn:putative enzyme; energy  
metabolism, carbon:) (db:genpept-bct2) (ec:1.7.99.4) (de:escherichia coli  
k-12 mg1655 section 199 of 400 of the completegenome.) (nt:f828; 99 pct  
identical to 801 residues of a 809 aa) (le:9991) (re:12477) (di:complement)  
AE000309 AE000309 g1788534 Escherichia coli 562 -11532885 5000690202  
(de:(ecoli\_2155) (pn:probable nitrate reductase) (gn:napa) (gtcfc:2.6)  
(ec:1.7.99.4) (napa\_ecoli) (keggfc:2.5) (rileyfc:5.7.0) (db:gtc-escherichia  
coli)) ECOLI\_2155 ECOLI\_2155 Escherichia coli 562 10123600

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824292	7573	29729	522	173
<u>Description</u>				

6500729028 ansb:b2957 l-asparaginase:l-asparaginase ii  
precursor:l-asparagine amidohydrolase ii (gtcfc:2.6:5.2:6.5:6.6)  
(ec:3.5.1.1) (keggfc:2.5:5.2:6.5) (rileyfc:1.1.2) (db:gtc-escherichia coli)  
b2957 b2957 Escherichia coli 562 -11532886 60347 ansb (ec:3.5.1.1)  
(de:amidohydrolase ii)) (db:swissprot) ASG2\_ECOLI P00805 ESCHERICHIA COLI  
562 -11532886 125005 ansb asparaginase:ii precursor (cl:asparaginase)  
(ec:3.5.1.1) (db:pir1.dat) (mp:63.8 min) XDEC A35132 Escherichia coli 562  
-11532886 234958 (sr:e.coli (strain k12 isolate jml08) dna, clones  
lambda-ansb an) (db:genpept-bct1) (de:e.coli l-asparaginase ii (ansb) gene,  
complete cds.) (nt:l-asparaginase ii (ansb) (ec 3.5.1.1)) (le:346) (re:1392)  
(di:direct) ECOANSBA M34234 g145277 Escherichia coli 562 -11532886 239170  
(sr:e.coli (strain k-12) dna) (db:genpept-bct1) (ec:3.5.1.1) (de:e.coli  
l-asparaginase ii (ansb) gene, complete cds.) (nt:l-asparaginase ii (ansb)  
precursor) (le:385) (re:1431) (di:direct) ECOLASNII M34277 g146597  
Escherichia coli 562 -11532886 7500877238 ansb l-asparaginase  
(db:genpept-bct1) (ec:3.5.1.1) (de:escherichia coli k-12 genome;  
approximately 65 to 68 minutes.) (nt:cg site no. 30045) (le:54076)  
(re:55122) (di:complement) ECU28377 U28377 g882486 Escherichia coli 562  
-11532886 233800 ansb periplasmic l-asparaginase ii (fn:enzyme; degradation  
of small molecules: amino) (db:genpept-bct2) (ec:3.5.1.1) (de:escherichia  
coli k-12 mg1655 section 268 of 400 of the completegenome.) (nt:f348; 100  
pct identical to asg2\_ecoli sw: p00805;) (le:5704) (re:6750) (di:complement)  
AE000378 AE000378 g1789327 Escherichia coli 562 -11532886 5000690204  
(de:(ecoli\_2879) (pn:periplasmic l-asparaginase ii) (gn:ansb)  
(gtcfc:2.6:5.2:6.5) (ec:3.5.1.1) (asg2\_ecoli) (keggfc:2.5:5.2:6.5)  
(rileyfc:1.1.2) (db:gtc-escherichia coli)) ECOLI\_2879 ECOLI\_2879 Escherichia  
coli 562 10003073



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824310	7574	29730	516	172

Description

6500729029 metc:b3008 cystathionine  
 beta-lyase:cbl:beta-cystathionase:cysteine lyase  
 (gtcfc:2.6:2.7:5.2:5.4:5.5:6.4) (ec:4.4.1.8) (keggfc:2.5:2.6:5.4:5.5:6.4)  
 (rileyfc:1.4.2) (db:gtc-escherichia coli) b3008 b3008 Escherichia coli 562  
 -11532887 83542 metc (ec:4.4.1.8) (de:(cysteine lyase)) (db:swissprot)  
 METC\_ECOLI P06721 ESCHERICHIA COLI 562 -11532887 125696 metc cystathionine  
 beta-lyase::beta-cystathionase:cystine lyase (cl:o-succinylhomoserine  
 (thiol)-lyase) (ec:4.4.1.8) (db:pir1.dat) (mp:65 min) WZECCB A25153  
 Escherichia coli 562 -11532887 7500885518 metc beta-cystathionase  
 (sr:e.coli k12 dna, clone pip29) (db:genpept-bct1) (ec:4.4.1.8) (de:e.coli  
 (metc) gene encoding beta-cystathionase, complete cds.) (le:499) (re:1686)  
 (di:direct) ECOMETC M12858 g146824 Escherichia coli 562 -11532887 235123  
 metc cystathionine beta-lyase beta-cystathionase (fn:enzyme; amino acid  
 biosynthesis: methionine) (db:genpept-bct2) (ec:4.4.1.8) (de:escherichia  
 coli k-12 mg1655 section 273 of 400 of the completegenome.) (nt:o395; 99 pct  
 identical to metc\_ecoli sw:) (le:2700) (re:3887) (di:direct) AE000383  
 AE000383 g1789383 Escherichia coli 562 -11532887 5000690205  
 (de:(ecoli\_2930) (pn:cystathionine beta-lyase) (gn:metc)  
 (gtcfc:2.6:5.4:5.5:6.4) (ec:4.4.1.8) (metc\_ecoli) (keggfc:2.5:5.4:5.5:6.4)  
 (rileyfc:1.4.2) (db:gtc-escherichia coli)) ECOLI\_2930 ECOLI\_2930 Escherichia  
 coli 562 10025756

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824313	7575	29731	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824320	7576	29732	693	230

Description

6500729030 nirb:b3365 nadh-nitrate oxidoreductase apoprotein:nitrite reductase:nadph large subunit (gtcfc:2.6:2.8) (ec:1.6.6.4) (keggfc:2.5) (rileyfc:1.2.6) (db:gtc-escherichia coli) b3365 b3365 Escherichia coli 562 -11532888 86027 nirb (ec:1.6.6.4) (de:nitrite reductase (nad(p)h) large subunit,) (db:swissprot) NIRB\_ECOLI P08201 ESCHERICHIA COLI 562 -11532888 7000685967 nirb nitrite reductase nadh (ec:1.6.6.4) (db:pir2.dat) H65130 H65130 Escherichia coli 562 -11532888 7500886474 nirb nadh-nitrate oxidoreductase apoprotein (db:genpept-bct1) (ec:1.6.6.4) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 451; alternate name nird; sequence) (le:274758) (re:277301) (di:direct) ECOUW67 U18997 g606299 Escherichia coli 562 -11532888 236598 nirb nitrite reductase nad p h subunit (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (ec:1.6.6.4) (de:escherichia coli k-12 mg1655 section 302 of 400 of the completegenome.) (nt:o847; cg site no. 451; alternate name nird;) (le:5115) (re:7658) (di:direct) AE000412 AE000412 g1789765 Escherichia coli 562 -11532888 5000690208 (de:(ecoli\_3283) (pn:nitrite reductase:nad:ph subunit) (gn:nirb) (gtcfc:2.6) (ec:1.6.6.4) (nirb\_ecoli) (keggfc:2.5) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI\_3283 ECOLI\_3283 Escherichia coli 562 10028194

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824322	7577	29733	636	211

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824338	7578	29734	183	61

Description

6500729031 nird:b3366 nadph small subunit:nitrite reductase:nadph small subunit (gtcfc:2.6:2.8) (ec:1.6.6.4) (keggfc:2.5) (rileyfc:1.2.6) (db:gtc-escherichia coli) b3366 b3366 Escherichia coli 562 -11532889 86031 nird (ec:1.6.6.4) (de:nitrite reductase (nad(p)h) small subunit,) (db:swissprot) NIRD\_ECOLI P23675 ESCHERICHIA COLI 562 -11532889 7000685968 nird nitrite reductase nadh:small chain (ec:1.6.6.4) (db:pir2.dat) A65131 A65131 Escherichia coli 562 -11532889 7500886475 nird (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (le:277298) (re:277624) (di:direct) ECOUW67 U18997 g606300 Escherichia coli 562 -11532889 236599 nird nitrite reductase nad p h subunit (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (ec:1.6.6.4) (de:escherichia coli k-12 mg1655 section 302 of 400 of the completegenome.) (nt:o108; 100 pct identical amino acid sequence and) (le:7655) (re:7981) (di:direct) AE000412 AE000412 g1789766 Escherichia coli 562 -11532889 5000690209 (de:(ecoli\_3284) (pn:nitrite reductase:nad:ph subunit,) (gn:nird) (gtcfc:2.6) (ec:1.6.6.4) (nird\_ecoli) (keggfc:2.5) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI\_3284 ECOLI\_3284 Escherichia coli 562 10028198

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824342	7579	29735	804	268

Description

6500729032 nirc:b3367 (gtcfc:2.6:2.8) (ec:1.6.6.4) (keggfc:2.5) (rileyfc:1.2.6) (db:gtc-escherichia coli) b3367 b3367 Escherichia coli 562 -11532890 7000691873 nirc nirc protein (cl:formate dehydrogenase foch) (db:pir2.dat) (mp:26 min) B65131 B65131 Escherichia coli 562 -11532890 236600 (db:genpept-bct1) (de:e. coli nirb, nird, nirc and cysg genes.) (nt:put. nirc gene product (aa 1-184)) (le:3650) (re:4204) (di:direct) ECNIRBC X14202 g42123 Escherichia coli 562 -11532890 7500960399 nirc (fn:nadh-nitrate reductase activity) (db:genpept-bct1) (ec:1.6.6.4) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 452) (le:278002) (re:278556) (di:direct) ECOUW67 U18997 g606301 Escherichia coli 562 -11532890 233485 nirc nitrite reductase activity (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (ec:1.6.6.4) (de:escherichia coli k-12 mg1655 section 302 of 400 of the completegenome.) (nt:o184; cg site no. 452; this 184 aa orf is 100 pct) (le:8359) (re:8913) (di:direct) AE000412 AE000412 g1789767 Escherichia coli 562 -11532890 5000690210 (de:(ecoli\_3285) (pn:nitrite reductase activity) (gn:nirc) (gtcfc:2.6) (ec:1.6.6.4) (nirc\_ecoli) (keggfc:2.5) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI\_3285 ECOLI\_3285 Escherichia coli 562 10124017

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824345	7580	29736	291	96

Description

6500729033 tnaa:b3708 tryptophanase (gtcfc:2.6:5.14:6.6) (ec:4.1.99.1)  
(keggfc:2.5:5.14) (rileyfc:1.1.2) (db:gtc-escherichia coli) b3708 b3708  
Escherichia coli 562 -11532891 7000688890 tnaa tryptophanase  
(cl:tryptophanase) (ec:4.1.99.1) (db:pir1.dat) (mp:83 min) WZEC E65173  
Escherichia coli 562 -11532891 7500953335 tnaa::cg site no. 101  
tryptophanase (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52)  
(db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.)  
(le:78112) (re:79542) (di:direct) ECOUW82 L10328 g290556 Escherichia coli  
562 -11532891 236944 tnaa tryptophanase (fn:enzyme; degradation of small  
molecules: amino) (db:genpept-bct2) (ec:4.1.99.1) (de:escherichia coli k-12  
mg1655 section 338 of 400 of the completegenome.) (nt:o476; 100 pct  
identical to 471 amino acids) (le:432) (re:1862) (di:direct) AE000448  
AE000448 g1790144 Escherichia coli 562 -11532891 5000690211  
(de:(ecoli\_3626) (pn:tryptophanase) (gn:tnaa) (gtcfc:2.6:5.14) (ec:4.1.99.1)  
(tnaa\_ecoli) (keggfc:2.5:5.14) (rileyfc:1.1.2) (db:gtc-escherichia coli))  
ECOLI\_3626 ECOLI\_3626 Escherichia coli 562 10124076

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824348	7581	29737	408	135

Description

6500729034 asna:b3744 aspartate--ammonia ligase:asparagine synthetase a (gtcfc:2.6:5.2:6.5) (ec:6.3.1.1) (keggfc:2.5:5.2:6.5) (rileyfc:1.4.2) (db:gtc-escherichia coli) b3744 b3744 Escherichia coli 562 -11532892 60368 asna (ec:6.3.1.1) (de:aspartate--ammonia ligase, (asparagine synthetase a)) (db:swissprot) ASNA\_ECOLI P00963 ESCHERICHIA COLI 562 -11532892 125958 asna aspartate--ammonia ligase::asparagine synthetase (cl:aspartate--ammonia ligase) (ec:6.3.1.1) (db:pir1.dat) (mp:84 min) AJECNA A01191 Escherichia coli 562 -11532892 235311 asna asparagine synthetase a (sr:escherichia coli k12 dna) (db:genpept-bct1) (de:e.coli replication origin (oric) and asna gene coding forasparagine synthetase a.) (le:1539) (re:2531) (di:direct) ECOORI J01657 g147026 Escherichia coli 562 -11532892 236981 asna asparagine synthetase a (sr:escherichia coli, clone (minichromosome) pcm959, dna) (db:genpept-bct1) (de:e.coli replication origin (oric) and asna gene coding forasparagine synthetase a.) (le:2111) (re:3103) (di:direct) ECOORIASN K00826 g147033 Escherichia coli 562 -11532892 7500877248 asna::cg site no. 995 asparagine synthetase a (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:116544) (re:117536) (di:direct) ECOUW82 L10328 g290593 Escherichia coli 562 -11532892 235306 asna asparagine synthetase a (fn:enzyme; amino acid biosynthesis: asparagine) (db:genpept-bct2) (ec:6.3.1.1) (de:escherichia coli k-12 mg1655 section 341 of 400 of the completengenome.) (nt:o330; 100 pct identical to asna\_ecoli sw: p00963;) (le:4252) (re:5244) (di:direct) AE000451 AE000451 g1790183 Escherichia coli 562 -11532892 5000690212 (de:(ecoli\_3662) (pn:asparagine synthetase a) (gn:asna) (gtcfc:2.6:5.2:6.5) (ec:6.3.1.1) (asna\_ecoli) (keggfc:2.5:5.2:6.5) (rileyfc:1.4.2) (db:gtc-escherichia coli)) ECOLI\_3662 ECOLI\_3662 Escherichia coli 562 10003094

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824349	7582	29738	516	172

Description

6500729035 glna:b3870 glutamine synthetase:glutamate--ammonia ligase (gtcfc:2.6:5.1:11.4:12.13) (ec:6.3.1.2) (keggfc:2.5:5.1:7.3:12.1) (rileyfc:1.4.1) (db:gtc-escherichia coli) b3870 b3870 Escherichia coli 562 -11532893 125982 glna glutamate--ammonia ligase::glutamine synthetase (cl:glutamate--ammonia ligase) (ec:6.3.1.2) (db:pir1.dat) (mp:87 min) AJECQ S40815 Escherichia coli 562 -11532893 7500953379 glna glutamine synthetase (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 705) (le:18265) (re:19674) (di:complement) ECOUW87 L19201 g304975 Escherichia coli 562 -11532893 237089 glna glutamine synthetase (fn:enzyme; amino acid biosynthesis: glutamine) (db:genpept-bct2) (ec:6.3.1.2) (de:escherichia coli k-12 mg1655 section 352 of 400 of the completegenome.) (nt:f469; 100 pct identical to glna\_ecoli sw: p06711;) (le:6558) (re:7967) (di:complement) AE000462 AE000462 g1790301 Escherichia coli 562 -11532893 5000690213 (de:(ecoli\_3769) (pn:glutamine synthetase) (gn:glna) (gtcfc:2.6:5.1:11.4) (ec:6.3.1.2) (glna\_ecoli) (keggfc:2.5:5.1:7.3) (rileyfc:1.4.1) (db:gtc-escherichia coli)) ECOLI\_3769 ECOLI\_3769 Escherichia coli 562 10066504

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824361	7583	29739	990	329

Description

6500729036 cysk:cysz:b2414 cysteine synthase a:o-acetylserine sulphydrylase a:o-acetylserine:thiol-lyase a:csase a:sulfate starvation-induced protein 5:ssi5 (gtcfc:2.7:5.3:5.5:6.4) (ec:4.2.99.8) (keggfc:2.6:5.5:6.4) (rileyfc:1.4.3) (db:gtc-escherichia coli) b2414 b2414 Escherichia coli 562 -11532894 7000688893 cysk cysteine synthase:a:o-acetylserine thiol -lyase a:o-acetylserine sulphydrylase a:protein ssi5 (cl:threonine dehydratase) (ec:4.2.99.8) (db:pir1.dat) (mp:52 min) SYECAC E65015 Escherichia coli 562 -11532894 7500953341 o-acetylserine sulphydrylase aa 1 -323 (db:genpept-bct1) (de:e. coli cysk gene for o-acetylserine sulphydrylase.) (le:777) (re:1748) (di:direct) ECCYSK X12615 g41201 Escherichia coli 562 -11532894 232625 cysk cysteine synthase a:o-acetylserine (fn:enzyme; amino acid biosynthesis: cysteine) (db:genpept-bct2) (ec:4.2.99.8) (de:escherichia coli k-12 mg1655 section 219 of 400 of the completegenome.) (nt:o323; 99 pct identical to 322 aa protein) (le:2228) (re:3199) (di:direct) AE000329 AE000329 g1788754 Escherichia coli 562 -11532894 5000690215 (de:(ecoli\_2355) (pn:cysteine synthase a, o-acetylserine sulphydrylase a) (gn:cysk) (gtcfc:2.7:5.5:6.4) (ec:4.2.99.8) (cysk\_ecoli) (keggfc:2.6:5.5:6.4) (rileyfc:1.4.3) (db:gtc-escherichia coli)) ECOLI\_2355 ECOLI\_2355 Escherichia coli 562 10123675

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824363	7584	29740	270	89

# Description

6500729037 hypothetical protein (gtcfc:14.1) (ec:4.2.99.8)  
(keggfc:2.6:5.5:6.4) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2420 b2420  
Escherichia coli 562 -11532895 7000691643 hypothetical protein b2420  
(db:pir2.dat) C65016 C65016 Escherichia coli 562 -11532895 224982 molr  
molybdate metabolism regulator. (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #418(54.6-54.9 min.)) (nt:similar to (swissprot accession  
number p33345)) (le:6117) (re:6851) (di:direct) D90871 D90871 g1799839  
Escherichia coli 562 -11532895 224991 molr molybdate metabolism regulator.  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #419(54.7-55.1  
min.)) (nt:similar to (swissprot accession number p33345)) (le:878)  
(re:1612) (di:direct) D90872 D90872 g1799849 Escherichia coli 562 -11532895  
7500960190 b2420 orf:hypothetical protein (fn:orf; unknown)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 219 of 400 of the  
completegenome.) (nt:o244) (le:7568) (re:8302) (di:direct) AE000329 AE000329  
g1788760 Escherichia coli 562 -11532895 5000690216 (de:(ecoli\_2361)  
(pn:function not assigned) (gtcfc:2.7:5.5:6.4) (ec:4.2.99.8)  
(keggfc:2.6:5.5:6.4) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2361  
ECOLI\_2361 Escherichia coli 562 10120191

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824375	7585	29741	210	69

# Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824377	7586	29742	471	156

# Description

GTC ORF with score 126 to: (fn:cyclization of farnesyl pyrophosphate to)  
(sr:penicillium roqueforti (library: nr1 849) dna) (db:genpept-pln1)  
(de:penicillium roqueforti aristolochene synthase (ari1) gene, completecds.)  
(nt:putative) (le:220:615:940) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824379	7587	29743	306	101

# Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824384	7588	29744	1269	422

Description

6500729038 cysm:b2421 cysteine synthase b:o-acetylserine sulfhydrylase  
b:o-acetylserine:thiol-lyase b:csase b (gtcfc:2.7:5.5) (ec:4.2.99.8)  
(keggfc:2.6:5.5:6.4) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2421 b2421  
Escherichia coli 562 -11532896 67679 cysm (ec:4.2.99.8) (de:(o-acetylserine  
(thiol)-lyase b) (csase b)) (db:swissprot) CYSM\_ECOLI P16703 ESCHERICHIA  
COLI 562 -11532896 125651 cysm cysteine synthase:b:o-acetylserine thiol  
-lyase b:o-acetylserine sulfhydrylase b (cl:threonine dehydratase)  
(ec:4.2.99.8) (db:pir1.dat) (mp:52 min) SYECBC D35402 Escherichia coli 562  
-11532896 224983 cysm cysteine synthase ec 4.2.99.8 b (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #418(54.6-54.9 min.)) (nt:similar to  
(pir accession number d35402)) (le:7040) (re:7951) (di:complement) D90871  
D90871 g1799840 Escherichia coli 562 -11532896 224992 cysm cysteine  
synthase ec 4.2.99.8 b (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #419(54.7-55.1 min.)) (nt:similar to (pir accession number  
d35402)) (le:1801) (re:2712) (di:complement) D90872 D90872 g1799850  
Escherichia coli 562 -11532896 7500879918 cysm o-acetylserine thiol  
-lyase-b (sr:e.coli k12 dna) (db:genpept-bct1) (ec:4.2.99.8) (de:e.coli  
thiosulfate binding protein (cysp), sulfate permease (cyst,cysw, cysa) and  
o-acetylserine (thiol)-lyase-b (cysm) genes,complete cds.) (le:4505)  
(re:5416) (di:direct) ECOCYS M32101 g145662 Escherichia coli 562 -11532896  
234096 cysm cysteine synthase b:o-acetylserine (fn:enzyme; amino acid  
biosynthesis: cysteine) (db:genpept-bct2) (ec:4.2.99.8) (de:escherichia coli  
k-12 mg1655 section 219 of 400 of the completegenome.) (nt:f303; 100 pct  
identical to cysm\_ecoli sw:) (le:8491) (re:9402) (di:complement) AE000329  
AE000329 g2367138 Escherichia coli 562 -11532896



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824404	7589	29745	717	238

Description

6500729039 cysc:b2750 adenosine 5-phosphosulfate kinase:adenylylsulfate  
kinase:aps kinase:atp adenosine-5-phosphosulfate 3-phosphotransferase  
(gtcfc:2.7:4.1:6.4) (ec:2.7.1.25) (keggfc:2.6:4.1:6.4) (rileyfc:1.3.5)  
(db:gtc-escherichia coli) b2750 b2750 Escherichia coli 562 -11532897  
7000690851 cysc adenylylsulfate kinase:precursor (cl:adenylylsulfate  
kinase:adenylylsulfate kinase homology) (ec:2.7.1.25) (db:pir2.dat) (mp:59  
min) B65056 B65056 Escherichia coli 562 -11532897 239324 atp  
adenylylsulfate 3-phosphotransferase (sr:escherichia coli (strain k-12) dna)  
(db:genpept-bct1) (ec:2.7.1.25) (de:escherichia coli adenylylsulfate  
3'-phosphotransferase (atp),complete cds.) (le:1) (re:606) (di:direct)  
ECOATP M86936 g145395 Escherichia coli 562 -11532897 7500954072 cysc  
adenosine 5-phosphosulfate kinase (db:genpept-bct1) (ec:2.7.1.25)  
(de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg  
site no. 896) (le:45690) (re:46295) (di:complement) ECU29579 U29579 g882643  
Escherichia coli 562 -11532897 233876 cysc adenosine 5-phosphosulfate  
kinase (fn:enzyme; central intermediary metabolism: sulfur)  
(db:genpept-bct2) (ec:2.7.1.25) (de:escherichia coli k-12 mg1655 section 248  
of 400 of the completegenome.) (nt:f201; 99 pct identical to cysc\_ecoli sw:  
23846 but) (le:8361) (re:8966) (di:complement) AE000358 AE000358 g1789107  
Escherichia coli 562 -11532897 5000690217 (de:(ecoli\_2679) (pn:adenosine  
5"-phosphosulfate kinase) (gn:cysc) (gtcfc:2.7:4.1:6.4) (ec:2.7.1.25)  
(cysc\_ecoli) (keggfc:2.6:4.1:6.4) (rileyfc:1.3.5) (db:gtc-escherichia coli))  
ECOLI\_2679 ECOLI\_2679 Escherichia coli 562 10123804

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824412	7590	29746	834	278

#### Description

6500729040 cyns:b2751 atp sulfurylase:atp sulfate adenylyltransferase subunit:sulfate adenylyltransferase subunit 1:atp-sulfurylase (gtcfc:2.7:4.1:6.4) (ec:2.7.7.4) (keggfc:2.6:4.1:6.4) (rileyfc:1.3.5) (db:gtc-escherichia coli) b2751 b2751 Escherichia coli 562 -11532898 67682 cyns (ec:2.7.7.4) (de:sulfurylase)) (db:swissprot) CYSN\_ECOLI P23845 ESCHERICHIA COLI 562 -11532898 164663 cyns sulfate adenylyltransferase:large chain (cl:translation elongation factor tu homology) (ec:2.7.7.4) (db:pir2.dat) (mp:59 min) JN0327 JN0327 Escherichia coli 562 -11532898 239325 cyns atp sulfurylase (sr:escherichia coli (individual\_isolate kl16, strain k-12) dna) (db:genpept-bct1) (de:e.coli k-12 atp sulfurylase (cysd and cyns) and aps kinase (cysc)genes, complete cds.) (le:1497) (re:2924) (di:direct) ECOCYSDNC M74586 g145673 Escherichia coli 562 -11532898 7500879919 cyns atp sulfurylase atp:sulfate adenylyltransferase (db:genpept-bct1) (ec:2.7.7.4) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg site no. 18436) (le:46295) (re:47722) (di:complement) ECU29579 U29579 g882644 Escherichia coli 562 -11532898 234103 cyns atp-sulfurylase atp:sulfate (fn:enzyme; central intermediary metabolism: sulfur) (db:genpept-bct2) (ec:2.7.7.4) (de:escherichia coli k-12 mg1655 section 248 of 400 of the completegenome.) (nt:f475; 100 pct identical to cyns\_ecoli sw: p23845;) (le:8966) (re:10393) (di:complement) AE000358 AE000358 g1789108 Escherichia coli 562 -11532898 5000690218 (de:(ecoli\_2680) (pn:atp-sulfurylase:atp:sulfate adenylyltransferase, subunit 1, probably a gtpase) (gn:cyns) (gtcfc:2.7:4.1:6.4) (ec:2.7.7.4) (cyns\_ecoli) (keggfc:2.6:4.1:6.4) (rileyfc:1.3.5) (db:gtc-escherichia coli)) ECOLI\_2680 ECOLI\_2680 Escherichia coli 562 10010280

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824433	7591	29747	342	113

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824439	7592	29748	198	65

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824443	7593	29749	765	254

Description

6500729041 cysd:b2752 atp sulfurylase:atp sulfate adenylyltransferase:sulfate  
adenylate transferase subunit 2:atp-sulfurylase (gtcfc:2.7:4.1:6.4)  
(ec:2.7.7.4) (keggfc:2.6:4.1:6.4) (rileyfc:1.3.5) (db:gtc-escherichia coli)  
b2752 b2752 Escherichia coli 562 -11532899 7000689403 cysd sulfate  
adenylyltransferase:small chain:atp-sulfurylase:sulfurylase (cl:nodulation  
protein nodp) (ec:2.7.7.4) (db:pir2.dat) (mp:59 min) D65056 D65056  
Escherichia coli 562 -11532899 7500955386 cysd atp sulfurylase atp:sulfate  
adenyltransferase (db:genpept-bct1) (ec:2.7.7.4) (de:escherichia coli k-12  
genome; approximately 61 to 62 minutes.) (nt:cg site no. 895) (le:47724)  
(re:48632) (di:complement) ECU29579 U29579 g882645 Escherichia coli 562  
-11532899 239326 cysd atp:sulfurylase atp:sulfate (fn:enzyme; central  
intermediary metabolism: sulfur) (db:genpept-bct2) (ec:2.7.7.4)  
(de:escherichia coli k-12 mg1655 section 248 of 400 of the completegenome.)  
(nt:f302; 99 pct identical to cysd\_ecoli sw: p21156; cg) (le:10395)  
(re:11303) (di:complement) AE000358 AE000358 g1789109 Escherichia coli 562  
-11532899 5000690219 (de:(ecoli\_2681) (pn:sulfurylase:atp:sulfate  
adenylyltransferase, subunit 2) (gn:cysd) (gtcfc:2.7:4.1:6.4) (ec:2.7.7.4)  
(cysd\_ecoli) (keggfc:2.6:4.1:6.4) (rileyfc:1.3.5) (db:gtc-escherichia coli))  
ECOLI\_2681 ECOLI\_2681 Escherichia coli 562 10123805

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824444	7594	29750	579	192

Description

6500729042 cysh:b2762 3-phosphoadenosine 5-phosphosulfate sulfotransferase  
 (gtcfc:2.7:5.5) (ec:2.8.2.-) (keggfc:2.6:5.5) (rileyfc:1.3.5)  
 (db:gtc-escherichia coli) b2762 b2762 Escherichia coli 562 -11532900 124178  
 cysh 3-phosphoadenosine 5-phosphosulfate reductase::3-phosphoadenylylsulfate  
 reductase:thioredoxin dependent:paps reductase:paps sulfotransferase  
 (cl:3'-phosphoadenosine 5'-phosphosulfate reductase) (ec:1.8.99.4)  
 (db:pirl.dat) (mp:59 min) RDECPA S14221 Escherichia coli 562 -11532900  
 239336 paps-reductase (db:genpept-bct1) (de:escherichia coli cysh and cysi  
 (partial) genes for paps-reductaseand sulfite reductase.) (le:769) (re:1503)  
 (di:direct) ECCYSH Y07525 g41198 Escherichia coli 562 -11532900 7500953278  
 cysh 3-phosphoadenosine 5-phosphosulfate (db:genpept-bct1) (ec:2.8.2.-)  
 (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg  
 site no. 892) (le:59880) (re:60614) (di:complement) ECU29579 U29579 g882655  
 Escherichia coli 562 -11532900 232623 cysh 3-phosphoadenosine  
 5-phosphosulfate reductase (fn:enzyme; central intermediary metabolism:  
 sulfur) (db:genpept-bct2) (ec:2.8.2.-) (de:escherichia coli k-12 mg1655  
 section 250 of 400 of the completegenome.) (nt:f244; 100 pct identical to  
 cysh\_ecoli sw: p17854;) (le:210) (re:944) (di:complement) AE000360 AE000360  
 g1789121 Escherichia coli 562 -11532900 5000690220 (de:(ecoli\_2691)  
 (pn:phosphoadenylylsulfate reductase) (gn:cysh) (gtcfc:2.7:5.5) (ec:2.8.2.-)  
 (cysh\_ecoli) (keggfc:2.6:5.5) (rileyfc:1.3.5) (db:gtc-escherichia coli))  
 ECOLI\_2691 ECOLI\_2691 Escherichia coli 562 10066046

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824450	7595	29751	927	308
<u>Description</u>				
6500729043 cysi:b2763 nadph hemoprotein alpha subunit:sulfite reductase:nadph hemoprotein beta-component:sir-hp (gtcfc:2.7:6.4) (ec:1.8.1.2) (keggfc:2.6:6.4) (rileyfc:1.3.5) (db:gtc-escherichia coli) b2763 b2763 Escherichia coli 562 -11532901 7000688851 cysi:cysq sulfite reductase nadph:hemoprotein:sulfite reductase nadph alpha chain (cl:sulfite reductase (ferredoxin)) (ec:1.8.1.2) (db:pir1.dat) (mp:59 min) RDECSH G65057 Escherichia coli 562 -11532901 7500953211 cysi sulfite reductase nadph hemoprotein alpha (db:genpept-bct1) (ec:1.8.1.2) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg site no.891; alternate gene name cysq) (le:60689) (re:62401) (di:complement) ECU29579 U29579 g882656 Escherichia coli 562 -11532901 239337 cysi sulfite reductase:alpha subunit (fn:enzyme; central intermediary metabolism: sulfur) (db:genpept-bct2) (ec:1.8.1.2) (de:escherichia coli k-12 mg1655 section 250 of 400 of the completegenome.) (nt:f570; 99 pct identical to cysi_ecoli sw: p17846; cg) (le:1019) (re:2731) (di:complement) AE000360 AE000360 g1789122 Escherichia coli 562 -11532901 5000690221 (de:(ecoli_2692) (pn:sulfite reductase, alpha subunit) (gn:cysi) (gtcfc:2.7:6.4) (ec:1.8.1.2) (cysi_ecoli) (keggfc:2.6:6.4) (rileyfc:1.3.5) (db:gtc-escherichia coli)) ECOLI_2692 ECOLI_2692 Escherichia coli 562 10123813				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824451	7596	29752	750	249
<u>Description</u>				
6500729044 cysj:b2764 nadph flavoprotein beta subunit:sulfite reductase:nadph flavoprotein alpha-component:sir-fp (gtcfc:2.7:6.4) (ec:1.8.1.2) (keggfc:2.6:6.4) (rileyfc:1.3.5) (db:gtc-escherichia coli) b2764 b2764 Escherichia coli 562 -11532902 7000691919 cysj sulfite reductase nadph:flavoprotein beta chain (cl:sulfite reductase (nadph):flavodoxin homology:nadph--ferrihemoprotein reductase homology) (ec:1.8.1.2) (db:pir2.dat) H65057 H65057 Escherichia coli 562 -11532902 7500953859 cysj sulfite reductase nadph flavoprotein beta (db:genpept-bct1) (ec:1.8.1.2) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg site no. 890; alternate gene name cysp) (le:62401) (re:64200) (di:complement) ECU29579 U29579 g882657 Escherichia coli 562 -11532902 239338 cysj sulfite reductase nadph:flavoprotein beta (fn:enzyme; central intermediary metabolism: sulfur) (db:genpept-bct2) (ec:1.8.1.2) (de:escherichia coli k-12 mg1655 section 250 of 400 of the completegenome.) (nt:f599; 98 pct identical to cysj_ecoli sw: p38038; cg) (le:2731) (re:4530) (di:complement) AE000360 AE000360 g1789123 Escherichia coli 562 -11532902 5000690222 (de:(ecoli_2693) (pn:sulfite reductase, flavoprotein beta subunit) (gn:cysj) (gtcfc:2.7:6.4) (ec:1.8.1.2) (cysj_ecoli) (keggfc:2.6:6.4) (rileyfc:1.3.5) (db:gtc-escherichia coli)) ECOLI_2693 ECOLI_2693 Escherichia coli 562 10123814				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824468	7600	29756	573	190
<u>Description</u>				
<p>6500729045 cyse:b3607 serine acetyltransferase:sat (gtcfc:2.7:5.3:5.5) (ec:2.3.1.30) (keggfc:2.6:5.5) (rileyfc:1.4.3) (db:gtc-escherichia coli) b3607 b3607 Escherichia coli 562 -11532903 67651 cyse (ec:2.3.1.30) (de:serine acetyltransferase, (sat)) (db:swissprot) CYSE_ECOLI P05796 ESCHERICHIA COLI 562 -11532903 123359 cyse serine o-acetyltransferase (cl:serine acetyltransferase:serine acetyltransferase homology) (ec:2.3.1.30) (db:pir1.dat) (mp:81 min) XYECSA A27896 Escherichia coli 562 -11532903 234116 (sr:e.coli dna (strain kl16)) (db:genpept-bct1) (de:e.coli serine acetyltransferase (cyse) gene, complete cds.) (nt:serine acetyltransferase) (le:223) (re:1044) (di:direct) ECOCYSE M15745 g145676 Escherichia coli 562 -11532903 236844 (sr:e.coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli cysteine regulon 33 kd (cyse) and 16 kd protein (cysx) genes, complete cds.) (nt:33 kd protein (cyse)) (le:221) (re:1042) (di:direct) ECOCYSXE M34333 g145694 Escherichia coli 562 -11532903 500684674 cyse serine acetyltransferase (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (ec:2.3.1.30) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 894) (le:195991) (re:196812) (di:complement) ECOUW76 U00039 g466745 Escherichia coli 562 -11532903 500684675 cyse serine acetyltransferase (fn:enzyme; amino acid biosynthesis: cysteine) (db:genpept-bct2) (ec:2.3.1.30) (de:escherichia coli k-12 mg1655 section 328 of 400 of the completegenome.) (nt:f273; 100 pct identical amino acid sequence and) (le:9537) (re:10358) (di:complement) AE000438 AE000438 g1790035 Escherichia coli 562 -11532903 7502851834 cyse (db:genpept-pat) (de:dna expression cassette mtce10 with bacterial csye gene from patentwo9218635.) (le:870) (re:1691) (di:direct) A31758 A31758 g1926472 synthetic construct 32630 -11532903 7502851835 cyse (db:genpept-pat) (de:dna expression cassette mtcekl with bacterial cyse and cysk genesfrom patent wo9218635.) (le:885) (re:1706) (di:direct) A31762 A31762 g1926476 synthetic construct 32630 -11532903 234105 cyse serine acetyltransferase (db:genpept-bct1) (ec:2.3.1.30) (de:escherichia coli k-12 mg1655 section 328 of 400 of the completegenome.) (nt:f273; 100 pct identical amino acid sequence and) (le:9537) (re:10358) (di:complement) ECAE000438 AE000438 g1790035 Escherichia coli 562 -11532903 5000690223 (de:(ecoli_3527) (pn:serine acetyltransferase) (gn:cyse) (gtcfc:2.7:5.5) (ec:2.3.1.30) (cyse_ecoli) (keggfc:2.6:5.5) (rileyfc:1.4.3) (db:gtc-escherichia coli)) ECOLI_3527 ECOLI_3527 Escherichia coli 562 10010249</p>				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824470	7601	29757	312	103

Description

6500729046 metb:b3939 cystathionine  
gamma-synthase:cgs:o-succinylhomoserine:thiol-lyase  
(gtcfc:2.7:5.2:5.3:5.4:5.5:6.4) (ec:4.2.99.9) (keggfc:2.6:5.3:5.4:5.5:6.4)  
(rileyfc:1.4.2) (db:gtc-escherichia coli) b3939 b3939 Escherichia coli 562  
-11532904 83536 metb (ec:4.2.99.9) (de:(thiol)-lyase)) (db:swissprot)  
METB\_ECOLI P00935 ESCHERICHIA COLI 562 -11532904 125695 metb  
o-succinylhomoserine thiol -lyase::cystathionine gamma-synthase  
(cl:o-succinylhomoserine (thiol)-lyase) (ec:4.2.99.9) (db:pir1.dat) (mp:89  
min) SYECCG A01158 Escherichia coli 562 -11532904 237156 (sr:e.coli  
(escherichia coli k12) dna, clone pmad4) (db:genpept-bct1) (de:e.coli metb  
and met1 (5' end) genes coding for cystathionine gamma-synthase and  
aspartokinase ii-homoserine dehydrogenase ii.) (nt:cystathione  
gamma-synthase (metb)) (le:231) (re:13... ECOMETLB1 K01546 g146846  
Escherichia coli 562 -11532904 7500885516 metb cystathionine gamma-synthase  
(sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda)  
(db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.)  
(nt:cg site no. 515) (le:90305) (re:91465) (di:direct) ECOUW87 L19201  
g305042 Escherichia coli 562 -11532904 235133 metb cystathionine  
gamma-synthase (fn:enzyme; amino acid biosynthesis: methionine)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 358 of 400 of the  
completeness genome.) (nt:o386; cg site no. 515) (le:223) (re:1383) (di:direct)  
AE000468 AE000468 g1790375 Escherichia coli 562 -11532904 5000690224  
(de:(ecoli\_3837) (pn:cystathionine gamma-synthase) (gn:metb)  
(gtcfc:2.7:5.3:5.4:5.5:6.4) (ec:4.2.99.9) (metb\_ecoli)  
(keggfc:2.6:5.3:5.4:5.5:6.4) (rileyfc:1.4.2) (db:gtc-escherichia coli))  
ECOLI\_3837 ECOLI\_3837 Escherichia coli 562 10025750

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824477	7602	29758	204	67

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824488	7603	29759	1449	482

Description

6500729047 meta:b4013 homoserine o-succinyltransferase:homoserine o-transsuccinylase (gtcfc:2.7:5.2:5.4) (ec:2.3.1.46) (keggfc:2.6:5.4) (rileyfc:1.4.2) (db:gtc-escherichia coli) b4013 b4013 Escherichia coli 562 -11532905 7000688857 meta homoserine o-succinyltransferase::homoserine o-transsuccinylase (cl:homoserine succinyltransferase) (ec:2.3.1.46) (db:pir1.dat) (mp:91) XYECM D65208 Escherichia coli 562 -11532905 237219 meta homoserine transsuccinylase (fn:enzyme; amino acid biosynthesis: methionine) (db:genpept-bct2) (ec:2.3.1.46) (de:escherichia coli k-12 mg1655 section 364 of 400 of the completegenome.) (nt:o309; 99 pct identical amino acid sequence and) (le:6411) (re:7340) (di:direct) AE000474 AE000474 g1790443 Escherichia coli 562 -11532905 7500953238 meta homoserine transsuccinylase (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (ec:2.3.1.46) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 516) (le:79522) (re:80451) (di:direct) ECOUW89 U00006 g396348 Escherichia coli 562 -11532905 5000690225 (de:(ecoli\_3899) (pn:homoserine transsuccinylase) (gn:meta) (gtcfc:2.7:5.4) (ec:2.3.1.46) (meta\_ecoli) (keggfc:2.6:5.4) (rileyfc:1.4.2) (db:gtc-escherichia coli)) ECOLI\_3899 ECOLI\_3899 Escherichia coli 562 10124130

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824502	7604	29760	234	77

Description

6500729048 ssea:b2521 putative thiosulfate sulfurtransferase (gtcfc:2.7) (ec:2.8.1.1) (keggfc:14.1) (rileyfc:1.3.5) (db:gtc-escherichia coli) b2521 b2521 Escherichia coli 562 -11532906 7000691898 ssea probable thiosulfate sulfurtransferase (cl:thiosulfate sulfurtransferase) (ec:2.8.1.1) (db:pir2.dat) H65028 H65028 Escherichia coli 562 -11532906 7500960433 ssea putative thiosulfate sulfurtransferase (fn:putative enzyme; not classified) (db:genpept-bct2) (ec:2.8.1.1) (de:escherichia coli k-12 mg1655 section 228 of 400 of the completegenome.) (nt:o334; 100 pct identical to thtr\_ecoli sw: p31142) (le:11735) (re:12739) (di:direct) AE000338 AE000338 g1788869 Escherichia coli 562 -11532906

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824504	7605	29761	1032	343

Description

6500729049 aslb:atsb:b3800 putative arylsulfatase regulatory protein (gtcfc:2.7) (keggfc:14.2) (rileyfc:1.3.5) (db:gtc-escherichia coli) b3800 b3800 Escherichia coli 562 -11532907 7500877242 aslb:atsb (de:putative arylsulfatase regulatory protein) (db:swissprot) ASLB\_ECOLI P25550 ESCHERICHIA COLI 562 -11532907 7000691892 atsb:aslb probable arylsulfatase regulatory protein atsb:arylsulfatase regulator (cl:probable arylsulfatase regulatory protein atsb) (db:pir2.dat) A65184 A65184 Escherichia coli 562 -11532907 7500877244 aslb putative arylsulfatase regulator (fn:regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 346 of 400 of the completegenome.) (nt:o411; 99 pct identical to aslb\_ecoli sw: p25550;) (le:100) (re:1335) (di:direct) AE000456 AE000456 g2367292 Escherichia coli 562 -11532907

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824518	7606	29762	591	196

Description

GTC ORF with score 110 to: (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #263(30.5-30.9 min.).) (nt:orf\_id:o263#22; similar to (swissprot accession) (le:14961) (re:18323) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824521	7607	29763	507	168
<u>Description</u>				
6500729050 asla:atsa:b3801 asla:arylsulfatase:aryl-sulphate sulphohydrolase (gtcfc:2.7:3.7:8.5) (ec:3.1.6.1) (keggfc:3.7:8.5) (rileyfc:1.3.5) (db:gtc-escherichia coli) b3801 b3801 Escherichia coli 562 -11532908 60358 asla:atsa (ec:3.1.6.1) (de:arylsulfatase, (aryl-sulphate sulphohydrolase)) (db:swissprot) ASLA_ECOLI P25549 ESCHERICHIA COLI 562 -11532908 139823 asla:atsa arylsulfatase::asla protein (cl:animal sulfatase) (ec:3.1.6.1) (db:pir2.dat) (mp:86 min) S30691 S30691 Escherichia coli 562 -11532908 7500877241 atsa (db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (nt:similar to arylsulfatases of klebsiella pneumoniae) (le:37466) (re:39121) (di:complement) ECOUW85 M87049 g148200 Escherichia coli 562 -11532908 237025 asla arylsulfatase (fn:enzyme; central intermediary metabolism: sulfur) (db:genpept-bct2) (ec:3.1.6.1) (de:escherichia coli k-12 mg1655 section 346 of 400 of the completegenome.) (nt:f551; 100 pct identical to asla_ecoli sw:) (le:1494) (re:3149) (di:complement) AE000456 AE000456 g1790233 Escherichia coli 562 -11532908 5000690245 (de:(ecoli_3707) (pn:arylsulfatase) (gn:asla) (gtcfc:3.7:8.4:8.5) (ec:3.1.6.1) (asla_ecoli) (keggfc:3.7:8.5) (rileyfc:1.3.5) (db:gtc-escherichia coli)) ECOLI_3707 ECOLI_3707 Escherichia coli 562 10003084				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824526	7608	29764	483	160
<u>Description</u>				
6500729051 cysq:amta:b4214 cysq protein (gtcfc:2.7) (keggfc:14.2) (rileyfc:1.3.5) (db:gtc-escherichia coli) b4214 b4214 Escherichia coli 562 -11532909 162728 cysq:amta ammonium transport system structural protein (db:pir2.dat) S56439 S56439 Escherichia coli 562 -11532909 7500959675 cysq (fn:ammonium transport protein) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:alternate gene name amta) (le:127587) (re:128327) (di:direct) ECOUW93 U14003 g537055 Escherichia coli 562 -11532909 237419 cysq affects pool of (fn:phenotype; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 382 of 400 of the completegenome.) (nt:o246; 99 pct identical amino acid sequence and) (le:9327) (re:10067) (di:direct) AE000492 AE000492 g1790659 Escherichia coli 562 -11532909				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824529	7609	29765	1053	350

Description

6500729052 mltd:dnir:b0211 regulatory protein dnir and hypothetical  
yafg:membrane-bound lytic murein transglycosylase d precursor:murein  
hydrolase d:regulatory protein dnir (gtcfc:11.1:12.13) (ec:3.2.1.-)  
(keggfc:4.3:4.4) (rileyfc:1.2.6) (db:gtc-escherichia coli) b0211 b0211  
Escherichia coli 562 -11532910 68961 mltd:dnir (ec:3.2.1.-) (de:(murein  
hydrolase d) (regulatory protein dnir)) (db:swissprot) MLTD\_ECOLI P23931  
ESCHERICHIA COLI 562 -11532910 7000685854 dnir regulatory protein dnir:yafg  
protein (db:pir2.dat) E64745 E64745 Escherichia coli 562 -11532910  
7500885688 dnir dnir (db:genpept-bct1) (de:escherichia coli chromosome  
minutes 4-6.) (le:63672) (re:65030) (di:complement) ECU70214 U70214 g1552781  
Escherichia coli 562 -11532910 239832 dnir transcriptional regulator for  
nitrite reductase (fn:regulator; energy metabolism, carbon: anaerobic)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 20 of 400 of the  
completegenome.) (nt:f452; residues 232-452 are 99 pct identical to)  
(le:1626) (re:2984) (di:complement) AE000130 AE000130 g1786405 Escherichia  
coli 562 -11532910

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824540	7610	29766	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824543	7611	29767	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824549	7612	29768	357	118

#### Description

6500729053 cyoe:b0428 cytochrome o ubiquinol oxidase c subunit:cytochrome o ubiquinol oxidase operon protein cyoe (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b0428 b0428 Escherichia coli 562 -11532911 67534 cyoe (de:cytochrome o ubiquinol oxidase operon protein cyoe) (db:swissprot) CYOE\_ECOLI P18404 ESCHERICHIA COLI 562 -11532911 162887 cyoe heme o synthase:protoheme ix farnesyltransferase (cl:heme o synthase) (db:pir2.dat) E42226 E42226 Escherichia coli 562 -11532911 7500879868 cyoe cytochrome o ubiquinol oxidase c subunit (sr:e.coli (strain k12) dna) (db:genpept-bct1) (de:e.coli cytochrome o ubiquinol oxidase (cyoa, cyob, cyoc, cyod andcyoe genes, complete cds.) (le:4706) (re:5596) (di:direct) ECOCYOA J05492 g145656 Escherichia coli 562 -11532911 234091 cyoe protoheme ix farnesyltransferase haeme o (fn:enzyme; energy metabolism, carbon: aerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 39 of 400 of the completegenome.) (nt:f296; 100 pct identical to cyoe\_ecoli sw: p18404) (le:2255) (re:3145) (di:complement) AE000149 AE000149 g1786631 Escherichia coli 562 -11532911

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824551	7613	29769	495	164

#### Description

6500729054 cyod:b0429 cytochrome o ubiquinol oxidase c subunit:cytochrome o ubiquinol oxidase operon protein cyod (gtcfc:2.8) (ec:1.10.3.-) (keggfc:14.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b0429 b0429 Escherichia coli 562 -11532912 67533 cyod (de:cytochrome o ubiquinol oxidase operon protein cyod) (db:swissprot) CYOD\_ECOLI P18403 ESCHERICHIA COLI 562 -11532912 162886 cyod bo-type ubiquinol oxidase:chain iv:cytochrome o chain iv (ec:1.10.3.-) (db:pir2.dat) D42226 D42226 Escherichia coli 562 -11532912 7500879867 cyod cytochrome o ubiquinol oxidase c subunit (sr:e.coli (strain k12) dna) (db:genpept-bct1) (de:e.coli cytochrome o ubiquinol oxidase (cyoa, cyob, cyoc, cyod andcyoe genes, complete cds.) (le:4365) (re:4694) (di:direct) ECOCYOA J05492 g145655 Escherichia coli 562 -11532912 234090 cyod cytochrome o ubiquinol oxidase subunit iv (fn:enzyme; energy metabolism, carbon: aerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 39 of 400 of the completegenome.) (nt:f109; 100 pct identical to cyod\_ecoli sw: p18403) (le:3157) (re:3486) (di:complement) AE000149 AE000149 g1786632 Escherichia coli 562 -11532912

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824555	7614	29770	807	268

Description

GTC ORF with score 206 to: (cl:yeast 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase:1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x homology:1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain y homology) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824573	7615	29771	1188	395

Description

6500729055 cyoc:b0430 cytochrome o ubiquinol oxidase subunit iii (gtcfc:2.8) (ec:1.10.3.-) (keggfc:14.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b0430 b0430 Escherichia coli 562 -11532913 67532 cyoc (ec:1.10.3.-) (de:cytochrome o ubiquinol oxidase subunit iii,) (db:swissprot) CYOC\_ECOLI P18402 ESCHERICHIA COLI 562 -11532913 162897 cyoc bo-type ubiquinol oxidase:chain iii:cytochrome o chain iii (cl:cytochrome-c oxidase chain iii) (ec:1.10.3.-) (db:pir2.dat) C42226 C42226 Escherichia coli 562 -11532913 240207 cyoc cytochrome o ubiquinol oxidase c subunit (sr:e.coli (strain k12) dna) (db:genpept-bct1) (de:e.coli cytochrome o ubiquinol oxidase (cyoa, cyob, cyoc, cyod andcyoe genes, complete cds.) (le:3751) (re:4365) (di:direct) ECOCYOA J05492 g145654 Escherichia coli 562 -11532913 7500879866 cyoc cytochrome o ubiquinol oxidase (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:27496) (re:28110) (di:complement) ECU82664 U82664 g1773114 Escherichia coli 562 -11532913 234089 cyoc cytochrome o ubiquinol oxidase subunit iii (fn:enzyme; energy metabolism, carbon: aerobic) (db:genpept-bct2) (ec:1.10.3.-) (de:escherichia coli k-12 mg1655 section 39 of 400 of the completegenome.) (nt:f204; 100 pct identical to cyoc\_ecoli sw: p18402) (le:3486) (re:4100) (di:complement) AE000149 AE000149 g1786633 Escherichia coli 562 -11532913

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824579	7616	29772	669	222

Description

6500729056 cyob:b0431 cytochrome o ubiquinol oxidase subunit i:ubiquinol oxidase polypeptide i:cytochrome o:bo subunit 1:oxidase bo:3 subunit 1:cytochrome o ubiquinol oxidase subunit 1 (gtcfc:2.8) (ec:1.10.3.-) (keggfc:14.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b0431 b0431 Escherichia coli 562 -11532914 67530 cyob (ec:1.10.3.-) (de:subunit 1)) (db:swissprot) CYOB\_ECOLI P18401 ESCHERICHIA COLI 562 -11532914 137078 cyob bo-type ubiquinol oxidase:chain i:cytochrome bo chain i (cl:cytochrome-c oxidase chain i:cytochrome-c oxidase chain i homology) (ec:1.10.3.-) (db:pir2.dat) B42226 B42226 Escherichia coli 562 -11532914 240208 cyob cytochrome o ubiquinol oxidase b subunit i (sr:e.coli (strain k12) dna) (db:genpept-bct1) (de:e.coli cytochrome o ubiquinol oxidase (cyoa, cyob, cyoc, cyod andcyoe genes, complete cds.) (le:1770) (re:3761) (di:direct) ECOCYOA J05492 g145653 Escherichia coli 562 -11532914 7500879864 cyob cytochrome o ubiquinol oxidase (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:28100) (re:30091) (di:complement) ECU82664 U82664 g1773115 Escherichia coli 562 -11532914 234088 cyob cytochrome o ubiquinol oxidase subunit i (fn:enzyme; energy metabolism, carbon: aerobic) (db:genpept-bct2) (ec:1.10.3.-) (de:escherichia coli k-12 mg1655 section 39 of 400 of the completegenome.) (nt:f663; 100 pct identical to cyob\_ecoli sw: p18401) (le:4090) (re:6081) (di:complement) AE000149 AE000149 g1786634 Escherichia coli 562 -11532914

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824583	7617	29773	309	102
<u>Description</u>				
6500729057 cyoa:b0432 cytochrome o ubiquinol oxidase subunit ii:ubiquinol oxidase polypeptide ii precursor:cytochrome o:bo subunit 2:oxidase bo:3 subunit 2:cytochrome o ubiquinol oxidase subunit 2 (gtcfc:2.8) (ec:1.10.3.-) (keggfc:14.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b0432 b0432 Escherichia coli 562 -11532915 67528 cyoa (ec:1.10.3.-) (de:oxidase subunit 2)) (db:swissprot) CYOA_ECOLI P18400 ESCHERICHIA COLI 562 -11532915 162896 cyoa bo-type ubiquinol oxidase:chain ii precursor:cytochrome o chain ii (cl:bo-type ubiquinol oxidase chain ii precursor) (ec:1.10.3.-) (db:pir2.dat) (mp:10 min) A42226 A42226 Escherichia coli 562 -11532915 240209 cyoa cytochrome o ubiquinol oxidase subunit ii (sr:e.coli (strain k12) dna) (db:genpept-bct1) (de:e.coli cytochrome o ubiquinol oxidase (cyoa, cyob, cyoc, cyod andcyoe genes, complete cds.) (le:801) (re:1748) (di:direct) ECOCYOA J05492 g145652 Escherichia coli 562 -11532915 7500879862 cyoa cytochrome o ubiquinol oxidase subunit ii (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:30113) (re:31060) (di:complement) ECU82664 U82664 g1773116 Escherichia coli 562 -11532915 234087 cyoa cytochrome o ubiquinol oxidase subunit ii (fn:enzyme; energy metabolism, carbon: aerobic) (db:genpept-bct2) (ec:1.10.3.-) (de:escherichia coli k-12 mg1655 section 39 of 400 of the completegenome.) (nt:f315; 100 pct identical to cyoa_ecoli sw: p18400) (le:6103) (re:7050) (di:complement) AE000149 AE000149 g1786635 Escherichia coli 562 -11532915				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824600	7618	29774	519	172
<u>Description</u>				
6500729058 flda:b0684 flavodoxin 1 (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b0684 b0684 Escherichia coli 562 -11532916 135963 flda flavodoxin a:flavodoxin 1 (cl:flavodoxin:flavodoxin homology) (db:pir2.dat) (mp:15.9 min) A37319 A37319 Escherichia coli 562 -11532916 223147 flda flavodoxin (sr:escherichia coli(strain:k12) dna, clone:kohara clone #172) (db:genpept-bct1) (de:escherichia coli genomic dna. (15.0 - 15.4 min).) (le:10762) (re:11292) (di:complement) D90707 D90707 g1651291 Escherichia coli 562 -11532916 223151 flda flavodoxin (sr:escherichia coli(strain:k12) dna, clone:kohara clone #173) (db:genpept-bct1) (de:escherichia coli genomic dna. (15.3 - 15.6 min).) (le:557) (re:1087) (di:complement) D90708 D90708 g1651296 Escherichia coli 562 -11532916 7500953770 flda flavodoxin (sr:e.coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli flavodoxin (flda) gene, complete cds.) (le:380) (re:910) (di:direct) ECOFLDA M59426 g145986 Escherichia coli 562 -11532916 234363 flda flavodoxin 1 (fn:enzyme; energy metabolism, carbon: electron) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 62 of 400 of the completegenome.) (nt:f176; 100 pct identical to flav_ecoli sw: p23243) (le:2920) (re:3450) (di:complement) AE000172 AE000172 g1786900 Escherichia coli 562 -11532916 7502851836 flda flavodoxin. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #172) (db:genpept) (de:escherichia coli genomic dna. (15.1 - 15.5 min).) (nt:orf_id:o173#2; similar to pir accession number) (le:10762) (re:11292) (di:complement) D90707 D90707 g1651291 Escherichia coli 562 -11532916 7502851837 flda flavodoxin. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #173) (db:genpept) (de:escherichia coli genomic dna. (15.3 - 15.7 min).) (nt:orf_id:o173#2; similar to pir accession number) (le:557) (re:1087) (di:complement) D90708 D90708 g1651296 Escherichia coli 562 -11532916				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824605	7619	29775	492	163
<u>Description</u>				
6500729059 cyda:cyd-1:b0733 cytochrome d ubiquinol oxidase subunit i:cytochrome bd-i oxidase subunit i (gtcfc:2.8) (ec:1.10.3.-) (keggfc:14.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b0733 b0733 Escherichia coli 562 -11532917 7000690867 cyda:cyd-1 cytochrome d complex terminal oxidase:chain i:cytochrome d ubiquinol oxidase subunit i (cl:cytochrome d complex terminal oxidase chain i) (ec:1.10.3.-) (db:pir2.dat) (mp:17 min) D64809 D64809 Escherichia coli 562 -11532917 7500959717 cyda cytochrome d terminal oxidase:polypeptide (fn:enzyme; energy metabolism, carbon: electron) (db:genpept-bct2) (ec:1.10.3.-) (de:escherichia coli k-12 mg1655 section 66 of 400 of the completegenome.) (nt:o522; 99 pct identical to cyda_ecoli sw: p11026) (le:8609) (re:10180) (di:direct) AE000176 AE000176 g1786953 Escherichia coli 562 -11532917				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824622	7620	29776	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824627	7621	29777	267	88

Description

6500729060 cydb:cyd-2:b0734 cytochrome d ubiquinol oxidase subunit ii:cytochrome bd-i oxidase subunit ii (gtcfc:2.8) (ec:1.10.3.-) (keggfc:14.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b0734 b0734 Escherichia coli 562 -11532918 67471 cydb:cyd-2 (ec:1.10.3.-) (de:bd-i oxidase subunit ii)) (db:swissprot) CYDB\_ECOLI P11027 ESCHERICHIA COLI 562 -11532918 162894 cydb:cyd-2 cytochrome d complex:chain ii:cytochrome d ubiquinol oxidase subunit ii (cl:cytochrome d ubiquinol oxidase) (ec:1.10.3.-) (db:pir2.dat) (mp:17 min) B28940 B28940 Escherichia coli 562 -11532918 223179 cydb cytochrome d ubiquinol oxidase subunit ii (sr:escherichia coli(strain:k12) dna, clone:kohara clone #178) (db:genpept-bct1) (de:escherichia coli genomic dna.(16.5 - 16.8 min).) (le:6232) (re:7371) (di:direct) D90713 D90713 g1651328 Escherichia coli 562 -11532918 7500879836 cyd cytochrome oxidase d subunit ii (sr:e.coli k12 dna) (db:genpept-bct1) (de:e.coli cytochrome d oxidase subunits i and ii (cyd) genes, completecds.) (le:2562) (re:3701) (di:direct) ECOCYD J03939 g145640 Escherichia coli 562 -11532918 234077 cydb cytochrome d terminal oxidase polypeptide (fn:enzyme; energy metabolism, carbon: electron) (db:genpept-bct2) (ec:1.10.3.-) (de:escherichia coli k-12 mg1655 section 66 of 400 of the completegenome.) (nt:o379; 100 pct identical to cydb\_ecoli sw: p11027) (le:10196) (re:11335) (di:direct) AE000176 AE000176 g1786954 Escherichia coli 562 -11532918 7502851838 cyd2 cytochrome d ubiquinol oxidase subunit ii ec (sr:escherichia coli(strain:k12) dna, clone:kohara clone #178) (db:genpept) (de:escherichia coli genomic dna. (16.5 - 16.9 min).) (nt:orf\_id:o178#3; similar to swissprot accession) (le:6232) (re:7371) (di:direct) D90713 D90713 g1651328 Escherichia coli 562 -11532918

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824628	7622	29778	1257	418

Description

6500729061 dmsa:b0894 anaerobic dimethyl sulfoxide reductase chain a precursor:dmsa reductase (gtcfc:2.8) (ec:1.8.99.-) (keggfc:14.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b0894 b0894 Escherichia coli 562 -11532919 68811 dmsa (ec:1.-.-.-) (de:(dmsa reductase)) (db:swissprot) DMSA\_ECOLI P18775 ESCHERICHIA COLI 562 -11532919 162931 dmsa dimethylsulfoxide reductase:chain a precursor:anaerobic (ec:1.8.-.-) (db:pir2.dat) (mp:20 min) S03785 S03785 Escherichia coli 562 -11532919 223259 dmsa dimethylsulfoxide reductase chain a (sr:escherichia coli(strain:k12) dna, clone:kohara clone #215) (db:genpept-bct1) (de:escherichia coli genomic dna.(20.0 - 20.3 min).) (le:10229) (re:12586) (di:direct) D90727 D90727 g1651421 Escherichia coli 562 -11532919 7500880380 dmsa anaerobic dimethyl sulfoxide reductase (sr:escherichia coli (strain c600) dna) (db:genpept-bct1) (de:e.coli dmsa, dmsb and dmsc genes encoding anaerobic dimethylsulfoxide reductase, complete cds.) (le:869) (re:3226) (di:direct) ECODMS J03412 g145755 Escherichia coli 562 -11532919 234173 dmsa anaerobic dimethyl sulfoxide reductase subunit (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 81 of 400 of the completegenome.) (nt:o785; 100 pct identical to dmsa\_ecoli sw: p18775) (le:8754) (re:11111) (di:direct) AE000191 AE000191 g1787121 Escherichia coli 562 -11532919 7502851839 dmsa dimethylsulfoxide reductase chain a (sr:escherichia coli(strain:k12) dna, clone:kohara clone #215) (db:genpept) (de:escherichia coli genomic dna. (20.1 - 20.4 min).) (nt:orf\_id:o215#7; similar to pir accession number) (le:10229) (re:12586) (di:direct) D90727 D90727 g1651421 Escherichia coli 562 -11532919

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824645	7623	29779	828	276

Description

GTC ORF with score 100 to: (fn:splicing factor) (sr:house mouse) (db:genpept-rod) (de:mus musculus suppressor of white apricot homolog 2 (swap2) mrna,complete cds.) (nt:contains rs (arginine/serine-rich) domain) (le:103) (re:1941) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824656	7624	29780	318	105

# Description

6500729062 dmhc:b0896 anaerobic dimethyl sulfoxide reductase chain c:dmso reductase anchor subunit (gtcfc:2.8) (ec:1.8.99.-) (keggfc:14.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b0896 b0896 Escherichia coli 562 -11532920 68815 dmhc (de:subunit)) (db:swissprot) DMSC\_ECOLI P18777 ESCHERICHIA COLI 562 -11532920 162932 dmhc probable dimethylsulfoxide reductase:chain c:anaerobic (cl:probable dimethylsulfoxide reductase chain c) (ec:1.8.-.-) (db:pir2.dat) (mp:20 min) S03787 S03787 Escherichia coli 562 -11532920 223261 dmhc dimethylsulfoxide reductase chain c (sr:escherichia coli(strain:k12) dna, clone:kohara clone #215) (db:genpept-bct1) (de:escherichia coli genomic dna.(20.0 - 20.3 min).) (le:13216) (re:14079) (di:direct) D90727 D90727 g1651423 Escherichia coli 562 -11532920 7500880385 dmhc anaerobic dimethyl sulfoxide reductase (sr:escherichia coli (strain c600) dna) (db:genpept-bct1) (de:e.coli dmsa, dmsb and dmhc genes encoding anaerobic dimethylsulfoxide reductase, complete cds.) (le:3862) (re:4725) (di:direct) ECODMS J03412 g145757 Escherichia coli 562 -11532920 234175 dmhc anaerobic dimethyl sulfoxide reductase subunit (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 81 of 400 of the completegenome.) (nt:o287; 100 pct identical to dmhc\_ecoli sw: p18777) (le:11741) (re:12604) (di:direct) AE000191 AE000191 g1787123 Escherichia coli 562 -11532920 7502851840 dmhc dimethylsulfoxide reductase chain c. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #215) (db:genpept) (de:escherichia coli genomic dna. (20.1 - 20.4 min).) (nt:orf\_id:o215#9; similar to pir accession number) (le:13216) (re:14079) (di:direct) D90727 D90727 g1651423 Escherichia coli 562 -11532920

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824665	7625	29781	1029	343

Description

6500729063 hyac:b0974 probable ni/fe-hydrogenase 1 b-type cytochrome subunit (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b0974 b0974 Escherichia coli 562 -11532921 67137 hyac (de:probable ni/fe-hydrogenase 1 b-type cytochrome subunit) (db:swissprot) CYBH\_ECOLI P19929 ESCHERICHIA COLI 562 -11532921 131327 hyac hydrogenase:nife b-type cytochrome chain (cl:hyac protein) (ec:1.18.99.1) (db:pir1.dat) (mp:21 min) BVECYC JV0074 Escherichia coli 562 -11532921 223306 hyac hyac protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #225) (db:genpept-bct1) (de:escherichia coli genomic dna. (22.2 - 22.6 min).) (le:989) (re:1696) (di:direct) D90735 D90735 g1651475 Escherichia coli 562 -11532921 7500879664 (sr:e.coli (strain le392) dna) (db:genpept-bct1) (de:e.coli hya operon encoding hydrogenase isozyme 1 large and smallsubunit (hyab and a) genes and hyac-f protein genes, complete cds.) (nt:hyac protein) (le:3115) (re:3822) (di:direct) ECOHYA M34825 g146422 Escherichia coli 562 -11532921 234822 hyac probable ni/fe-hydrogenase 1 b-type cytochrome (fn:putative enzyme; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 89 of 400 of the completengenome.) (nt:o235; 100 pct identical to cybh\_ecoli sw: p19929) (le:5123) (re:5830) (di:direct) AE000199 AE000199 g1787208 Escherichia coli 562 -11532921 7502851841 hyac hyac protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #225) (db:genpept) (de:escherichia coli genomic dna. (22.3 - 22.7 min).) (nt:orf\_id:o225#1; similar to pir accession number) (le:985) (re:1692) (di:direct) D90735 D90735 g1651475 Escherichia coli 562 -11532921

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824692	7626	29782	1392	463

Description

6500729064 hyad:b0975 hydrogenase-1 operon protein hyad (gtcfc:2.8)  
(keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b0975 b0975  
Escherichia coli 562 -11532922 78411 hyad (ec:3.4.-.-) (de:hydrogenase 1  
maturation protease,) (db:swissprot) HYAD\_ECOLI P19930 ESCHERICHIA COLI 562  
-11532922 135168 hyad hydrogenase 1 formation factor hyad (cl:hydrogenase-1  
operon protein hyad) (db:pir1.dat) (mp:21 min) QQECHD JV0075 Escherichia  
coli 562 -11532922 223307 hyad hydrogenase-1 operon protein hyad  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #225)  
(db:genpept-bct1) (de:escherichia coli genomic dna. (22.2 - 22.6 min).)  
(le:1693) (re:2280) (di:direct) D90735 D90735 g1651476 Escherichia coli 562  
-11532922 7500883683 (sr:e.coli (strain le392) dna) (db:genpept-bct1)  
(de:e.coli hya operon encoding hydrogenase isozyme 1 large and smallsubunit  
(hyab and a) genes and hyac-f protein genes, complete cds.) (nt:hyad  
protein) (le:3819) (re:4406) (di:direct) ECOHYA M34825 g146423 Escherichia  
coli 562 -11532922 234823 hyad processing of hyaa and hyab proteins  
(fn:factor; energy metabolism, carbon: aerobic) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 89 of 400 of the completegenome.)  
(nt:o195; 98 pct identical to hyad\_ecoli sw: p19930) (le:5827) (re:6414)  
(di:direct) AE000199 AE000199 g1787209 Escherichia coli 562 -11532922  
7502851842 hyad hydrogenase-1 operon protein hyad. (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #225) (db:genpept) (de:escherichia  
coli genomic dna. (22.3 - 22.7 min).) (nt:orf\_id:o225#2; similar to  
swissprot accession) (le:1689) (re:2276) (di:direct) D90735 D90735 g1651476  
Escherichia coli 562 -11532922

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824693	7627	29783	609	202

# Description

6500729065 hyae:b0976 hydrogenase-1 operon protein hyae (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b0976 b0976 Escherichia coli 562 -11532923 78412 hyae (de:hydrogenase-1 operon protein hyae) (db:swissprot) HYAE\_ECOLI P19931 ESCHERICHIA COLI 562 -11532923 135167 hyae hydrogenase 1 formation factor hyae (cl:hydrogenase-1 operon protein hyae) (db:pir1.dat) (mp:21 min) QQECHE JV0076 Escherichia coli 562 -11532923 223308 hyae hydrogenase-1 operon protein hyae (sr:escherichia coli(strain:k12) dna, clone:kohara clone #225) (db:genpept-bct1) (de:escherichia coli genomic dna. (22.2 - 22.6 min).) (le:2277) (re:2675) (di:direct) D90735 D90735 g1651477 Escherichia coli 562 -11532923 7500883684 (sr:e.coli (strain le392) dna) (db:genpept-bct1) (de:e.coli hya operon encoding hydrogenase isozyme 1 large and smallsubunit (hyab and a) genes and hyac-f protein genes, complete cds.) (nt:hyae protein) (le:4403) (re:4801) (di:direct) ECOHYA M34825 g146424 Escherichia coli 562 -11532923 234824 hyae processing of hyaa and hyab proteins (fn:factor; energy metabolism, carbon: aerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 89 of 400 of the completegenome.) (nt:o132; 100 pct identical to hyae\_ecoli sw: p19931) (le:6411) (re:6809) (di:direct) AE000199 AE000199 g1787210 Escherichia coli 562 -11532923 7502851843 hyae hydrogenase-1 operon protein hyae. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #225) (db:genpept) (de:escherichia coli genomic dna. (22.3 - 22.7 min).) (nt:orf\_id:o225#3; similar to swissprot accession) (le:2273) (re:2671) (di:direct) D90735 D90735 g1651477 Escherichia coli 562 -11532923

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824694	7628	29784	225	74

Description

6500729066 hyaf:b0977 hydrogenase-1 operon protein hyaf (gtcfc:2.8)  
(keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b0977 b0977  
Escherichia coli 562 -11532924 78413 hyaf (de:hydrogenase-1 operon protein  
hyaf) (db:swissprot) HYAF\_ECOLI P19932 ESCHERICHIA COLI 562 -11532924  
135169 hyaf hydrogenase 1 formation factor hyaf (cl:hydrogenase-1 operon  
protein hyaf) (db:pir1.dat) (mp:21 min) QQECHF JV0077 Escherichia coli 562  
-11532924 223309 hyaf hydrogenase-1 operon protein hyaf (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #225) (db:genpept-bct1)  
(de:escherichia coli genomic dna. (22.2 - 22.6 min).) (le:2672) (re:3529)  
(di:direct) D90735 D90735 g1651478 Escherichia coli 562 -11532924  
7500883685 (sr:e.coli (strain le392) dna) (db:genpept-bct1) (de:e.coli hya  
operon encoding hydrogenase isozyme 1 large and smallsubunit (hyab and a)  
genes and hyac-f protein genes, complete cds.) (nt:hyaf protein) (le:4798)  
(re:5655) (di:direct) ECOHYA M34825 g146425 Escherichia coli 562 -11532924  
234825 hyaf nickel incorporation into hydrogenase-1 (fn:phenotype; energy  
metabolism, carbon: aerobic) (db:genpept-bct2) (de:escherichia coli k-12  
mg1655 section 89 of 400 of the completegenome.) (nt:o285; 100 pct identical  
to hyaf\_ecoli sw: p19932) (le:6806) (re:7663) (di:direct) AE000199 AE000199  
g1787211 Escherichia coli 562 -11532924 7502851844 hyaf hydrogenase-1  
operon protein hyaf. (sr:escherichia coli(strain:k12) dna, clone:kohara  
clone #225) (db:genpept) (de:escherichia coli genomic dna. (22.3 - 22.7  
min).) (nt:orf\_id:o225#4; similar to swissprot accession) (le:2668)  
(re:3525) (di:direct) D90735 D90735 g1651478 Escherichia coli 562 -11532924



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824695	7629	29785	237	78

Description

6500729067 appc:cyxa:cbda:b0978 probable cytochrome oxidase subunit  
i:cytochrome bd-ii oxidase subunit i (gtcfc:2.8) (ec:1.10.3.-) (keggfc:14.1)  
(rileyfc:1.2.6) (db:gtc-escherichia coli) b0978 b0978 Escherichia coli 562  
-11532925 59881 appc:cyxa:cbda (ec:1.10.3.-) (de:cytochrome bd-ii oxidase  
subunit i,) (db:swissprot) APPC\_ECOLI P26459 ESCHERICHIA COLI 562 -11532925  
162741 appc cytochrome bd-ii oxidase chain i::appc protein (cl:cytochrome d  
complex terminal oxidase chain i) (ec:1.10.3.-) (db:pir2.dat) S17958 S17958  
Escherichia coli 562 -11532925 223310 appc appc protein (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #225) (db:genpept-bct1)  
(de:escherichia coli genomic dna. (22.2 - 22.6 min).) (le:3663) (re:5207)  
(di:direct) D90735 D90735 g1651479 Escherichia coli 562 -11532925  
7500876999 appc appc (sr:escherichia coli k12) (db:genpept-bct1)  
(de:appc=cytochrome d oxidase, subunit i homolog...appa=ph 2.5  
acidphosphatase (escherichia coli, k12, genomic, 4 genes, 3124 nt).)  
(nt:cytochrome d oxidase, subunit i homolog; this) (le:197) (re:1741)  
(di:di... S63811 S63811 g238657 Escherichia coli 562 -11532925 258545 appc  
probable third cytochrome oxidase:subunit i (fn:putative enzyme; energy  
metabolism, carbon:) (db:genpept-bct2) (ec:1.10.3.-) (de:escherichia coli  
k-12 mg1655 section 89 of 400 of the completegenome.) (nt:o514; 100 pct  
identical to appc\_ecoli sw: p26459) (le:7797) (re:9341) (di:direct) AE000199  
AE000199 g1787212 Escherichia coli 562 -11532925 7502851845 appc cytochrome  
bd-ii oxidase subunit i ec (sr:escherichia coli(strain:k12) dna,  
clone:kohara clone #225) (db:genpept) (de:escherichia coli genomic dna.  
(22.3 - 22.7 min).) (nt:orf\_id:o225#5; similar to swissprot accession)  
(le:3659) (re:5203) (di:direct) D90735 D90735 g1651479 Escherichia coli 562  
-11532925

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824702	7630	29786	756	251

Description

6500729068 appb:cyxb:cbdb:b0979 probable cytochrome oxidase subunit ii:cytochrome bd-ii oxidase subunit ii (gtcfc:2.8) (ec:1.10.3.-) (keggfc:14.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b0979 b0979 Escherichia coli 562 -11532926 59879 appb:cyxb:cbdb (ec:1.10.3.-) (de:cytochrome bd-ii oxidase subunit ii,) (db:swissprot) APPB\_ECOLI P26458 ESCHERICHIA COLI 562 -11532926 223311 appb appb protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #225) (db:genpept-bct1) (de:escherichia coli genomic dna. (22.2 - 22.6 min).) (le:5219) (re:6355) (di:direct) D90735 D90735 g1651480 Escherichia coli 562 -11532926 7500876997 appb probable third cytochrome oxidase:subunit ii (fn:putative enzyme; energy metabolism, carbon:) (db:genpept-bct2) (ec:1.10.3.-) (de:escherichia coli k-12 mg1655 section 89 of 400 of the completegenome.) (nt:o378; 99 pct identical to appb\_ecoli sw: p26458) (le:9353) (re:10489) (di:direct) AE000199 AE000199 g1787213 Escherichia coli 562 -11532926 7502851846 appb cytochrome bd-ii oxidase subunit ii ec (sr:escherichia coli(strain:k12) dna, clone:kohara clone #225) (db:genpept) (de:escherichia coli genomic dna. (22.3 - 22.7 min).) (nt:orf\_id:o225#6; similar to swissprot accession) (le:5215) (re:6351) (di:direct) D90735 D90735 g1651480 Escherichia coli 562 -11532926

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824710	7631	29787	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824714	7632	29788	228	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824724	7633	29789	1965	655

Description

6500729069 torr:b0995 torcad operon transcriptional regulatory protein torr (gtcfc:2.8:12.13:10.2) (keggfc:12.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b0995 b0995 Escherichia coli 562 -11532927 101830 torr (de:torcad operon transcriptional regulatory protein torr) (db:swissprot) TORR\_ECOLI P38684 ESCHERICHIA COLI 562 -11532927 7000686816 torr torcad operon transcription regulator torr:tmao response regulator:torcad response regulator (cl:ompr protein:response regulator homology) (db:pir2.dat) A64841 A64841 Escherichia coli 562 -11532927 223317 torr torcad operon transcriptional regulatory protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept-bct1) (de:escherichia coli genomic dna. (22.5 - 22.9 min).) (le:11757) (re:12449) (di:complement) D90736 D90736 g1651487 Escherichia coli 562 -11532927 223322 torr torcad operon transcriptional regulatory protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #227) (db:genpept-bct1) (de:escherichia coli genomic dna. (22.7 - 23.0 min).) (le:2759) (re:3451) (di:complement) D90737 D90737 g1651493 Escherichia coli 562 -11532927 7500893274 torr response transcriptional regulator for tora (fn:regulator; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 91 of 400 of the completegenome.) (nt:f230; 99 pct identical to torr\_ecoli sw: p38684) (le:6035) (re:6727) (di:complement) AE000201 AE000201 g1787229 Escherichia coli 562 -11532927 7502851847 torr torcad response regulator (sr:escherichia coli(strain:k12) dna, clone:kohara clone #227) (db:genpept) (de:escherichia coli genomic dna. (22.8 - 23.1 min).) (nt:orf\_id:o227#2; similar to pir accession number) (le:2759) (re:3451) (di:complement) D90737 D90737 g1651493 Escherichia coli 562 -11532927 7502851848 torr torcad response regulator (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept) (de:escherichia coli genomic dna. (22.6 - 23.0 min).) (nt:orf\_id:o227#2; similar to pir accession number) (le:11757) (re:12449) (di:complement) D90736 D90736 g1651487 Escherichia coli 562 -11532927

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824741	7634	29790	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824749	7635	29791	474	157

Description

6500729070 ndh:b1109 nadh dehydrogenase (gtcfc:2.8) (ec:1.6.99.3)  
(keggfc:14.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b1109 b1109  
Escherichia coli 562 -11532928 122884 ndh nadh dehydrogenase (cl:nadh  
dehydrogenase) (ec:1.6.99.3) (db:pir1.dat) (mp:22 min) DEECR A00461  
Escherichia coli 562 -11532928 223366 ndh nadh dehydrogenase  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #237)  
(db:genpept-bct1) (de:escherichia coli genomic dna.(24.9 - 25.3 min).)  
(le:8026) (re:9330) (di:direct) D90746 D90746 g1651546 Escherichia coli 562  
-11532928 7500953206 nadh dehydrogenase (db:genpept-bct1) (de:e. coli gene  
ndh coding for respiratory nadh dehydrogenase (acomponent of the electron  
transport chain). this enzyme catalysethe transfer of electrons from nadh  
to the respiratory chain andthus links the major catabolic and energ...  
ECNDHX V00306 g581140 Escherichia coli 562 -11532928 233473 ndh respiratory  
nadh dehydrogenase (fn:enzyme; energy metabolism, carbon: aerobic)  
(db:genpept-bct2) (ec:1.6.99.3) (de:escherichia coli k-12 mg1655 section 101  
of 400 of the completegenome.) (nt:o434; 99 pct identical to dhna\_ecoli sw:  
p00393 but) (le:4397) (re:5701) (di:direct) AE000211 AE000211 g1787352  
Escherichia coli 562 -11532928 7502851849 ndh nadh dehydrogenase ec  
1.6.99.3 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #237)  
(db:genpept) (de:escherichia coli genomic dna. (25.0 - 25.4 min).)  
(nt:orf\_id:o237#8; similar to pir accession number) (le:8026) (re:9330)  
(di:direct) D90746 D90746 g1651546 Escherichia coli 562 -11532928

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824753	7636	29792	249	82

Description

6500729071 narl:frdr:b1221 nitrate/nitrite response regulator protein narl (gtcfc:2.8:12.13) (keggfc:12.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b1221 b1221 Escherichia coli 562 -11532929 304591 narl:frdr (de:nitrate/nitrite response regulator protein narl) (db:swissprot) NARL\_ECOLI P10957 ESCHERICHIA COLI 562 -11532929 130891 narl:frdr nitrate/nitrite response regulator protein narl (cl:regulatory protein coma:response regulator homology) (sr:strain k12, , strain k12) (sr:strain k12, ) (db:pir1.dat) (mp:27 min) RGEENL S09285 Escherichia coli 562 -11532929 223426 narl nitrate/nitrite response regulator protein narl (sr:escherichia coli(strain:k12) dna, clone:kohara clone #248) (db:genpept-bct1) (de:escherichia coli genomic dna (27.2-27.6 min).) (le:10303) (re:10953) (di:complement) D90757 D90757 g1651615 Escherichia coli 562 -11532929 233468 narl (db:genpept-bct1) (de:e. coli narx and narl genes.) (le:2222) (re:2872) (di:direct) ECNARXL X13360 g42102 Escherichia coli 562 -11532929 7502851850 narl (db:genpept-bct1) (de:e.coli narxl operon and partial nark gene.) (le:3171) (re:3821) (di:direct) ECNARXLO X69189 g42106 Escherichia coli 562 -11532929 233465 narl pleiotrophic regulation of anaerobic (fn:regulator; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 110 of 400 of the completgenome.) (nt:f216; 100 pct identical to narl\_ecoli sw: p10957) (le:5325) (re:5975) (di:complement) AE000220 AE000220 g1787473 Escherichia coli 562 -11532929 7502851851 frdr nitrate/nitrite response regulator protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #248) (db:genpept) (de:escherichia coli genomic dna. (27.3 - 27.7 min).) (nt:orf\_id:o248#11; similar to swissprot accession) (le:10303) (re:10953) (di:complement) D90757 D90757 g1651615 Escherichia coli 562 -11532929 85246 narl:frdr (de:nitrate/nitrite response regulator protein narl) (db:swissprot) NARL\_ECOLI P10957 ESCHERICHIA COLI 562 -11532929

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824757	7637	29793	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824771	7638	29794	705	235

Description

GTC ORF with score 131 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome xii cosmid 8083.) (nt:similar to kluyveromyces lactis deoxyribonucleic) (le:23775) (re:26219) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824774	7639	29795	876	291

Description

GTC ORF with score 190 to: (sr:thale cress) (db:genpept-pln2)  
(de:arabidopsis thaliana chromosome ii bac t19c21 genomic sequence, complete  
sequence.) (nt:unknown protein) (le:15334:15625:15833)  
(re:15498:15735:15970) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824791	7640	29796	489	163

Description

6500729072 narx:narr:b1222 nitrate/nitrite sensor protein narx  
(gtcfc:2.8:12.13) (ec:2.7.3.-) (keggfc:12.1) (rileyfc:1.2.6)  
(db:gtc-escherichia coli) b1222 b1222 Escherichia coli 562 -11532930 304590  
narx:narr (ec:2.7.3.-) (de:nitrate/nitrite sensor protein narx,)  
(db:swissprot) NARX\_ECOLI P10956 ESCHERICHIA COLI 562 -11532930 131459 narx  
nitrate/nitrite sensor protein narx (cl:regulatory protein narx)  
(ec:2.7.3.-) (db:pir1.dat) (mp:27 min) RGE CNX S26137 Escherichia coli 562  
-11532930 223427 narx nitrate/nitrite sensor protein narx (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #248) (db:genpept-bct1)  
(de:escherichia coli genomic dna (27.2-27.6 min).) (le:10946) (re:12742)  
(di:complement) D90757 D90757 g1651616 Escherichia coli 562 -11532930  
233467 narx (db:genpept-bct1) (de:e. coli narx and narl genes.) (le:433)  
(re:2229) (di:direct) ECNARXL X13360 g42101 Escherichia coli 562 -11532930  
7502851852 narx (db:genpept-bct1) (de:e.coli narxl operon and partial narx  
gene.) (le:1382) (re:3178) (di:direct) ECNARXLO X69189 g42105 Escherichia  
coli 562 -11532930 233464 narx nitrate/nitrate sensor:histidine protein  
kinase (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2)  
(ec:2.7.3.-) (de:escherichia coli k-12 mg1655 section 110 of 400 of the  
completegenome.) (nt:f598; 100 pct identical to narx\_ecoli sw: p10956)  
(le:5968) (re:7764) (di:complement) AE000220 AE000220 g1787474 Escherichia  
coli 562 -11532930 7502851853 narr nitrate/nitrite sensor protein narx ec  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #248) (db:genpept)  
(de:escherichia coli genomic dna. (27.3 - 27.7 min).) (nt:orf\_id:o248#12;  
similar to swissprot accession) (le:10946) (re:12742) (di:complement) D90757  
D90757 g1651616 Escherichia coli 562 -11532930 85258 narx:narr (ec:2.7.3.-)  
(de:nitrate/nitrite sensor protein narx,) (db:swissprot) NARX\_ECOLI P10956  
ESCHERICHIA COLI 562 -11532930

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824800	7641	29797	189	62

Description

GTC ORF with score 107 to: (db:genpept-bct1) (de:methylobacterium extorquens methylotrophy region containingmalylyl-coa lyase (mcla), putative abc transporter subunit a (abca), putative abc transporter subunit b (abcb), putative abc transporteratp-binding...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824814	7642	29798	597	198

Description

GTC ORF with score 162 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana chromosome ii bac t1d16 genomic sequence, complete sequence.) (nt:unknown protein) (le:29689:30544:31121:31563) (re:30462:30982:31191:31687) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824845	7643	29799	1293	430

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824854	7644	29800	564	187

Description

6500729073 cybb:b1418 (gtcfc:2.8) (ec:1.10.2.-) (keggfc:14.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b1418 b1418 Escherichia coli 562 -11532931 7000690866 cybb cytochrome b561 (cl:cytochrome b561) (db:pir2.dat) E64893 E64893 Escherichia coli 562 -11532931 7500959716 cybb cytochrome b 561 (fn:enzyme; energy metabolism, carbon: electron) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 129 of 400 of the completegenome.) (nt:o188; residues 41-177 are 100 pct identical) (le:3797) (re:4363) (di:direct) AE000239 AE000239 g1787687 Escherichia coli 562 -11532931

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824859	7645	29801	231	76

Description

6500729074 narp:b2193 nitrate/nitrite response regulator protein narp (gtcfc:2.8:12.13) (keggfc:12.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2193 b2193 Escherichia coli 562 -11532932 85247 narp (de:nitrate/nitrite response regulator protein narp) (db:swissprot) NARP\_ECOLI P31802 ESCHERICHIA COLI 562 -11532932 164159 narp nitrate/nitrite response regulator protein narp (cl:regulatory protein coma:response regulator homology) (db:pir2.dat) A40584 A40584 Escherichia coli 562 -11532932 7500886307 narp nitrate/nitrite response regulator (fn:narp, like narl, is a response regulator) (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli nitrate and nitrite response regulator protein(narp) gene, complete cds.) (le:15) (re:662) (di:direct) ECONARP L11273 g304917 Escherichia coli 562 -11532932 235219 narp nitrate/nitrite response regulator sensor (fn:regulator; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 199 of 400 of the completengenome.) (nt:o215; 100 pct identical to narp\_ecoli sw: p31802) (le:224) (re:871) (di:direct) AE000309 AE000309 g1788521 Escherichia coli 562 -11532932

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824861	7646	29802	216	71

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824875	7647	29803	747	248

Description

6500729075 glpa:b2241 anaerobic glycerol-3-phosphate dehydrogenase subunit  
a:g-3-p dehydrogenase (gtcfc:2.8:8.1) (ec:1.1.99.5) (keggfc:8.1)  
(rileyfc:1.2.6) (db:gtc-escherichia coli) b2241 b2241 Escherichia coli 562  
-11532933 74009 glpa (ec:1.1.99.5) (de:(g-3-p dehydrogenase))  
(db:swissprot) GLPA ECOLI P13032 ESCHERICHIA COLI 562 -11532933 122591 glpa  
glycerol-3-phosphate dehydrogenase:chain a:anaerobic  
(cl:glycerol-3-phosphate dehydrogenase (aerobic)) (ec:1.1.99.5)  
(db:pir1.dat) (mp:49 min) DEECNA A32006 Escherichia coli 562 -11532933  
224747 glpa glycerol-3-phosphate dehydrogenase ec 1.1.99.5 (sr:escherichia  
coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #377(50.5-50.9 min.)) (nt:similar to  
(pir accession number a32006)) (le:12931) (re:14559) (di:direct) D90855  
D90855 g1799588 Escherichia coli 562 -11532933 7500882485 glpa  
sn-glycerol-3-phosphate dehydrogenase (fn:enzyme; energy metabolism, carbon:  
anaerobic) (db:genpept-bct2) (ec:1.1.99.5) (de:escherichia coli k-12 mg1655  
section 204 of 400 of the completegenome.) (nt:o542; 99 pct identical to  
glpa\_ecoli sw: p13032) (le:3098) (re:4726) (di:direct) AE000314 AE000314  
g1788574 Escherichia coli 562 -11532933 5000690564 (de:(ecoli\_2190)  
(pn:sn-glycerol-3-phosphate dehydrogenase:anaerobic, large subunit)  
(gn:glpa) (gtcfc:8.1) (ec:1.1.99.5) (glpa\_ecoli) (keggfc:8.1)  
(rileyfc:1.2.6) (db:gtc-escherichia coli) ECOLI\_2190 ECOLI\_2190 Escherichia  
coli 562 10065538

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824877	7648	29804	831	276

Description

6500729076 glpb:b2242 anaerobic glycerol-3-phosphate dehydrogenase subunit b:g-3-p dehydrogenase (gtcfc:2.8:8.1) (ec:1.1.99.5) (keggfc:8.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2242 b2242 Escherichia coli 562 -11532934 74012 glpb (ec:1.1.99.5) (de:(g-3-p dehydrogenase)) (db:swissprot) GLPB\_ECOLI P13033 ESCHERICHIA COLI 562 -11532934 122592 glpb glycerol-3-phosphate dehydrogenase:chain b:anaerobic (cl:glycerol-3-phosphate dehydrogenase (anaerobic) chain b) (ec:1.1.99.5) (db:pir1.dat) (mp:49 min) DEECNB B32006 Escherichia coli 562 -11532934 224748 glpb glycerol-3-phosphate dehydrogenase ec 1.1.99.5 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #377(50.5-50.9 min.)) (nt:similar to (pir accession number b32006)) (le:14549) (re:15808) (di:direct) D90855 D90855 g1799589 Escherichia coli 562 -11532934 7500882487 glpb glycerol-3-phosphate dehydrogenase subunit b (sr:escherichia coli (strain jm83) (clone: pglp1.) dna) (db:genpept-bct1) (de:e.coli glpabc operon encoding glycerol-3-phosphate dehydrogenase,complete cds.) (le:1841) (re:3100) (di:direct) ECOGLPA M20938 g146178 Escherichia coli 562 -11532934 234511 glpb sn-glycerol-3-phosphate dehydrogenase (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (ec:1.1.99.5) (de:escherichia coli k-12 mg1655 section 204 of 400 of the completegenome.) (nt:o419; 99 pct identical to glpb\_ecoli sw: p13033) (le:4716) (re:5975) (di:direct) AE000314 AE000314 g1788575 Escherichia coli 562 -11532934 5000690565 (de:(ecoli\_2191) (pn:sn-glycerol-3-phosphate dehydrogenase:anaerobic, membrane anchor subunit) (gn:glpb) (gtcfc:8.1) (ec:1.1.99.5) (glpb\_ecoli) (keggfc:8.1) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI\_2191 ECOLI\_2191 Escherichia coli 562 10016542

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824889	7649	29805	471	156
<u>Description</u>				

6500729077 glpc:b2243 anaerobic glycerol-3-phosphate dehydrogenase subunit c:g-3-p dehydrogenase (gtcfc:2.8:8.1) (ec:1.1.99.5) (keggfc:8.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2243 b2243 Escherichia coli 562 -11532935 74015 glpc (de:dehydrogenase) (db:swissprot) GLPC\_ECOLI P13034 ESCHERICHIA COLI 562 -11532935 7000685413 glpc glycerol-3-phosphate dehydrogenase:anaerobic chain c (cl:glycerol-3-phosphate dehydrogenase (anaerobic) chain c:ferredoxin 2(4fe-4s) homology) (ec:1.1.99.5) (db:pir1.dat) (mp:49 min) DEECNC A64995 Escherichia coli 562 -11532935 224749 glpc glycerol-3-phosphate dehydrogenase ec 1.1.99.5 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #377(50.5-50.9 min.)) (nt:similar to (pir accession number c32006)) (le:15805) (re:16995) (di:direct) D90855 D90855 g1799590 Escherichia coli 562 -11532935 7500882489 glpc sn-glycerol-3-phosphate dehydrogenase (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 204 of 400 of the completegenome.) (nt:o396; 99 pct identical glpc\_ecoli sw: p13034) (le:5972) (re:7162) (di:direct) AE000314 AE000314 g1788576 Escherichia coli 562 -11532935 5000690566 (de:(ecoli\_2192) (pn:sn-glycerol-3-phosphate dehydrogenase:anaerobic, k-small subunit) (gn:glpc) (gtcfc:8.1) (ec:1.1.99.5) (glpc\_ecoli) (keggfc:8.1) (rileyfc:1.2.6) (db:gtc-escherichia coli)) ECOLI\_2192 ECOLI\_2192 Escherichia coli 562 10120045

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824892	7650	29806	264	87
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824900	7651	29807	396	131

#### Description

6500729078 narq:b2469 nitrate/nitrite sensor protein:nitrate/nitrite sensor protein narq (gtcfc:2.8:12.13) (ec:2.7.3.-) (keggfc:12.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2469 b2469 Escherichia coli 562 -11532936 235221 narq (ec:2.7.3.-) (de:nitrate/nitrite sensor protein narq,) (db:swissprot) NARQ\_ECOLI P27896 ESCHERICHIA COLI 562 -11532936 7000685929 narq nitrate/nitrite sensor protein narq (cl:nitrate/nitrite sensor protein narq) (ec:2.7.3.-) (db:pir2.dat) D65022 D65022 Escherichia coli 562 -11532936 225031 narq nitrate/nitrite sensor protein narq ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #422(55.5-55.8 min.)) (nt:similar to (swissprot accession number p27896)) (le:8824) (re:10524) (di:direct) D90875 D90875 g1799892 Escherichia coli 562 -11532936 7500886309 narq (db:genpept-bct1) (de:e.coli narq gene.) (le:58) (re:1758) (di:direct) ECNARQ X65714 g581139 Escherichia coli 562 -11532936 7502851854 narq nitrate sensor protein (fn:histidine protein kinase (like narx involved in) (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli nitrate sensor protein (narq) gene, complete cds.) (le:19) (re:1719) (di:direct) ECONARQB M94724 g146928 Escherichia coli 562 -11532936 233461 narq sensor for nitrate reductase system:protein (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (ec:2.7.3.-) (de:escherichia coli k-12 mg1655 section 223 of 400 of the completegenome.) (nt:o566; 100 pct identical to narq\_ecoli sw:) (le:9774) (re:11474) (di:direct) AE000333 AE000333 g1788812 Escherichia coli 562 -11532936 85250 narq (ec:2.7.3.-) (de:nitrate/nitrite sensor protein narq,) (db:swissprot) NARQ\_ECOLI P27896 ESCHERICHIA COLI 562 -11532936

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824901	7652	29808	480	159

#### Description

GTC ORF with score 302 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome ii cosmid c2d10.) (nt:spbc2d10.12, len:368, similarity:mus musculus,) (le:21268:21377:21491:22380) (re:21336:21449:22332:22448) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824907	7653	29809	240	79

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824919	7654	29810	312	103

Description

6500729079 fdx:b2525 ferredoxin:2fe-2s (gtcfc:2.8) (keggfc:14.2)  
(rileyfc:1.2.6) (db:gtc-escherichia coli) b2525 b2525 Escherichia coli 562  
-11532937 135744 fdx ferredoxin 2fe-2s ) (cl:ferredoxin (2fe-2s):ferredoxin  
(2fe-2s) homology) (db:pir2.dat) JC1110 JC1110 Escherichia coli 562  
-11532937 225104 fdx ferredoxin 2fe-2s ) (sr:escherichia coli (strain:k12)  
dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic  
dna, kohara clone #429(56.9-57.2 min.)) (nt:similar to (pir accession  
number jc1110)) (le:14656) (re:14991) (di:complement) D90882 D90882 g1799928  
Escherichia coli 562 -11532937 225108 fdx ferredoxin 2fe-2s )  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #430(57.2-57.5  
min.)) (nt:similar to (pir accession number jc1110)) (le:511) (re:846)  
(di:complement) D90883 D90883 g1799933 Escherichia coli 562 -11532937  
7500953745 fdx ferredoxin (sr:escherichia coli (strain k-12) dna)  
(db:genpept-bct1) (de:escherichia coli ferredoxin (2fe-2s) protein (fdx)  
gene, completecds.) (le:181) (re:516) (di:direct) ECOFDX M88654 g145915  
Escherichia coli 562 -11532937 234312 fdx 2fe-2s ferredoxin, electron  
carrer protein) (fn:carrier; energy metabolism, carbon: electron)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 229 of 400 of the  
completegenome.) (nt:f111; 100 pct identical to fer\_ecoli sw: p25528)  
(le:3030) (re:3365... AE000339 AE000339 g1788874 Escherichia coli 562  
-11532937

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824920	7655	29811	594	197

Description

6500729080 hmpa:hmp:fsrb:b2552 flavohemoprotein:haemoglobin-like protein:flavohemoglobin: dihydropteridine reductase:ferrisiderophore reductase b (gtcfc:2.8:9.6) (ec:1.6.99.7) (keggfc:9.7) (rileyfc:1.2.6) (db:gtc-escherichia coli) (gtcfc:energy metabolism-electron transport:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) b2552 b2552 Escherichia coli 562 -11532938 304575 hmpa:hmp:fsrb (ec:1.6.99.7) (de:b) (nitric oxide dioxygenase) (nod)) (db:swissprot) HMPA\_ECOLI P24232 ESCHERICHIA COLI 562 -11532938 163184 hmpa::hmp flavohemoglobin hmp:ferrisiderophore reductase fsrb:flavohemoprotein (cl:flavohemoglobin:cytochrome-b5 reductase homology:globin homology) (db:pir1.dat) S15992 S15992 Escherichia coli 562 -11532938 225149 fsrb flavohemoprotein haemoglobin-like protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #432(57.5-57.9 min.)) (nt:similar to (swissprot accession number p24232)) (le:13864) (re:15054) (di:direct) D90885 D90885 g1799976 Escherichia coli 562 -11532938 5000690657 hmp hmp haemoprotein (db:genpept-bct1) (de:e.coli hmp and glnb genes for hmp haemoprotein and p-ii protein.) (le:293) (re:1483) (di:direct) ECHMPGLNB X58872 g41731 Escherichia coli 562 -11532938 233125 hmpa dihydropteridine reductase:ferrisiderophore (fn:enzyme; energy metabolism, carbon: electron) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 231 of 400 of the completegenome.) (nt:o396; 100 pct identical to hmpa\_ecoli sw: p24232) (le:6450) (re:7640) (di:direct) AE000341 AE000341 g1788903 Escherichia coli 562 -11532938 77373 hmpa:hmp:fsrb (ec:1.6.99.7) (de:b)) (db:swissprot) HMPA\_ECOLI P24232 ESCHERICHIA COLI 562 -11532938

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824921	7656	29812	441	146

#### Description

6500729081 hydn:b2713 4fe-4s iron-sulfur protein:electron transport protein hydn (gtcfc:2.8:2.7) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2713 b2713 Escherichia coli 562 -11532939 78434 hydn (de:electron transport protein hydn) (db:swissprot) HYDN\_ECOLI P30132 ESCHERICHIA COLI 562 -11532939 7000685583 hydn 4fe-4s iron-sulfur protein (cl:nrfc protein:ferredoxin 2(4fe-4s) homology) (db:pir2.dat) E65051 E65051 Escherichia coli 562 -11532939 239287 hydn 4fe-4s iron-sulfur protein:putative (fn:electron transport from formate to hydrogen,) (sr:escherichia coli (strain:k-12) cell\_line:klf43/kl259 dna) (db:genpept-bct1) (de:e.coli hyda gene for hyda and hydn gene for 4fe-4s iron-sulfurprotein, complete cds.) (nt:this cds is located between ... ECOHYDA D14422 g216575 Escherichia coli 562 -11532939 7500883710 hydn 4fe-4s iron-sulfur protein (fn:electron transport from formate to hydrogen) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg site no. 33521) (le:9882) (re:10409) (di:complement) ECU29579 U29579 g882606 Escherichia coli 562 -11532939 234826 hydn involved in electron transport from formate to (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 245 of 400 of the completegenome.) (nt:f175; 100 pct identical to hydn\_ecoli sw: p30132) (le:5188) (re:5715) (di:complement) AE000355 AE000355 g1789067 Escherichia coli 562 -11532939

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824922	7657	29813	651	216

#### Description

6500729082 hypa:b2726 hypa protein (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2726 b2726 Escherichia coli 562 -11532940 239300 hypa (de:hypa protein) (db:swissprot) HYP\_A\_ECOLI P24189 ESCHERICHIA COLI 562 -11532940 163226 hypa hypa protein (cl:hydrogenase accessory protein) (db:pir2.dat) S15197 S15197 Escherichia coli 562 -11532940 7500883718 hypa hypa product (db:genpept-bct1) (de:e. coli hyp operon encoding hydrogenase isoenzymes.) (le:102) (re:452) (di:direct) ECHYP X54543 g41775 Escherichia coli 562 -11532940 7502851855 hypa (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg site no. 33104; orf\_o116) (le:22951) (re:23301) (di:direct) ECU29579 U29579 g882619 Escherichia coli 562 -11532940 233180 hypa pleiotrophic effects on 3 hydrogenase isozymes (fn:phenotype; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 246 of 400 of the completegenome.) (nt:o116; 100 pct identical to hypa\_ecoli sw: p24189;) (le:8184) (re:8534) (di:direct) AE000356 AE000356 g1789081 Escherichia coli 562 -11532940 78459 hypa (de:hypa protein) (db:swissprot) HYP\_A\_ECOLI P24189 ESCHERICHIA COLI 562 -11532940

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824924	7658	29814	384	127

Description

6500729083 hycp:b2728 hydrogenase isoenzymes formation protein hycp (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2728 b2728 Escherichia coli 562 -11532941 239302 hycp (de:hydrogenase isoenzymes formation protein hycp) (db:swissprot) HYPC\_ECOLI P24191 ESCHERICHIA COLI 562 -11532941 163223 hycp hydrogenase expression/formation protein hycp (cl:hydrogenase expression/formation protein hycp) (db:pir2.dat) S15199 S15199 Escherichia coli 562 -11532941 7500883732 hycp hydrogenase isoenzyme hycp (db:genpept-bct1) (de:e. coli hyp operon encoding hydrogenase isoenzymes.) (le:1319) (re:1591) (di:direct) ECHYP X54543 g41777 Escherichia coli 562 -11532941 7502851856 hycp (fn:required for formation of all 3 hydrogenase) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg site no. 33113; orf\_o90) (le:24168) (re:24440) (di:direct) ECU29579 U29579 g882621 Escherichia coli 562 -11532941 233182 hycp pleiotrophic effects on 3 hydrogenase isozymes (fn:phenotype; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 246 of 400 of the completegenome.) (nt:o90; 100 pct identical to hycp\_ecoli sw: p24191; cg) (le:9401) (re:9673) (di:direct) AE000356 AE000356 g1789083 Escherichia coli 562 -11532941 78471 hycp (de:hydrogenase isoenzymes formation protein hycp) (db:swissprot) HYPC\_ECOLI P24191 ESCHERICHIA COLI 562 -11532941

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824945	7659	29815	399	132

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824949	7660	29816	318	106

Description

6500729084 hypd:b2729 hydrogenase isoenzymes formation protein hypd (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2729 b2729 Escherichia coli 562 -11532942 7500883738 hypd (de:hydrogenase isoenzymes formation protein hypd) (db:swissprot) HYPD\_ECOLI P24192 ESCHERICHIA COLI 562 -11532942 163224 hypd hydrogenase expression/formation protein hypd (cl:hydrogenase expression/formation protein hypd) (db:pir2.dat) S15200 S15200 Escherichia coli 562 -11532942 7502851857 hypd hydrogenase isoenzyme hypd (db:genpept-bct1) (de:e. coli hyp operon encoding hydrogenase isoenzymes.) (le:1591) (re:2712) (di:direct) ECHYP X54543 g41778 Escherichia coli 562 -11532942 233183 hypd pleiotrophic effects on 3 hydrogenase isozymes (fn:phenotype; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 246 of 400 of the completegenome.) (nt:o373; 99 pct identical to hypd\_ecoli sw: p24192; cg) (le:9673) (re:10794) (di:direct) AE000356 AE000356 g1789084 Escherichia coli 562 -11532942 78477 hypd (de:hydrogenase isoenzymes formation protein hypd) (db:swissprot) HYPD\_ECOLI P24192 ESCHERICHIA COLI 562 -11532942

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824965	7661	29817	330	109

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824967	7662	29818	498	165

Description

6500729085 hype:b2730 hydrogenase isoenzymes formation protein hype (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2730 b2730 Escherichia coli 562 -11532943 7500883740 hype (de:hydrogenase isoenzymes formation protein hype) (db:swissprot) HYPE\_ECOLI P24193 ESCHERICHIA COLI 562 -11532943 163227 hype hydrogenase isoenzymes formation protein hype (cl:hydrogenase expression/formation protein hype) (db:pir2.dat) S15201 S15201 Escherichia coli 562 -11532943 7502851858 hype hype product (db:genpept-bct1) (de:e. coli hyp operon encoding hydrogenase isoenzymes.) (le:2751) (re:3719) (di:direct) ECHYP X54543 g41779 Escherichia coli 562 -11532943 233184 hype plays structural role in maturation of all 3 (fn:factor; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 246 of 400 of the completegenome.) (nt:o322; 99 pct identical to hype\_ecoli sw: p24193; cg) (le:10833) (re:11801) (di:direct) AE000356 AE000356 g1789085 Escherichia coli 562 -11532943 78483 hype (de:hydrogenase isoenzymes formation protein hype) (db:swissprot) HYPE\_ECOLI P24193 ESCHERICHIA COLI 562 -11532943

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824968	7663	29819	240	80

Description

6500729086 hybg:b2990 hydrogenase-2 operon protein hybg (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2990 b2990 Escherichia coli 562 -11532944 78419 hybg (de:hydrogenase-2 operon protein hybg) (db:swissprot) HYBG\_ECOLI P37185 ESCHERICHIA COLI 562 -11532944 163220 hybg hydrogenase-2 operon protein hybg (cl:hydrogenase expression/formation protein hycp) (db:pir2.dat) G55516 G55516 Escherichia coli 562 -11532944 239203 hybg (db:genpept-bct1) (de:escherichia coli tg1 hyb operon, hydrogenase-2 large subunit (hybc)gene and hyba, hybb, hybd, hybe, hybf, and hybg genes, completecds.) (le:5303) (re:5551) (di:direct) ECU09177 U09177 g544489 Escherichia coli 562 -11532944 7500883690 hybg hydrogenase-2 operon protein hybg (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf\_f82; cg site no. 33403) (le:94107) (re:94355) (di:complement) ECU28377 U28377 g882519 Escherichia coli 562 -11532944 238552 hybg hydrogenase-2 operon protein:may effect (fn:phenotype; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 272 of 400 of the completegenome.) (nt:f82; 100 pct identical to hybg\_ecoli sw: p37185; cg) (le:1146) (re:1394) (di:complement) AE000382 AE000382 g1789364 Escherichia coli 562 -11532944

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824978	7664	29820	420	139

Description

GTC ORF with score 370 to: (db:genpept-pln2) (de:emerella nidulans spindle assembly checkpoint protein slsb (slsb)gene, complete cds.) (nt:similar to saccharomyces cerevisiae spindle) (le:1113:1175:1501) (re:1122:1430:2308) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824979	7665	29821	783	261

Description

GTC ORF with score 1046 to: (db:genpept-pln2) (de:emerella nidulans spindle assembly checkpoint protein slsb (slsb)gene, complete cds.) (nt:similar to saccharomyces cerevisiae spindle) (le:1113:1175:1501) (re:1122:1430:2308) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824982	7666	29822	783	260

Description

6500729087 hybf:b2991 hydrogenase-2 operon protein hybf (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2991 b2991 Escherichia coli 562 -11532945 78418 hybf (de:hydrogenase-2 operon protein hybf) (db:swissprot) HYBF\_ECOLI P37184 ESCHERICHIA COLI 562 -11532945 163219 hybf:hybe hydrogenase-2 operon protein hybf (cl:hydrogenase accessory protein) (db:pir2.dat) F55516 F55516 Escherichia coli 562 -11532945 7500883689 hybf hydrogenase-2 operon protein hybf (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf\_f113; cg site no. 33427) (le:94368) (re:94709) (di:complement) ECU28377 U28377 g882520 Escherichia coli 562 -11532945 239204 hybf may modulate levels of hydrogenase-2 (fn:regulator; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 272 of 400 of the completegenome.) (nt:f113; 100 pct identical to pir: f55516; cg site) (le:1407) (re:1748) (di:complement) AE000382 AE000382 g1789365 Escherichia coli 562 -11532945

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501824988	7667	29823	414	137

Description

6500729088 hybe:b2992 hydrogenase-2 operon protein hybe (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2992 b2992 Escherichia coli 562 -11532946 7000690905 hybe hydrogenase-2 operon protein hybe (db:pir2.dat) F65085 F65085 Escherichia coli 562 -11532946 7500959766 hybe hydrogenase-2 operon protein hybe (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf\_f162; cg site no. 33424) (le:94702) (re:95190) (di:complement) ECU28377 U28377 g882521 Escherichia coli 562 -11532946 239205 hybe member of hyb operon (fn:phenotype; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 272 of 400 of the completegenome.) (nt:f162; 99 pct identical to hybe\_ecoli sw: p37183; cg) (le:1741) (re:2229) (di:complement) AE000382 AE000382 g1789366 Escherichia coli 562 -11532946

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501824994	7668	29824	711	236

Description

6500729089 hybd:b2993 hydrogenase-2 operon protein hybd (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2993 b2993 Escherichia coli 562 -11532947 78416 hybd (ec:3.4.-.-) (de:hydrogenase 2 maturation protease,) (db:swissprot) HYBD\_ECOLI P37182 ESCHERICHIA COLI 562 -11532947 7000685578 hybd hydrogenase-2 operon protein hybd (cl:hydrogenase-1 operon protein hyad) (db:pir2.dat) G65085 G65085 Escherichia coli 562 -11532947 7500883687 hybd hydrogenase-2 operon protein hybd (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf\_f164; cg site no. 33421) (le:95183) (re:95677) (di:complement) ECU28377 U28377 g882522 Escherichia coli 562 -11532947 239206 hybd probable processing element for hydrogenase-2 (fn:putative enzyme; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 272 of 400 of the completegenome.) (nt:f164; 100 pct identical to 159 aa of hybd\_ecoli) (le:2222) (re:2716) (di:complement) AE000382 AE000382 g1789367 Escherichia coli 562 -11532947

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825009	7669	29825	423	140

Description

6500729090 hybb:b2995 probable hydrogenase-2 cytochrome b subunit:probable ni/fe-hydrogenase 2 b-type cytochrome subunit (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b2995 b2995 Escherichia coli 562 -11532948 7000691894 hybb probable hydrogenase-2 cytochrome b subunit (db:pir2.dat) A65086 A65086 Escherichia coli 562 -11532948 7500960425 hybb probable cytochrome ni/fe component of (fn:putative enzyme; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 272 of 400 of the completegenome.) (nt:f392; 100 pct identical to hybb\_ecoli sw: p37180;) (le:4416) (re:5594) (di:complement) AE000382 AE000382 g2367183 Escherichia coli 562 -11532948

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825014	7670	29826	306	101

Description

6500729091 glpr:b3423 glycerol-3-phosphate regulon repressor (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b3423 b3423  
 Escherichia coli 562 -11532949 7000690889 glpr glpr protein (db:pir2.dat) B65138 B65138 Escherichia coli 562 -11532949 236657 glpr (fn:glycerol-3-phosphate regulon repressor) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 688) (le:340586) (re:341344) (di:complement) ECOUW67 U18997 g606358 Escherichia coli 562 -11532949 234521 glpr repressor of the glp operon (fn:regulator; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 308 of 400 of the completegenome.) (nt:f252; cg site no. 688) (le:6974) (re:7732) (di:complement) AE000418 AE000418 g1789829 Escherichia coli 562 -11532949 7500959745 glpr repressor protein (fn:negative regulatory protein for the glp) (db:genpept-bct2) (de:escherichia coli glycerophosphate dehydrogenase (glpd) gene,partial cds; and the translation start site has been verified(glpe), the translation start site has been verified (glpg), and... ECOGLPDAA M96795 g1293534 Escherichia coli 562 -11532949

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825023	7671	29827	636	211

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825025	7672	29828	681	227

Description

GTC ORF with score 205 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c17h11.) (nt:coded for by c. elegans cdna yk136e11.3; coded for) (le:19425:19626:20313) (re:19579:19849:20496) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825037	7673	29829	192	63

Description

GTC ORF with score 168 to: (sr:baker's yeast) (db:genpept-pln1) (de:ykl522=mitochondrial adp/atp carrier protein homolog...ykl527=hlhistone homolog (saccharomyces cerevisiae, genomic, 5 genes, 8294nt).) (nt:mitochondrial adp/atp carrier protein ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825041	7674	29830	564	187

Description

GTC ORF with score 469 to: (sr:baker's yeast) (db:genpept-pln1)  
 (de:ykl522=mitochondrial adp/ATP carrier protein homolog...ykl527=hlhistone  
 homolog (saccharomyces cerevisiae, genomic, 5 genes, 8294nt).)  
 (nt:mitochondrial adp/ATP carrier protein ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825045	7675	29831	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825049	7676	29832	840	279

Description

GTC ORF with score 159 to: (fn:essential for slug migration)  
 (db:genpept-inv) (de:dictyostelium discoideum miga (miga) gene, complete  
 cds.) (nt:n-terminus of this protein is similar to other btb) (le:884:2998)  
 (re:2899:3423) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825051	7677	29833	723	240

Description

6500729092 glpg:b3424 glpg protein (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6)  
 (db:gtc-escherichia coli) b3424 b3424 Escherichia coli 562 -11532950  
 7000688979 glpg glpg protein (cl:glpg protein) (db:pir1.dat) (mp:75 min)  
 BVECGG C65138 Escherichia coli 562 -11532950 234520 glpg protein of glp  
 regulon (fn:phenotype; energy metabolism, carbon: anaerobic)  
 (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 308 of 400 of the  
 completegenome.) (nt:f276; cg site no. 18262; 100 pct identical) (le:7749)  
 (re:8579) (di:complement) AE000418 AE000418 g2367225 Escherichia coli 562  
 -11532950 7500953636 glpg (fn:unknown) (db:genpept-bct2) (de:escherichia  
 coli glycerophosphate dehydrogenase (glpd) gene,partial cds; and the  
 translation start site has been verified(glpe), the translation start site  
 has been verified (glpg), andrepressor protein (glpr) genes, ... ECOGLPDAA  
 M96795 g1293533 Escherichia coli 562 -11532950

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825071	7678	29834	399	132

Description

6500729093 glpe:b3425 protein:glpe protein (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b3425 b3425 Escherichia coli 562 -11532951 74024 glpe (de:glpe protein) (db:swissprot) GLPE\_ECOLI P09390 ESCHERICHIA COLI 562 -11532951 7000685415 glpe glpe protein (cl:glpe protein) (db:pir1.dat) (mp:75 min) BVECGE D65138 Escherichia coli 562 -11532951 236659 glpe (fn:gene of glp regulon) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 18265) (le:342236) (re:342562) (di:complement) ECOUW67 U18997 g606360 Escherichia coli 562 -11532951 234519 glpe protein of glp regulon (fn:phenotype; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 308 of 400 of the completegenome.) (nt:f108; cg site no. 18265; 100 pct identical) (le:8624) (re:8950) (di:complement) AE000418 AE000418 g1789831 Escherichia coli 562 -11532951 7500882494 glpe (fn:unknown) (db:genpept-bct2) (de:escherichia coli glycerophosphate dehydrogenase (glpd) gene,partial cds; and the translation start site has been verified(glpe), the translation start site has been verified (glpg), andrepressor protein (glpr) genes, ... ECOGLPDAA M96795 g146184 Escherichia coli 562 -11532951

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825074	7679	29835	567	188

Description

6500729094 glpd:glyd:b3426 aerobic glycerol-3-phosphate dehydrogenase (gtcfc:2.8:8.1) (ec:1.1.99.5) (keggfc:8.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b3426 b3426 Escherichia coli 562 -11532952 74019 glpd:glyd (ec:1.1.99.5) (de:aerobic glycerol-3-phosphate dehydrogenase,) (db:swissprot) GLPD\_ECOLI P13035 ESCHERICHIA COLI 562 -11532952 122590 glpd glycerol-3-phosphate dehydrogenase::aerobic:sn-glycerol-3-phosphate dehydrogenase (cl:glycerol-3-phosphate dehydrogenase (aerobic)) (ec:1.1.99.5) (db:pir1.dat) (mp:75 min) DEECGD A39186 Escherichia coli 562 -11532952 7500882492 glpd glycerophosphate dehydrogenase (sr:e.coli (sub-species k-12) dna) (db:genpept-bct1) (de:e.coli sn-glycerol 3-phosphate dehydrogenase (glpd) gene, completecds.) (le:205) (re:1710) (di:direct) ECOSNGLPD M55989 g147838 Escherichia coli 562 -11532952 236007 glpd sn-glycerol-3-phosphate dehydrogenase aerobic (fn:enzyme; energy metabolism, carbon: aerobic) (db:genpept-bct2) (ec:1.1.99.5) (de:escherichia coli k-12 mg1655 section 308 of 400 of the completegenome.) (nt:o501; cg site no. 693; alternate name glyd; 99 pct) (le:9140) (re:10645) (di:direct) AE000418 AE000418 g2367226 Escherichia coli 562 -11532952

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825091	7680	29836	600	199

Description

6500729095 llldr:lctr:b3604 lctr:putative l-lactate dehydrogenase operon regulatory protein (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b3604 b3604 Escherichia coli 562 -11532953 82265 llldr:lctr (de:putative l-lactate dehydrogenase operon regulatory protein) (db:swissprot) LLDR\_ECOLI P33233 ESCHERICHIA COLI 562 -11532953 164398 lctr probable regulatory protein lctr (cl:regulatory protein fadr) (db:pir2.dat) B49904 B49904 Escherichia coli 562 -11532953 236841 lctr (fn:unknown) (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli lct operon encoding l-lactate permease (lctp)gene, (lctr) gene, and l-lactate dehydrogenase (lctd) gene,complete cds.) (nt:lctr contains a helix-turn-helix doma... ECOLCTPRD L13970 g404694 Escherichia coli 562 -11532953 7500885083 lctr (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:aug is 2nd start) (le:193304) (re:194080) (di:direct) ECOUW76 U00039 g466742 Escherichia coli 562 -11532953 234960 llldr transcriptional regulator (fn:regulator; energy metabolism, carbon: aerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 328 of 400 of the completegenome.) (nt:o258) (le:6850) (re:7626) (di:direct) AE000438 AE000438 g1790032 Escherichia coli 562 -11532953

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825092	7681	29837	201	66

Description

6500729096 fdhe:b3891 fdhe protein (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b3891 b3891 Escherichia coli 562 -11532954 71255 fdhe (de:fdhe protein) (db:swissprot) FDHE\_ECOLI P13024 ESCHERICHIA COLI 562 -11532954 163023 fdhe fdhe protein (db:pir2.dat) (mp:88 min) S40835 S40835 Escherichia coli 562 -11532954 7500881378 fdhe (fn:necessary for nitrogen inducible formate) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:41938) (re:42867) (di:complement) ECOUW87 L19201 g304995 Escherichia coli 562 -11532954 237109 fdhe affects formate dehydrogenase-n (fn:phenotype; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:f309; 100 pct identical amino acid sequence and) (le:9858) (re:10787) (di:complement) AE000464 AE000464 g1790324 Escherichia coli 562 -11532954 7502851859 fdhe affects formate dehydrogenase-n (fn:phenotype; energy metabolism, carbon: anaerobic) (db:genpept) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:f309; 100 pct identical amino acid sequence and) (le:9858) (re:10787) (di:complement) AE000464 AE000464 g1790324 Escherichia coli 562 -11532954



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825093	7682	29838	351	116

Description

GTC ORF with score 159 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completedcds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825095	7683	29839	423	140

Description

6500729097 fdhd:b3895 fdhd protein (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b3895 b3895 Escherichia coli 562 -11532955 71251 fdhd (de:fdhd protein) (db:swissprot) FDHD\_ECOLI P32177 ESCHERICHIA COLI 562 -11532955 163022 fdhd fdhd protein (db:pir2.dat) S40839 S40839 Escherichia coli 562 -11532955 7500881376 fdhd (fn:necessary for nitrate inducible formate) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:similar to wolinella succinogenes fdhd) (le:47655) (re... ECOUW87 L19201 g304999 Escherichia coli 562 -11532955 237113 fdhd affects formate dehydrogenase-n (fn:phenotype; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 355 of 400 of the completegenome.) (nt:o277; 100 pct identical to fdhd\_ecoli sw:) (le:193) (re:1026) (di:direct) AE000465 AE000465 g1790329 Escherichia coli 562 -11532955

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825098	7684	29840	228	75

Description

237141 fpr:mvra:b3924 ferredoxin--nadp reductase:fnr:flavodoxin  
reductase:flxr:methyl viologen resistance protein a:da1  
(gtcf:2.8:9.10:13.3) (ec:1.18.1.2) (keggfc:9.10) (rileyfc:1.2.6)  
(db:gtc-escherichia coli) b3924 b3924 Escherichia coli 562 -11532956 163029  
fpr:ai:163029 ferredoxin--nadp+ reductase::methyl viologen-resistance  
protein (ec:1.18.1.2) (db:pir2.dat) (mp:88 min) S40867 S40867 Escherichia  
coli 562 -11532956 6500729098 fpr ferredoxin nadp+ reductase  
(sr:escherichia coli (individual\_isolate c-600, strain k-12) dna)  
(db:genpept-bct1) (de:escherichia coli ferredoxin (flavodoxin) nadp+  
reductase (fpr)gene, complete cds.) (le:45) (re:791) (di:direct) ECOFPR  
L04757 g290446 Escherichia coli 562 -11532956 7500959737 (sr:escherichia  
coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1)  
(de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:75359)  
(re:76105) (di:complement) ECOUW87 L19201 g305027 Escherichia coli 562  
-11532956 234393 fpr ferredoxin-nadp reductase (fn:enzyme; central  
intermediary metabolism: pool,) (db:genpept-bct2) (ec:1.18.1.2)  
(de:escherichia coli k-12 mg1655 section 357 of 400 of the completegenome.)  
(nt:f248; 100 pct identical amino acid sequence and) (le:852) (re:1598)  
(di:complement) AE000467 AE000467 g1790359 Escherichia coli 562 -11532956

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825111	7685	29841	1605	534

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825153	7686	29842	621	206
<u>Description</u>				
6500729099 qor:hc: b4051 quinone oxidoreductase: nadph: quinone reductase: zeta-crystallin homolog protein (gtcfc: 2.8: 9.12) (ec: 1.6.5.5) (keggfc: 14.1) (rileyfc: 1.2.6) (db: gtc-escherichia coli) b4051 b4051 Escherichia coli 562 -11532957 92706 qor: hc: (ec: 1.6.5.5) (de: crystallin homolog protein) (db: swissprot) QOR ECOLI P28304 ESCHERICHIA COLI 562 -11532957 164453 qor quinone oxidoreductase (cl: alcohol dehydrogenase: long-chain alcohol dehydrogenase homology) (ec: 1.6.5.5) (db: pir2.dat) S45529 S45529 Escherichia coli 562 -11532957 237257 qor quinone oxidoreductase (sr: escherichia coli (strain k-12) dna) (db: genpept-bct1) (de: escherichia coli helicase (dnab) gene, 5' end, and quinone oxidoreductase (qor) gene, complete cds.) (le: 553) (re: 1536) (di: direct) ECODNABA L02312 g145766 Escherichia coli 562 -11532957 234183 qor quinone oxidoreductase (fn: enzyme; energy metabolism, carbon: electron) (db: genpept-bct2) (ec: 1.6.5.5) (de: escherichia coli k-12 mg1655 section 368 of 400 of the complete genome.) (nt: f327; 100 pct identical amino acid sequence and) (le: 4087) (re: 5070) (di: complement) AE000478 AE000478 g1790485 Escherichia coli 562 -11532957 7500889206 qor quinone oxidoreductase (sr: escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db: genpept-bct2) (de: e. coli chromosomal region from 89.2 to 92.8 minutes.) (le: 128492) (re: 129475) (di: complement) ECOUW89 U00006 g396386 Escherichia coli 562 -11532957				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825161	7687	29843	300	99

Description

6500729100 nrfa:b4070 cytochrome c552 precursor (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b4070 b4070 Escherichia coli 562 -11532958 237276 nrfa (de:cytochrome c552 precursor) (db:swissprot) NRFA\_ECOLI P32050 ESCHERICHIA COLI 562 -11532958 122900 nrfa formate-dependent nitrite reductase:cytochrome c552 (cl:formate-dependent nitrite reductase cytochrome c552) (ec:1.7.-.-) (db:pir1.dat) S39590 S39590 Escherichia coli 562 -11532958 7500886581 nrfa (db:genpept-bct1) (de:e.coli nrfa gene.) (le:303) (re:1739) (di:direct) ECNRFA X72298 g853826 Escherichia coli 562 -11532958 233507 nrfa periplasmic cytochrome c 552:plays a role in (fn:carrier; energy metabolism, carbon: electron) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 370 of 400 of the completegenome.) (nt:o478; 100 pct identical to nrfa\_ecoli sw:) (le:7867) (re:9303) (di:direct) AE000480 AE000480 g1790506 Escherichia coli 562 -11532958 7502851860 nrfa (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:matches ps00190: cytochrome c family heme-binding) (le:153004) (re:154440) (di:direct) ECOUW89 U00006 g396405 Escherichia coli 562 -11532958 86499 nrfa (de:cytochrome c552 precursor) (db:swissprot) NRFA\_ECOLI P32050 ESCHERICHIA COLI 562 -11532958

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825176	7688	29844	411	136

Description

6500729101 nrfb:b4071 cytochrome c-type protein nrfb precursor (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b4071 b4071 Escherichia coli 562 -11532959 7000688847 nrfb nrfb protein precursor (cl:nrfb protein) (db:pir1.dat) B57987 F65215 Escherichia coli 562 -11532959 237277 nrfb formate-dependent nitrite reductase:a (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 370 of 400 of the completegenome.) (nt:o190; 100 pct identical to 188 amino acids) (le:9342) (re:9914) (di:direct) AE000480 AE000480 g1790507 Escherichia coli 562 -11532959 7500953207 nrfb (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:matches ps00190: cytochrome c family heme-binding) (le:154479) (re:155051) (di:direct) ECOUW89 U00006 g409802 Escherichia coli 562 -11532959

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825178	7689	29845	531	177

Description

6500729102 nrfc:b4072 nrfc protein (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b4072 b4072 Escherichia coli 562 -11532960  
 7500886585 nrfc (de:nrfc protein) (db:swissprot) NRFC\_ECOLI P32708  
 ESCHERICHIA COLI 562 -11532960 122904 nrfc nrfc protein (cl:nrfc protein:ferredoxin 2(4fe-4s) homology) (db:pir1.dat) C57987 C57987  
 Escherichia coli 562 -11532960 7502851861 nrfc (db:genpept-bct1) (de:e.coli nrfa gene.) (nt:member of coof family containing 4fe /4s iron) (le:2347) (re:3018) (di:direct) ECNRFA X72298 g404304 Escherichia coli 562 -11532960  
 233509 nrfc formate-dependent nitrite reductase:fe-s (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 370 of 400 of the completegenome.) (nt:o223; 99 pct identical amino acid sequence and) (le:9911) (re:10582) (di:direct) AE000480 AE000480  
 g2367345 Escherichia coli 562 -11532960 86503 nrfc (de:nrfc protein) (db:swissprot) NRFC\_ECOLI P32708 ESCHERICHIA COLI 562 -11532960

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825179	7690	29846	576	191

Description

GTC ORF with score 94 to: (sr:norway rat) (db:genpept-rod) (de:rattus norvegicus brain-enriched guanylate kinase-associatedprotein 2 mrna, complete cds.) (nt:protein enriched in the postsynaptic density) (le:75) (re:1892) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825198	7691	29847	315	104

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825202	7692	29848	891	296

Description

6500729103 nrfd:b4073 nrfd protein (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b4073 b4073 Escherichia coli 562 -11532961  
7000688848 nrfd nrfd protein (cl:nrfd protein) (db:pir1.dat) D57987 H65215 Escherichia coli 562 -11532961 237279 nrfd formate-dependent nitrate reductase complex (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 370 of 400 of the completegenome.) (nt:o318; 99 pct identical amino acid sequence and) (le:10579) (re:11535) (di:direct) AE000480 AE000480 g1790509 Escherichia coli 562 -11532961 7500953208 nrfd (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:similar to wolinella succinogenes polysulfide) (le:155716) (re:156672) (di:direct) ECOUW89 U00006 g396408 Escherichia coli 562 -11532961

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825208	7693	29849	612	204

Description

6500729104 nrfe:b4074 cytochrome c-type biogenesis protein nrfe (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b4074 b4074 Escherichia coli 562 -11532962 7000688849 nrfe cytochrome c-type biogenesis protein nrfe (cl:nrfe protein) (db:pir1.dat) E57987 A65216 Escherichia coli 562 -11532962 237280 nrfe formate-dependent nitrite reductase:possible (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 371 of 400 of the completegenome.) (nt:o552; 97 pct identical amino acid sequence and) (le:70) (re:1728) (di:direct) AE000481 AE000481 g1790511 Escherichia coli 562 -11532962 7500953209 nrfe (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:matches ps00327: bacterial rhodopsins retinal) (le:156752) (re:158410) (di:direct) ECOUW89 U00006 g409803 Escherichia coli 562 -11532962 7502851862 nrfe formate-dependent nitrite reductase:possible (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept) (de:escherichia coli k-12 mg1655 section 371 of 400 of the completegenome.) (nt:o552; 97 pct identical amino acid sequence and) (le:70) (re:1728) (di:direct) AE000481 AE000481 g1790511 Escherichia coli 562 -11532962

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825218	7694	29850	450	149

Description

6500729105 nrff:b4075 cytochrome c-type biogenesis protein nrff precursor (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b4075 b4075 Escherichia coli 562 -11532963 237281 nrff (de:cytochrome c-type biogenesis protein nrff precursor) (db:swissprot) NRFF\_ECOLI P32711 ESCHERICHIA COLI 562 -11532963 122909 nrff cytochrome c-type biogenesis protein nrff precursor (cl:nrff protein) (db:pir1.dat) F57987 F57987 Escherichia coli 562 -11532963 7500886591 nrff (db:genpept-bct1) (de:e.coli nrfa gene.) (nt:similar to cc12 protein from rhodobacter) (le:5702) (re:6085) (di:direct) ECNRFA X72298 g404307 Escherichia coli 562 -11532963 233512 nrff part of formate-dependent nitrite reductase (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 371 of 400 of the completegenome.) (nt:o127c; 100 pct identical to nrff\_ecoli sw:) (le:1721) (re:2104) (di:direct) AE000481 AE000481 g1790512 Escherichia coli 562 -11532963 7502851863 nrff (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:similar to rhodobacter capsulatus gene ccl2) (le:158403) (re:158786) (di:direct) ECOUW89 U00006 g396410 Escherichia coli 562 -11532963 7502851864 nrff part of formate-dependent nitrite reductase (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept) (de:escherichia coli k-12 mg1655 section 371 of 400 of the completegenome.) (nt:o127c; 100 pct identical to nrff\_ecoli sw:) (le:1721) (re:2104) (di:direct) AE000481 AE000481 g1790512 Escherichia coli 562 -11532963 86509 nrff (de:cytochrome c-type biogenesis protein nrff precursor) (db:swissprot) NRFF\_ECOLI P32711 ESCHERICHIA COLI 562 -11532963

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825229	7695	29851	573	190

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825230	7696	29852	1173	391

Description

6500729106 nrfg:b4076 nrfg protein (gtcfc:2.8) (keggfc:14.2) (rileyfc:1.2.6) (db:gtc-escherichia coli) b4076 b4076 Escherichia coli 562 -11532964 237282 nrfg (de:nrfg protein) (db:swissprot) NRFG\_ECOLI P32712 ESCHERICHIA COLI 562 -11532964 122910 nrfg nrfg protein (cl:nrfg protein) (db:pir1.dat) A57987 A57987 Escherichia coli 562 -11532964 7500886592 nrfg (db:genpept-bct1) (de:e.coli nrfa gene.) (nt:hydrophobic protein of unknown function) (le:6082) (re:6678) (di:direct) ECNRFA X72298 g404308 Escherichia coli 562 -11532964 233513 nrfg part of formate-dependent nitrite reductase (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 371 of 400 of the completegenome.) (nt:ol98; 100 pct identical amino acid sequence and) (le:2101) (re:2697) (di:direct) AE000481 AE000481 g1790513 Escherichia coli 562 -11532964 7502851865 nrfg (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:similar to synechococcus sp. hypothetical 28.7 kda) (le:158783) (re:159379) (di:direct) ECOUW89 U00006 g396411 Escherichia coli 562 -11532964 7502851866 nrfg part of formate-dependent nitrite reductase (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept) (de:escherichia coli k-12 mg1655 section 371 of 400 of the completegenome.) (nt:ol98; 100 pct identical amino acid sequence and) (le:2101) (re:2697) (di:direct) AE000481 AE000481 g1790513 Escherichia coli 562 -11532964 86511 nrfg (de:nrfg protein) (db:swissprot) NRFG\_ECOLI P32712 ESCHERICHIA COLI 562 -11532964

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825238	7697	29853	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825247	7698	29854	285	94

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825256	7699	29855	723	240

Description

6500729107 cybc:b4236 cytochrome b562 (gtcfc:2.8) (ec:1.10.2.-)  
(keggfc:14.1) (rileyfc:1.2.6) (db:gtc-escherichia coli) b4236 b4236  
Escherichia coli 562 -11532965 7500974873 cybc cytochrome b562  
(db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to  
00.1 minutes.) (le:150382) (re:150684) (di:direct) ECOUW93 U14003 g537078  
Escherichia coli 562 -11532965 237442 cybc cytochrome b 562 (fn:enzyme;  
energy metabolism, carbon: electron) (db:genpept-bct2) (de:escherichia coli  
k-12 mg1655 section 385 of 400 of the completgenome.) (nt:o100; this 100 aa  
orf is 97 pct identical to) (le:195) (re:497) (di:direct) AE000495 AE000495  
g1790684 Escherichia coli 562 -11532965

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825258	7700	29856	612	203

Description

6500729108 faba:b0954 d-3-hydroxydecanoyl-acyl  
carrier-protein:3-hydroxydecanoyl-acyl-carrier-protein  
dehydratase:beta-hydroxydecanoyl thioester dehydrase (gtcfc:3.1)  
(ec:4.2.1.60) (keggfc:3.1) (rileyfc:1.8.0) (db:gtc-escherichia coli) b0954  
b0954 Escherichia coli 562 -11532966 7000685213 faba  
3-hydroxydecanoyl-acyl-carrier-protein dehydratase,:beta-hydroxydecanoyl  
thiolester dehydrase) (cl:3-hydroxydecanoyl-(acyl-carrier-protein)  
dehydratase) (ec:4.2.1.60) (db:pir1.dat) (mp:22 min) DWECHD A64836  
Escherichia coli 562 -11532966 223297 faba  
3-hydroxydecanoyl-acyl-carrier-protein ) (sr:escherichia coli(strain:k12)  
dna, clone:kohara clone #222) (db:genpept-bct1) (de:escherichia coli genomic  
dna. (21.6 - 22.0 min).) (le:9304) (re:9822) (di:complement) D90733 D90733  
g1655500 Escherichia coli 562 -11532966 7500881300 faba  
d-3-hydroxydecanoyl-acyl carrier-protein (sr:e.coli (strain k-12) dna, clone  
prc1) (db:genpept-bct1) (ec:4.2.1.60) (de:e.coli faba gene encoding  
beta-hydroxydecanoyl thioester dehydrase,complete cds.) (le:111) (re:629)  
(di:direct) ECOFABAA J03186 g1256744 Escherichia coli 562 -11532966 234284  
faba beta-hydroxydecanoyl thioester dehydrase (fn:enzyme; fatty acid and  
phosphatidic acid) (db:genpept-bct2) (ec:4.2.1.60) (de:escherichia coli k-12  
mg1655 section 87 of 400 of the completgenome.) (nt:f172; 100 pct identical  
to faba\_ecoli sw: p18391) (le:8260) (re:8778) (di:complement) AE000197  
AE000197 g1787187 Escherichia coli 562 -11532966 5000690226 faba  
3-hydroxydecanoyl-acyl-carrier-protein ) (sr:escherichia coli(strain:k12)  
dna, clone:kohara clone #222) (db:genpept) (de:escherichia coli genomic dna.  
(21.7 - 22.1 min).) (nt:orf\_id:o222#7; similar to swissprot accession)  
(le:9304) (re:9822) (di:complement) D90733 D90733 g1655500 Escherichia coli  
562 -11532966 70968 faba (ec:4.2.1.60) (de:(beta-hydroxydecanoyl thioester  
dehydrase)) (db:swissprot) FABA\_ECOLI P18391 ESCHERICHIA COLI 562 -11532966

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825272	7701	29857	489	162

Description

6500729109 fabh:b1091 3-oxoacyl-acyl-carrier-protein synthase  
 iii:beta-ketoacyl-acp synthase iii:kas iii (gtcfc:3.1) (keggfc:3.1)  
 (rileyfc:1.8.0) (db:gtc-escherichia coli) b1091 b1091 Escherichia coli 562  
 -11532967 70998 fabh (ec:2.3.1.41) (de:ketoacyl-acp synthase iii) (kas  
 iii)) (db:swissprot) FABH\_ECOLI P24249 ESCHERICHIA COLI 562 -11532967  
 123381 fabh 3-oxoacyl-acyl-carrier-protein synthase, iii:beta-ketoacyl-acyl  
 carrier protein synthase iii) (cl:3-oxoacyl-(acyl-carrier-protein) synthase  
 iii) (ec:2.3.1.41) (db:pir1.dat) (mp:24.5 min) A42431 A42431 Escherichia  
 coli 562 -11532967 7500881311 fabh beta-ketoacyl-acyl carrier protein  
 synthase iii (fn:fatty acid biosynthesis) (sr:escherichia coli dna)  
 (db:genpept-bct1) (de:escherichia coli beta-ketoacyl-acyl carrier protein  
 synthase iii(fabh) gene, complete cds.) (le:196) (re:1149) (di:direct)  
 ECOFABH M77744 g145898 Escherichia coli 562 -11532967 234297 fabh  
 3-oxoacyl-acyl-carrier-protein synthase iii;) (fn:enzyme; fatty acid and  
 phosphatidic acid) (db:genpept-bct2) (ec:2.3.1.41) (de:escherichia coli k-12  
 mg1655 section 100 of 400 of the completegenome.) (nt:o317; 100 pct  
 identical to fabh\_ecoli sw: p24249) (le:64) (re:1017) (di:direct) AE000210  
 AE000210 g1787333 Escherichia coli 562 -11532967 5000690227  
 (de:(ecoli\_1053) (pn:3-oxoacyl-acyl-carrier-protein synthase iii; acetylcoa  
 acp transacylase:3-oxoacyl-) (gn:fabh) (gtcfc:3.1) (ec:2.3.1.41)  
 (fabh\_ecoli) (keggfc:3.1) (rileyfc:1.8.0) (db:gtc-escherichia coli))  
 ECOLI\_1053 ECOLI\_1053 Escherichia coli 562 10013573

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825285	7702	29858	234	77

Description

6500729110 fabd:tfpa:b1092 malonyl coa-acyl carrier protein transacylase:mct (gtcfc:3.1) (ec:2.3.1.39) (keggfc:3.1) (rileyfc:1.8.0) (db:gtc-escherichia coli) b1092 b1092 Escherichia coli 562 -11532968 123375 fabd:tfpa acyl-carrier-protein s-malonyltransferase,) (cl:(acyl-carrier-protein) s-malonyltransferase:(acyl-carrier-protein) s-malonyltransferase homology) (ec:2.3.1.39) (db:pir1.dat) (mp:24 min) B41856 B41856 Escherichia coli 562 -11532968 223356 fabd acyl-carrier-protein s-malonyltransferase) (sr:escherichia coli(strain:k12) dna, clone:kohara clone #236) (db:genpept-bct1) (de:escherichia coli genomic dna.(24.7 - 25.1 min).) (le:371) (re:1300) (di:direct) D90745 D90745 g1651535 Escherichia coli 562 -11532968 234290 fabd malonyl coa-acyl carrier protein transacylase (db:genpept-bct1) (de:e.coli fabh and fabd genes for 2-ketoacyl-acyl carrier proteinsynthase iii and malonyl coa-acyl carrier protein transacylase.) (le:371) (re:1300) (di:direct) ECFABHDG Z11565 g41364 Escherichia coli 562 -11532968 7500953237 fabd malonyl coenzyme a-acyl carrier protein (fn:fatty acid biosynthesis) (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli malonyl coenzyme a-acyl carrier protein (fabd)gene, complete cds.) (le:532) (re:1461) (di:direct) ECOFABD M87040 g145887 Escherichia coli 562 -11532968 232789 fabd malonyl-coa-acyl-carrier-protein transacylase) (fn:enzyme; fatty acid and phosphatidic acid) (db:genpept-bct2) (ec:2.3.1.39) (de:escherichia coli k-12 mg1655 section 100 of 400 of the completegenome.) (nt:o309; 99 pct identical to fabd\_ecoli sw: p25715) (le:1033) (re:1962) (di:direct) AE000210 AE000210 g1787334 Escherichia coli 562 -11532968 5000690228 fabd acyl-carrier-protein s-malonyltransferase (ec) (sr:escherichia coli(strain:k12) dna, clone:kohara clone #236) (db:genpept) (de:escherichia coli genomic dna. (24.8 - 25.2 min).) (nt:orf\_id:o236#1; similar to pir accession number) (le:371) (re:1300) (di:direct) D90745 D90745 g1651535 Escherichia coli 562 -11532968

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825288	7703	29859	276	91

Description

6500729111 fabg:b1093 3-oxoacyl-acyl-carrier protein reductase:3-ketoacyl-acyl carrier protein reductase (gtcfc:3.1:3.2:8.1) (ec:1.1.1.100) (keggfc:3.1) (rileyfc:1.8.0) (db:gtc-escherichia coli) b1093 b1093 Escherichia coli 562 -11532969 70991 fabg (ec:1.1.1.100) (de:acyl carrier protein reductase)) (db:swissprot) FABG\_ECOLI P25716 ESCHERICHIA COLI 562 -11532969 7000685215 fabg 3-oxoacyl-acyl-carrier-protein reductase,:3-ketoacyl-acp reductase) (cl:ribitol dehydrogenase:short-chain alcohol dehydrogenase homology) (ec:1.1.1.100) (db:pir1.dat) (mp:24 min) B42147 B64853 Escherichia coli 562 -11532969 223357 fabg 3-oxoacyl-acyl-carrier-protein reductase) (sr:escherichia coli(strain:k12) dna, clone:kohara clone #236) (db:genpept-bct1) (de:escherichia coli genomic dna.(24.7 - 25.1 min).) (le:1313) (re:2047) (di:direct) D90745 D90745 g1651536 Escherichia coli 562 -11532969 7500881307 fabg 3-oxoacyl-acyl-carrier-protein reductase) (fn:enzyme; fatty acid and phosphatidic acid) (db:genpept-bct2) (ec:1.1.1.100) (de:escherichia coli k-12 mg1655 section 100 of 400 of the completegenome.) (nt:o244; 99 pct identical to fabg\_ecoli sw: p25716) (le:1975) (re:2709) (di:direct) AE000210 AE000210 g1787335 Escherichia coli 562 -11532969 5000690229 fabg 3-oxoacyl-acyl-carrier-protein reductase (ec) (sr:escherichia coli(strain:k12) dna, clone:kohara clone #236) (db:genpept) (de:escherichia coli genomic dna. (24.8 - 25.2 min).) (nt:orf\_id:o236#2; similar to pir accession number) (le:1313) (re:2047) (di:direct) D90745 D90745 g1651536 Escherichia coli 562 -11532969

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825296	7704	29860	951	316

Description

6500729112 fabf:fabj:b1095 3-oxoacyl-acyl-carrier-protein synthase  
ii:beta-ketoacyl-acp synthase ii:kas ii (gtcfc:3.1) (ec:2.3.1.41)  
(keggfc:3.1) (rileyfc:1.8.0) (db:gtc-escherichia coli) b1095 b1095  
Escherichia coli 562 -11532970 162616 fabf:fabj  
3-oxoacyl-acyl-carrier-protein synthase, ii)  
(cl:3-oxoacyl-(acyl-carrier-protein) synthase  
i:3-oxoacyl-(acyl-carrier-protein) synthase i homology) (ec:2.3.1.41)  
(db:pir2.dat) I41060 I41060 Escherichia coli 562 -11532970 7500959666 fabf  
beta-ketoacyl-acyl carrier protein synthase ii (db:genpept-bct1)  
(de:escherichia coli beta-ketoacyl-acyl carrier protein synthase ii(fabf)  
gene, complete cds.) (nt:allele: wild type; 3-oxoacyl-acyl carrier) (le:91)  
(re:1332) (di:direct) ECU20767 U20767 g664870 Escherichia coli 562 -11532970  
232790 fabf 3-oxoacyl-acyl-carrier-protein synthase ii) (fn:enzyme; fatty  
acid and phosphatidic acid) (db:genpept-bct2) (ec:2.3.1.41) (de:escherichia  
coli k-12 mg1655 section 100 of 400 of the completegenome.) (nt:o413; 100  
pct identical amino to fabf\_ecoli) (le:3244) (re:4485) (di:direct) AE000210  
AE000210 g1787337 Escherichia coli 562 -11532970 238764 fabf beta  
ketoacyl-acyl carrier protein synthase (fn:condensation of malonyl-acp with  
acyl-acp) (db:genpept-bct2) (ec:2.3.1.41) (de:e.coli fabj gene encoding beta  
ketoacyl-acyl carrier proteinsynthase.) (nt:alternative name, fabj) (le:73)  
(re:1314) (di:direct) ECFABJ Z34979 g572680 Escherichia coli 562 -11532970  
5000690230 fabf 3-oxoacyl-acyl-carrier-protein synthase (ec)  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #236) (db:genpept)  
(de:escherichia coli genomic dna. (24.8 - 25.2 min).) (nt:orf\_id:o236#4;  
similar to pir accession number) (le:2582) (re:3823) (di:direct) D90745  
D90745 g4062664 Escherichia coli 562 -11532970

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825299	7705	29861	597	198

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825300	7706	29862	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825311	7707	29863	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825315	7708	29864	192	64

Description

6500729113 fabi:envm:b1288 enoyl-acyl-carrier-protein reductase  
nadh:nadh-dependent enoyl-acp reductase (gtcfc:3.1) (ec:1.3.1.9)  
(keggfc:3.1) (rileyfc:1.8.0) (db:gtc-escherichia coli) b1288 b1288  
Escherichia coli 562 -11532971 164612 fabi:envm enoyl-acyl-carrier-protein  
reductase (nadh),:enoyl-acp reductase:short-chain alcohol dehydrogenase  
homolog envm) (cl:enoyl-(acyl-carrier-protein) reductase (nadh):short-chain  
alcohol dehydrogenase homology) (ec:1.3.1.9) (db:pir2.dat) S48029 S48029  
Escherichia coli 562 -11532971 234251 envm enoyl-acp reductase  
(db:genpept-bct1) (de:e.coli envm gene.) (le:530) (re:1318) (di:direct)  
ECENVMACP X78733 g587106 Escherichia coli 562 -11532971 7500953788 envm  
(sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli short chain  
alcohol dehydrogenase homolog (envm)gene, complete cds.) (le:404) (re:1192)  
(di:direct) ECOENVM M97219 g145851 Escherichia coli 562 -11532971 232772  
fabi enoyl-acyl-carrier-protein reductase (nadh)) (fn:enzyme; fatty acid and  
phosphatidic acid) (db:genpept-bct2) (ec:1.3.1.9) (de:escherichia coli k-12  
mg1655 section 117 of 400 of the completegenome.) (nt:f262; 100 pct  
identical to fabi\_ecoli sw: p29132;) (le:1335) (re:2123) (di:co... AE000227  
AE000227 g1787545 Escherichia coli 562 -11532971 5000690231  
(de:(ecoli\_1248) (pn:enoyl-acp reductase:nadh) (gn:fabi) (gtcfc:3.1)  
(ec:1.3.1.9) (fabi\_ecoli) (keggfc:3.1) (rileyfc:1.8.0) (db:gtc-escherichia  
coli)) ECOLI\_1248 ECOLI\_1248 Escherichia coli 562 10087396

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825333	7709	29865	753	250

Description

6500729114 fabb:b2323 3-oxoacyl-acyl-carrier-protein synthase  
i:beta-ketoacyl-acp synthase i:kas i (gtcfc:3.1) (ec:2.3.1.41) (keggfc:3.1)  
(rileyfc:1.8.0) (db:gtc-escherichia coli) b2323 b2323 Escherichia coli 562  
-11532972 70974 fabb:fabc (ec:2.3.1.41) (de:ketoacyl-acp synthase i) (kas  
i)) (db:swissprot) FABB\_ECOLI P14926 ESCHERICHIA COLI 562 -11532972 123376  
fabb 3-oxoacyl-acyl-carrier-protein synthase, i:acetoacetyl-acp synthase  
i:beta-ketoacyl-acp synthase i) (cl:3-oxoacyl-(acyl-carrier-protein)  
synthase i:3-oxoacyl-(acyl-carrier-protein) synthase i homology)  
(ec:2.3.1.41) (db:pir1.dat) (mp:50 min) SYECA1 A31284 Escherichia coli 562  
-11532972 224867 fabb 3-oxoacyl-acyl-carrier-protein synthase i (ec)  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #407(52.4-52.8  
min.)) (nt:similar to (swissprot accession number p14926)) (le:11027)  
(re:12247) (di:complement) D90863 D90863 g1799716 Escherichia coli 562  
-11532972 234288 fabb 3-oxoacyl-acyl-carrier-protein synthase i)  
(fn:enzyme; fatty acid and phosphatidic acid) (db:genpept-bct2)  
(ec:2.3.1.41) (de:escherichia coli k-12 mg1655 section 211 of 400 of the  
completegenome.) (nt:f406; 99 pct identical to fabb\_ecoli sw: p14926)  
(le:3733) (re:4953) (di:complement) AE000321 AE000321 g1788663 Escherichia  
coli 562 -11532972 7500881302 fabb (db:genpept-bct2) (ec:2.3.1.41)  
(de:escherichia coli beta-ketoacyl-acp synthase i (fabb) gene, completecds.)  
(nt:beta-ketoacyl-acp synthase i) (le:237) (re:1457) (di:direct) ECOFABB  
M24427 g145884 Escherichia coli 562 -11532972 5000690232 (de:(ecoli\_2272)  
(pn:3-oxoacyl-acyl-carrier-protein synthase i) (gn:fabb) (gtcfc:3.1)  
(ec:2.3.1.41) (fabb\_ecoli) (keggfc:3.1) (rileyfc:1.8.0) (db:gtc-escherichia  
coli)) ECOLI\_2272 ECOLI\_2272 Escherichia coli 562 10013549

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825345	7710	29866	231	76

Description

6500729115 accc:fabg:b3256 biotin carboxylase:a subunit of acetyl-coa carboxylase:acc (gtcfc:9.6:3.1) (ec:6.3.4.14) (keggfc:3.1) (rileyfc:1.8.0) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:lipid metabolism-fatty acid biosynthesis) b3256 b3256 Escherichia coli 562 -11532973 57998 accc:fabg (ec:6.3.4.14:6.4.1.2) (de:carboxylase,) (acc)) (db:swissprot) ACCC\_ECOLI P24182 ESCHERICHIA COLI 562 -11532973 126062 accc:fabg acetyl-coa carboxylase::biotin carboxylase:biotin carboxylase (cl:biotin carboxylase:biotin carboxylase homology) (ec:6.4.1.2:6.3.4.14) (db:pir1.dat) (mp:72 min) JS0632 JS0632 Escherichia coli 562 -11532973 234294 fabe biotin carboxylase (fn:subunit of acetyl-coa carboxylase) (sr:escherichia coli (strain k-12) f- dna) (db:genpept-bct1) (de:e.coli biotin carboxylase and biotin carboxyl carrier protein(fabe) and orf1 35 kda protein genes, complete cds.) (nt:upstream of panf gene) (le:292... ECOACOAC M80458 g145175 Escherichia coli 562 -11532973 236495 fabg biotin carboxylase (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (ec:6.3.4.14) (de:escherichia coli biotin carboxyl carrier biotin carboxylase (fabg),complete cds, and pantothenate permease (panf) genes, 5' end.) (le:1282) (re:2631) (di:direct) ECOFABEGF M83198 g145893 Escherichia coli 562 -11532973 7500876290 accc biotin carboxylase (fn:subunit of acetyl-coa carboxylase) (db:genpept-bct1) (ec:6.3.4.14) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 29834; alternate name fabg) (le:186662) (re:188011) (di:direct) ECOUW67 U18997 g606196 Escherichia coli 562 -11532973 233714 accc acetyl coa carboxylase:biotin carboxylase (fn:enzyme; fatty acid and phosphatidic acid) (db:genpept-bct2) (ec:6.3.4.14) (de:escherichia coli k-12 mg1655 section 294 of 400 of the completegenome.) (nt:o449; cg site no. 29834; alternate name fabg; 100) (le:9655) (re:11004) (di:direct) AE000404 AE000404 g1789654 Escherichia coli 562 -11532973 5000689998 (de:(ecoli\_3180) (pn:biotin carboxylase subunit of acetyl coa carboxylase) (gn:accc) (gtcfc:1.10:1.8:3.1) (ec:6.3.4.14) (accc\_ecoli) (keggfc:1.8:1.10:3.1) (rileyfc:1.8.0) (db:gtc-escherichia coli)) ECOLI\_3180 ECOLI\_3180 Escherichia coli 562 10000778



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825354	7711	29867	270	89

Description

6500729116 fada:olda:b3845 small:beta subunit of the fatty acid-oxidizing multienzyme complex:3-ketoacyl-coa thiolase:fatty oxidation complex beta subunit:beta-ketothiolase:acetyl-coa acyltransferase (gtcfc:3.1:3.2:3.5:5.13:5.6) (ec:2.3.1.16) (keggfc:3.1:3.2:3.5:5.6:5.13) (rileyfc:1.1.3) (db:gtc-escherichia coli) b3845 b3845 Escherichia coli 562 -11532974 101338 fada:olda (ec:2.3.1.16) (de:subunit) (beta-ketothiolase) (acetyl-coa acyltransferase)) (db:swissprot) THIK\_ECOLI P21151 ESCHERICHIA COLI 562 -11532974 7000686792 fada acetyl-coa c-acyltransferase::3-ketoacyl-coa thiolase:beta-ketothiolase:degradative thiolase:fatty acid beta oxidation multienzyme complex small beta chain:thiolase i (cl:acetyl-coa acetyltransferase) (ec:2.3.1.16) (db:pir1.dat) (mp:87 min) XUEC F65189 Escherichia coli 562 -11532974 7500893070 fada thiolase i:3-ketoacyl-coa thiolase:acetyl-coa (fn:enzyme; degradation of small molecules: fatty) (db:genpept-bct2) (ec:2.3.1.16) (de:escherichia coli k-12 mg1655 section 350 of 400 of the completegenome.) (nt:f387; 100 pct identical to thik\_ecoli sw: p21151) (le:350) (re:1513) (di:complement) AE000460 AE000460 g2367316 Escherichia coli 562 -11532974

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825367	7712	29868	462	153

Description

6500729117 cdsa:cds:b0175 phosphatidate cytidyltransferase:cdp-diglyceride synthetase:cdp-diglyceride pyrophosphorylase:cdp-diacylglycerol synthase (gtcfc:3.1:8.1) (ec:2.7.7.41) (keggfc:8.1) (rileyfc:1.8.0) (db:gtc-escherichia coli) b0175 b0175 Escherichia coli 562 -11532975 63720 cdsa:cds (ec:2.7.7.41) (de:synthase)) (db:swissprot) CDSA\_ECOLI P06466 ESCHERICHIA COLI 562 -11532975 124060 cdsa:cds phosphatidate cytidyltransferase::cdp-diglyceride pyrophosphorylase:cdp-diglyceride synthetase (cl:phosphatidate cytidyltransferase) (ec:2.7.7.41) (db:pir1.dat) (mp:4 min) SYECDG A23898 Escherichia coli 562 -11532975 236165 cds cdp-diglyceride synthetase (sr:e.coli k-12 dna, clones ptis(138,139,141,157,161)) (db:genpept-bct1) (de:e.coli cds gene encoding cdp-diglyceride synthetase, complete cds.) (le:190) (re:939) (di:direct) ECOCDs M11330 g145476 Escherichia coli 562 -11532975 239803 cdsa phosphatidate cytidyltransferase (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (ec:2.7.7.41) (de:escherichia coli genome, 4.0 - 6.0 min region.) (le:5309) (re:6058) (di:direct) ECOTSF D83536 g1208947 Escherichia coli 562 -11532975 303242 cdsa phosphatidate cytidyltransferase (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:26860) (re:27609) (di:direct) ECU70214 U70214 g1552752 Escherichia coli 562 -11532975 233946 cdsa cdp-diglyceride synthetase (fn:enzyme; fatty acid and phosphatidic acid) (db:genpept-bct2) (ec:2.7.7.41) (de:escherichia coli k-12 mg1655 section 17 of 400 of the completegenome.) (nt:o249; 100 pct identical to cdsa\_ecoli sw: p06466) (le:1005) (re:1754) (di:direct) AE000127 AE000127 g1786372 Escherichia coli 562 -11532975 5000690558 (de:(ecoli\_175) (pn:cdp-diglyceride synthetase:ctp:phosphatidate cytidyltransferase) (gn:cdsa) (gtcfc:8.1) (ec:2.7.7.41) (cdsa\_ecoli) (keggfc:8.1) (rileyfc:1.8.0) (db:gtc-escherichia coli)) ECOLI\_175 ECOLI\_175 Escherichia coli 562 10006389

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501825370	7713	29869	1257	418

Description

6500729118 tesb:b0452 acyl-coa thioesterase ii (gtcfc:3.1) (ec:3.1.2.-)  
(keggfc:14.1) (rileyfc:1.8.0) (db:gtc-escherichia coli) b0452 b0452  
Escherichia coli 562 -11532976 7000690849 tesb acyl-coa thiolesterase:ii  
precursor (cl:acyl-coa thiolesterase ii) (ec:3.1.2.-) (db:pir2.dat) D64775  
D64775 Escherichia coli 562 -11532976 240229 tesb thioesterase ii  
(sr:e.coli dna) (db:genpept-bct1) (de:e.coli thioesterase ii (tesb) gene,  
complete cds.) (le:387) (re:1247) (di:direct) ECOTESB M63308 g147932  
Escherichia coli 562 -11532976 7500959672 tesb acyl-coa thioesterase ii  
(db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.)  
(le:53751) (re:54611) (di:complement) ECU82664 U82664 g1773136 Escherichia  
coli 562 -11532976 236077 tesb acyl-coa thioesterase ii (fn:enzyme; fatty  
acid and phosphatidic acid) (db:genpept-bct2) (ec:3.1.2.-) (de:escherichia  
coli k-12 mg1655 section 41 of 400 of the completegenome.) (nt:f286; 100 pct  
identical to tesb\_ecoli sw: p23911) (le:8752) (re:9612) (di:complement)  
AE000151 AE000151 g1786657 Escherichia coli 562 -11532976 5000690246  
(de:(ecoli\_436) (pn:acyl-coa thioesterase ii) (gn:tesb) (gtcfc:3.8)  
(ec:3.1.2.-) (tesb\_ecoli) (keggfc:11.1) (rileyfc:1.8.0) (db:gtc-escherichia  
coli)) ECOLI\_436 ECOLI\_436 Escherichia coli 562 10122832

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ORF Name

NT ID

AA ID

NT  
LENGTHAA  
LENGTH

7501825372

7714

29870

324

107

Description

6500729119 tesa:apea:b0494 acyl-coa thioesterase i:acyl-coa thioesterase i precursor:protease i (gtcfc:3.2:3.8:10.11) (ec:3.1.2.-) (keggfc:14.1) (rileyfc:1.8.0) (db:gtc-escherichia coli) b0494 b0494 Escherichia coli 562 -11532977 101053 tesa:apea:pldc (ec:3.1.2.-:3.1.1.5) (de:(lysophospholipase 11), (lecithinase b)) (db:swissprot) TESA\_ECOLI P29679 ESCHERICHIA COLI 562 -11532977 164425 tesa:apea acyl-coa thioesterase i:precursor:proteinase i:thioesterase i (ec:3.1.2.-) (db:pir2.dat) A49699 A49699 Escherichia coli 562 -11532977 236076 apea protease i (sr:escherichia coli (strain k-12) dna, clone pym028) (db:genpept-bct1) (de:e.coli gene for protease i, complete cds.) (le:108) (re:734) (di:direct) ECOAPEA D13180 g216527 Escherichia coli 562 -11532977 7500892938 tesa acyl-coa thioesterase i (sr:escherichia coli (sub\_strain w3110, strain k-12) (library: kohara) (db:genpept-bct1) (de:escherichia coli acyl-coa thioesterase i (tesa) gene, complete cds.) (le:457) (re:1083) (di:direct) ECOTESA L06182 g290474 Escherichia coli 562 -11532977 233806 tesa acyl-coa thioesterase i:also functions as (fn:enzyme; fatty acid and phosphatidic acid) (db:genpept-bct2) (ec:3.1.2.-) (de:escherichia coli k-12 mg1655 section 45 of 400 of the completegenome.) (nt:f208; 100 pct identical to tesa\_ecoli sw: p29679;) (le:7659) (re:8285) (di:complement) AE000155 AE000155 g1786702 Escherichia coli 562 -11532977 5000690247 (de:(ecoli\_477) (pn:acyl-coa thioesterase i; also functions as protease i) (gn:tesa) (gtcfc:3.8) (ec:3.1.2.-) (tesa\_ecoli) (keggfc:11.1) (rileyfc:1.8.0) (db:gtc-escherichia coli)) ECOLI\_477 ECOLI\_477 Escherichia coli 562 10042895

JP542 U.S. PTO  
09/417507



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825373	7715	29871	309	102

Description

6500729120 acpp:b1094 acyl carrier protein:acp (gtcfc:3.1) (keggfc:14.2) (rileyfc:1.8.0) (db:gtc-escherichia coli) b1094 b1094 Escherichia coli 562 -11532978 130667 acpp acyl carrier protein (cl:acyl carrier protein:acyl carrier protein homology) (db:pir1.dat) (mp:24 min) AYEC C42147 Escherichia coli 562 -11532978 223358 acpp acyl carrier protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #236) (db:genpept-bct1) (de:escherichia coli genomic dna.(24.7 - 25.1 min).) (le:2258) (re:2494) (di:direct) D90745 D90745 g1651537 Escherichia coli 562 -11532978 7500953597 acpp acyl carrier protein (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli 3-ketoacyl-acyl carrier protein reductase (fabg)and acyl carrier protein (acpp) genes, complete cds, and malonylcoa-acyl carrier protein transacylase (fabd) gene, 5' end.) (... ECOFABACP M84991 g145882 Escherichia coli 562 -11532978 234287 acpp acyl carrier protein (fn:carrier; fatty acid and phosphatidic acid) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 100 of 400 of the completegenome.) (nt:o78; 100 pct identical to acp\_ecoli sw: p02901 but) (le:2920) (re:3156) (di:direct) AE000210 AE000210 g1787336 Escherichia coli 562 -11532978 7500953598 acyl carrier protein (db:genpept-syn) (de:synthetic construct acyl carrier protein mrna, complete cds.) (nt:acp) (le:10) (re:246) (di:direct) AF072368 AF072368 g3249737 synthetic construct 32630 -11532978 5000690248 acpp acyl carrier protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #236) (db:genpept) (de:escherichia coli genomic dna. (24.8 - 25.2 min).) (nt:orf\_id:o236#3; similar to pir accession number) (le:2258) (re:2494) (di:direct) D90745 D90745 g1651537 Escherichia coli 562 -11532978

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825378	7716	29872	288	95

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825382	7717	29873	261	86

Description

GTC ORF with score 314 to: (sr:homo sapiens male bone marrow myeloblast cell\_line:kg-1 cdna t) (db:genpept-pri2) (de:human mrna for kiaa0224 gene, complete cds.) (nt:similar to putative atp-dependent rna helicase) (le:137) (re:3820) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825385	7718	29874	378	125

Description

GTC ORF with score 110 to: (sr:homo sapiens male bone marrow myeloblast cell\_line:kg-1 cdna t) (db:genpept-pri2) (de:human mrna for kiaa0224 gene, complete cds.) (nt:similar to putative atp-dependent rna helicase) (le:137) (re:3820) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825395	7719	29875	267	88

Description

6500729121 cfa:cdfa:b1661 cyclopropane-fatty-acyl-phospholipid synthase:cyclopropane fatty acid synthase:cfa synthase (gtcfc:3.1) (ec:2.1.1.79) (keggfc:14.1) (rileyfc:1.8.0) (db:gtc-escherichia coli) b1661 b1661 Escherichia coli 562 -11532979 162884 cfa cyclopropane-fatty-acyl-phospholipid synthase (ec:2.1.1.79) (db:pir2.dat) A44292 A44292 Escherichia coli 562 -11532979 224106 cfa cyclopropane fatty acid synthase (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #318(37.2-37.6 min.)) (nt:orf\_id:o319#5; similar to (pir accession number) (le:13006) (re:14154) (di:direct) D90809 D90809 g1742735 Escherichia coli 562 -11532979 224115 cfa cyclopropane fatty acid synthase (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #319(37.4-37.8 min.)) (nt:orf\_id:o319#5; similar to (pir accession number) (le:5400) (re:6548) (di:direct) D90810 D90810 g1742745 Escherichia coli 562 -11532979 300784 cfa cyclopropane fatty acid synthase (sr:escherichia coli (strain k-12) hfrc dna) (db:genpept-bct1) (de:escherichia coli cyclopropane fatty acid synthase (cfa) gene,complete cds.) (le:286) (re:1434) (di:direct) ECOCFAX M98330 g145514 Escherichia coli 562 -11532979 233969 cfa cyclopropane fatty acyl phospholipid synthase (fn:enzyme; fatty acid and phosphatidic acid) (db:genpept-bct2) (ec:2.1.1.79) (de:escherichia coli k-12 mg1655 section 151 of 400 of the completegenome.) (nt:o382; 100 pct identical to cfa\_ecoli sw: p30010; cg) (le:6129) (re:7277) (di:direct) AE000261 AE000261 g1787951 Escherichia coli 562 -11532979 5000690249 (de:(ecoli\_1620) (pn:cyclopropane-fatty-acyl-phospholipid synthase:cyclopropane fatty acid synthase:cfa synthase) (gn:cfa) (gtcfc:3.8) (ec:2.1.1.79) (cfa\_ecoli) (keggfc:11.1) (rileyfc:1.8.0) (db:gtc-escherichia coli)) ECOLI\_1620 ECOLI\_1620 Escherichia coli 562 10086669

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825398	7720	29876	189	62

Description

6500729122 eutc:b2440 ethanolamine ammonia-lyase light chain (gtcfc:3.1) (ec:4.3.1.7) (keggfc:14.1) (rileyfc:1.8.0) (db:gtc-escherichia coli) b2440 b2440 Escherichia coli 562 -11532980 70750 eutc (ec:4.3.1.7) (de:ethanolamine ammonia-lyase light chain,) (db:swissprot) EUTC\_ECOLI P19636 ESCHERICHIA COLI 562 -11532980 7000685193 eutc ethanolamine ammonia-lyase:light chain (ec:4.3.1.7) (db:pir2.dat) G65018 G65018 Escherichia coli 562 -11532980 225010 eutc ethanolamine ammonia-lyase light chain ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #420(54.9-55.2 min.)) (nt:similar to (swissprot accession number p19636)) (le:10348) (re:11235) (di:complement) D90873 D90873 g1799869 Escherichia coli 562 -11532980 225016 eutc ethanolamine ammonia-lyase light chain ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #421(55.1-55.5 min.)) (nt:similar to (swissprot accession number p19636)) (le:3244) (re:4131) (di:complement) D90874 D90874 g1799876 Escherichia coli 562 -11532980 7500881205 eutc ethanolamine ammonia-lyase:light chain (fn:enzyme; degradation of small molecules: amines) (db:genpept-bct2) (ec:4.3.1.7) (de:escherichia coli k-12 mg1655 section 221 of 400 of the completegenome.) (nt:f295; 100 pct identical to fragment eutc\_ecoli) (le:4140) (re:5027) (di:complement) AE000331 AE000331 g1788781 Escherichia coli 562 -11532980 5000690250 (de:(ecoli\_2380) (pn:ethanolamine-ammonia lyase light subunit) (gn:eutc) (gtcfc:3.8) (ec:4.3.1.7) (eutc\_ecoli) (keggfc:11.1) (rileyfc:1.8.0) (db:gtc-escherichia coli)) ECOLI\_2380 ECOLI\_2380 Escherichia coli 562 10120203

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825400	7721	29877	225	74

Description

6500729123 eutb:b2441 ethanolamine ammonia-lyase heavy chain (gtcfc:3.1) (ec:4.3.1.7) (keggfc:14.1) (rileyfc:1.8.0) (db:gtc-escherichia coli) b2441 b2441 Escherichia coli 562 -11532981 7000690873 eutb ethanolamine ammonia-lyase:heavy chain (ec:4.3.1.7) (db:pir2.dat) H65018 H65018 Escherichia coli 562 -11532981 7500959731 eutb ethanolamine ammonia-lyase:heavy chain (fn:enzyme; degradation of small molecules: amines) (db:genpept-bct2) (ec:4.3.1.7) (de:escherichia coli k-12 mg1655 section 221 of 400 of the completegenome.) (nt:f467; 100 pct identical to fragment eutb\_ecoli) (le:5048) (re:6451) (di:complement) AE000331 AE000331 g1788782 Escherichia coli 562 -11532981 5000690251 (de:(ecoli\_2381) (pn:ethanolamine-ammonia lyase heavy subunit) (gn:eutb) (gtcfc:3.8) (ec:4.3.1.7) (eutb\_ecoli) (keggfc:11.1) (rileyfc:1.8.0) (db:gtc-escherichia coli)) ECOLI\_2381 ECOLI\_2381 Escherichia coli 562 10123683

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825404	7722	29878	729	242
<u>Description</u>				
6500729124 acps:dpj:b2563 dpj protein:holo-acyl-carrier protein synthase:holo-acp synthase (gtcfc:3.1:9.5) (ec:2.7.8.7) (keggfc:9.5) (rileyfc:1.8.0) (db:gtc-escherichia coli) b2563 b2563 Escherichia coli 562 -11532982 162967 acps dpj protein (cl:holo-acp synthase) (db:pir2.dat) B42294 B42294 Escherichia coli 562 -11532982 235736 dpj dpj protein (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli pdxj and dpj protein gene, complete cds.) (le:801) (re:1181) (di:direct) ECOPDXJDPJ M74526 g147138 Escherichia coli 562 -11532982 239517 dpj (fn:unknown) (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli recombination and repair protein (reco) gene, 3'end, and pyridoxal phosphate biosynthetic protein (pdxj) gene,complete cds.) (le:975) (re:1355) (di:direct) ECORECOPDX M76470 g147556 Escherichia coli 562 -11532982 7500955963 dpj (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 55 minutes.) (le:11862) (re:12242) (di:complement) ECU36841 U36841 g1033152 Escherichia coli 562 -11532982 235384 acps coa:apo-acyl-carrier-protein ) (fn:enzyme; fatty acid and phosphatidic acid) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 233 of 400 of the completegenome.) (nt:f126; 100 pct identical to dpj_ecoli sw: p24224) (le:378) (re:758) (di:complement) AE000343 AE000343 g1788916 Escherichia coli 562 -11532982 5000690643 (de:(ecoli_2503) (pn:apo-acyl-carrier-protein pantetheinephosphotransferase, holo-acyl-carrier-protein synthase:coa:apo-acyl-carrier-protein pantetheinephosphotransferase ) (gn:acps) (gtcfc:9.5) (ec:2.7.8.7) (acps_ecoli) (keggfc:) ECOLI_2503 ECOLI_2503 Escherichia coli 562 10001046				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825420	7723	29879	732	243
<u>Description</u>				
Hypothetical protein				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825429	7724	29880	561	186

Description

6500729125 aas:b2836 2-acylglycerophosphoethanolamine acyltransferase / acyl-acyl carrier protein synthetase:2-acyl-gpe acyltransferase / acyl-acp synthetase (gtcfc:8.1:3.1:3.2) (ec:6.2.1.20) (keggfc:3.2) (rileyfc:1.8.0) (db:gtc-escherichia coli) b2836 b2836 Escherichia coli 562 -11532983 57860 aas (de:protein synthetase (2-acyl-gpe acyltransferase / acyl-acp synthetase)) (db:swissprot) AAS\_ECOLI P31119 ESCHERICHIA COLI 562 -11532983 7000684478 aas 2-acylglycerophosphoethanolamine acyl transferase/acyl carrier protein synthetase (db:pir2.dat) (mp:61.2 min) E65066 E65066 Escherichia coli 562 -11532983 7500876241 aas 2-acylglycerophosphoethanolamine acyl (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:cg site no. 29780) (le:55410) (re:57569) (di:complement) ECU29581 U29581 g882729 Escherichia coli 562 -11532983 239407 aas 2-acyl-glycerophospho-ethanolamine (fn:enzyme; fatty acid and phosphatidic acid) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 257 of 400 of the completegenome.) (nt:f719; 99 pct identical to aas\_ecoli sw: p31119; cg) (le:4566) (re:6725) (di:complement) AE000367 AE000367 g1789201 Escherichia coli 562 -11532983 5000690235 (de:(ecoli\_2764) (pn:2-acylglycerophospho-ethanolamine acyl transferase; acyl-acyl- carrier protein synthetase) (gn:aas) (gtcfc:3.2) (ec:6.2.1.20) (aas\_ecoli) (keggfc:3.2) (rileyfc:1.8.0) (db:gtc-escherichia coli)) ECOLI\_2764 ECOLI\_2764 Escherichia coli 562 10123856

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825439	7725	29881	978	325

Description

6500729126 cdh:b3918 cdp-diglyceride hydrolase:cdp-diacylglycerol pyrophosphatase:cdp-diacylglycerol phosphatidylhydrolase (gtcfc:3.1) (ec:3.6.1.26) (keggfc:14.1) (rileyfc:1.8.0) (db:gtc-escherichia coli) b3918 b3918 Escherichia coli 562 -11532984 63660 cdh (ec:3.6.1.26) (de:phosphatidylhydrolase)) (db:swissprot) CDH\_ECOLI P06282 ESCHERICHIA COLI 562 -11532984 125090 cdh cdpdiacylglycerol pyrophosphatase::cdp-diacylglycerol phosphatidylhydrolase (cl:cdpdiacylglycerol pyrophosphatase) (ec:3.6.1.26) (db:pir1.dat) (mp:88 min) PSECCD A01019 Escherichia coli 562 -11532984 237135 cdh cdp-diglyceride hydrolase (sr:e.coli k-12 dna, clones ptih237 and pti10 derivative) (db:genpept-bct1) (de:e.coli cdh gene coding for cdp-diglyceride hydrolase, complete cds.) (le:399) (re:1154) (di:direct) ECOCDH M11331 g145472 Escherichia coli 562 -11532984 7500878436 cdh cdp-diglyceride hydrolase (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 931) (le:71563) (re:72318) (di:direct) ECOUW87 L19201 g305021 Escherichia coli 562 -11532984 233944 cdh cdp-diacylglycerol phosphotidylhydrolase (fn:enzyme; fatty acid and phosphatidic acid) (db:genpept-bct2) (ec:3.6.1.26) (de:escherichia coli k-12 mg1655 section 356 of 400 of the completegenome.) (nt:o251; 100 pct identical to cdh\_ecoli sw: p06282; cg) (le:7206) (re:7961) (di:direct) AE000466 AE000466 g1790352 Escherichia coli 562 -11532984 5000690252 (de:(ecoli\_3816) (pn:cdp-diacylglycerol phosphotidylhydrolase) (gn:cdh) (gtcfc:3.8) (ec:3.6.1.26) (cdh\_ecoli) (keggfc:11.1) (rileyfc:1.8.0) (db:gtc-escherichia coli)) ECOLI\_3816 ECOLI\_3816 Escherichia coli 562 10006329

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825455	7726	29882	819	272

#### Description

6500729127 dgka:b4042 diacylglycerol kinase:dagk:diglyceride kinase:dgk (gtcfc:3.1:8.1) (ec:2.7.1.107) (keggfc:8.1) (rileyfc:1.8.0) (db:gtc-escherichia coli) b4042 b4042 Escherichia coli 562 -11532985 123837 dgka probable diacylglycerol kinase::diglyceride kinase (cl:diacylglycerol kinase) (ec:2.7.1.107) (db:pir1.dat) (mp:92 min) KIECDG A00667 Escherichia coli 562 -11532985 237248 dgk diglyceride kinase (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli plsb and dgk genes coding for sn-glycerol-3-phosphateacyltransferase and diglyceride kinase.) (le:15) (re:383) (di:complement) ECOPLSB K00127 g457112 Escherichia coli 562 -11532985 235499 dgka diacylglycerol kinase (fn:enzyme; fatty acid and phosphatidic acid) (db:genpept-bct2) (ec:2.7.1.107) (de:escherichia coli k-12 mg1655 section 367 of 400 of the completegenome.) (nt:ol22; 100 pct identical to kdgl\_ecoli sw: p00556;) (le:8732) (re:9100) (di:direct) AE000477 AE000477 g1790475 Escherichia coli 562 -11532985 7500953260 dgka diacylglycerol kinase (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (ec:2.7.1.107) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 862) (le:121879) (re:122247) (di:direct) ECOUW89 U00006 g396377 Escherichia coli 562 -11532985 5000690575 (de:(ecoli\_3928) (pn:diacylglycerol kinase) (gn:dgka) (gtcfc:8.1) (ec:2.7.1.107) (kdgl\_ecoli) (keggfc:8.1) (rileyfc:1.8.0) (db:gtc-escherichia coli)) ECOLI\_3928 ECOLI\_3928 Escherichia coli 562 10065970

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825464	7727	29883	183	60

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825465	7728	29884	204	67

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825466	7729	29885	198	65

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825474	7730	29886	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825476	7731	29887	186	61

Description

6500729128 fadd:oldd:bl805 long-chain-fatty-acid--coa ligase:long-chain acyl-coa synthetase (gtcfc:3.2) (ec:6.2.1.3) (keggfc:3.2) (rileyfc:1.1.3) (db:gtc-escherichia coli) bl805 bl805 Escherichia coli 562 -11532986 232794 fadd:oldd (ec:6.2.1.3) (de:synthetase)) (db:swissprot) LCFA\_ECOLI P29212 ESCHERICHIA COLI 562 -11532986 164009 fadd long-chain-fatty-acid--coa ligase::acyl coenzyme a synthetase (cl:acetate--coa ligase:acetate--coa ligase homology) (ec:6.2.1.3) (db:pir2.dat) S41589 B64941 Escherichia coli 562 -11532986 300932 fadd:oldd long-chain-fatty-acid--coa ligase ec 6.2.1.3 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #333(40.5-40.8 min.)) (nt:orf\_id:o333#1; similar to (swissprot accession) (le:9727) (re:11412) (di:complement) D90824 D90824 g1736438 Escherichia coli 562 -11532986 300937 fadd:oldd long-chain-fatty-acid--coa ligase ec 6.2.1.3 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #334(40.6-41.0 min.)) (nt:orf\_id:o333#1; similar to (swissprot accession) (le:767) (re:2452) (di:complement) D90825 D90825 g1736444 Escherichia coli 562 -11532986 5000690234 fadd long-chain-fatty-acid--coa ligase (db:genpept-bct1) (ec:6.2.1.3) (de:e.coli fadd gene for acyl coenzyme a synthetase.) (nt:acyl coenzyme a synthetase) (le:226) (re:1911) (di:direct) ECFADDACA X70994 g581070 Escherichia coli 562 -11532986 224295 fadd acyl-coa synthetase:long-chain-fatty-acid--coa (fn:enzyme; degradation of small molecules: fatty) (db:genpept-bct2) (ec:6.2.1.3) (de:escherichia coli k-12 mg1655 section 165 of 400 of the completegenome.) (nt:f561; 100 pct identical to lcfa\_ecoli sw: p29212;) (le:65) (re:1750) (di:complement) AE000275 AE000275 g1788107 Escherichia coli 562 -11532986 81584 fadd:oldd (ec:6.2.1.3) (de:synthetase)) (db:swissprot) LCFA\_ECOLI P29212 ESCHERICHIA COLI 562 -11532986 7000685714 fadd long-chain-fatty-acid--coa ligase::acyl coenzyme a synthetase (cl:acetate--coa ligase:acetate--coa ligase homology) (ec:6.2.1.3) (db:pir) S41589 S41589 Escherichia coli 562 -11532986 224290 fadd:oldd long-chain-fatty-acid--coa ligase ec 6.2.1.3 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #334(40.6-41.0 min.)) (nt:orf\_id:o333#1; similar to (swissprot accession) (le:767) (re:2452) (di:complement) D90825 D90825 g1736444 Escherichia coli 562 -11532986

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825479	7732	29888	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825498	7733	29889	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825500	7734	29890	927	308

Description

6500729129 sbma:b0377 sbma protein (gtcfc:3.2:13.3) (keggfc:14.2) (rileyfc:1.1.3:5.4.0) (db:gtc-escherichia coli) b0377 b0377 Escherichia coli 562 -11532987 97996 sbma (de:sbma protein) (db:swissprot) SBMA\_ECOLI P24212 ESCHERICHIA COLI 562 -11532987 7000686564 sbma sbma protein (cl:probable inner membrane transport protein baca) (db:pir2.dat) A64766 A64766 Escherichia coli 562 -11532987 7500891339 sbma sensitivity to microcin b17:possibly envelop (fn:putative membrane; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 34 of 400 of the completegenome.) (nt:o406; 99 pct identical to sbma\_ecoli sw: p24212) (le:6461) (re:7681) (di:direct) AE000144 AE000144 g1786575 Escherichia coli 562 -11532987 5000690236 (de:(ecoli\_361) (pn:sensitivity to microcin b17, possibly envelop protein) (gn:sbma) (gtcfc:3.3:13.3) (ec:) (sbma\_ecoli) (keggfc:11.2:11.2) (rileyfc:1.1.3:5.4.0) (db:gtc-escherichia coli)) ECOLI\_361 ECOLI\_361 Escherichia coli 562 10122803

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825531	7735	29891	252	83

Description

6500729130 fadr:oler:thdb:b1187 fatty acid--fatty acyl responsive dna-binding protein:fatty acid metabolism regulator protein (gtcfc:3.2) (keggfc:14.2) (rileyfc:1.1.3) (db:gtc-escherichia coli) b1187 b1187 Escherichia coli 562 -11532988 7000689514 fadr:oler:thdb dna-binding protein:fatty acid/fatty acyl-responsive (cl:regulatory protein fadr) (db:pir2.dat) (mp:25.5 min) H64864 H64864 Escherichia coli 562 -11532988 223404 fadr regulatory protein fadr (sr:escherichia coli(strain:k12) dna, clone:kohara clone #244) (db:genpept-bct1) (de:escherichia coli genomic dna. (26.4 - 26.7 min).) (le:6684) (re:7403) (di:direct) D90753 D90753 g1651590 Escherichia coli 562 -11532988 7500955820 fadr (db:genpept-bct1) (de:e. coli fadr gene.) (le:168) (re:887) (di:direct) ECFADR X08087 g992991 Escherichia coli 562 -11532988 232797 fadr negative regulator for fad regulon:and positive (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 107 of 400 of the completegenome.) (nt:o239; 100 pct identical to fadr\_ecoli sw: p09371) (le:1865) (re:2584) (di:direct) AE000217 AE000217 g1787436 Escherichia coli 562 -11532988 5000690237 fadr fatty acid metabolism regulator protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #244) (db:genpept) (de:escherichia coli genomic dna. (26.5 - 26.8 min).) (nt:orf\_id:o244#7; similar to swissprot accession) (le:6684) (re:7403) (di:direct) D90753 D90753 g1651590 Escherichia coli 562 -11532988

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825535	7736	29892	894	297

Description

GTC ORF with score 176 to: (sr:tomato tiny tim cultivar la154) (db:genpept-pln1) (de:deoxyuridine triphosphatase (tomatoes, tiny tim cultivar la154,mrna, 764 nt).) (nt:18 kda. this sequence comes from fig. 3; dntpase;) (le:13) (re:522) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825544	7737	29893	315	104

Description

GTC ORF with score 236 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k09h11.) (nt:similar to acyl-coa dehydrogenases and epoxide) (le:34034:34228:34416:34587) (re:34103:34324:34530:34772) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825545	7738	29894	738	245

Description

GTC ORF with score 248 to: (sr:caenorhabditis elegans strain=bristol n2)  
(db:genpept-inv) (de:caenorhabditis elegans cosmid k09h11.) (nt:similar to  
acyl-coa dehydrogenases and epoxide) (le:34034:34228:34416:34587)  
(re:34103:34324:34530:34772) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825572	7739	29895	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825573	7740	29896	1935	645

Description

6500729131 sbmc:b2009 hypothetical 18.1 kd protein in phse 5region:sbmc protein (gtcfc:3.2) (keggfc:14.2) (rileyfc:1.1.3) (db:gtc-escherichia coli) b2009 b2009 Escherichia coli 562 -11532989 97997 gyri:sbmc (de:dna gyrase inhibitory protein (sbmc protein)) (db:swissprot) GYRI\_ECOLI P33012 ESCHERICHIA COLI 562 -11532989 7000686565 sbmc sbmc protein:hypothetical 18.1 kd protein:phse 5region (db:pir2.dat) H64965 H64965 Escherichia coli 562 -11532989 224513 sbmc sbmc protein. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #348(44.5-44.9 min.)) (nt:orf\_id:o348#21; similar to (swissprot accession) (le:16355) (re:16828) (di:complement) D90838 D90838 g1736675 Escherichia coli 562 -11532989 301160 sbmc sbmc protein. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #349(44.6-45.0 min.)) (nt:orf\_id:o348#21; similar to (swissprot accession) (le:9441) (re:9914) (di:complement) D90839 D90839 g1736683 Escherichia coli 562 -11532989 238217 yeeb (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:sbcb region of e.coli k12 bhb2600.) (le:646) (re:1119) (di:complement) ECOHU43 U00009 g405952 Escherichia coli 562 -11532989 301153 sbmc (db:genpept-bct1) (de:e.coli sbmc gene.) (le:127) (re:600) (di:direct) ECSBMC X84885 g1129137 Escherichia coli 562 -11532989 234711 sbmc sbmc protein (fn:orf; unknown function) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 182 of 400 of the completegenome.) (nt:f157; 100 pct identical yeeb\_ecoli sw: p33012) (le:6104) (re:6577) (di:complement) AE000292 AE000292 g1788319 Escherichia coli 562 -11532989 224520 sbmc sbmc protein. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #349(44.6-45.0 min.)) (nt:orf\_id:o348#21; similar to (swissprot accession) (le:9441) (re:9914) (di:complement) D90839 D90839 g1736683 Escherichia coli 562 -11532989 5000690238 (de:(ecoli\_1957) (pn:sbmc protein) (gn:sbmc) (gtcfc:3.3) (ec:) (sbmc\_ecoli) (keggfc:11.2) (rileyfc:1.1.3) (db:gtc-escherichia coli)) ECOLI\_1957 ECOLI\_1957 Escherichia coli 562 10039876



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825578	7741	29897	507	168

Description

6500729132 atoc:az:b2220 acetoacetate metabolism regulatory protein  
atoc:ornithine / arginine decarboxylase inhibitor:ornithine decarboxylase  
antizyme (gtcfc:3.2:12.13) (keggfc:12.1) (rileyfc:1.1.3) (db:gtc-escherichia  
coli) b2220 b2220 Escherichia coli 562 -11532990 60604 atoc:az  
(de:decarboxylase inhibitor) (ornithine decarboxylase antizyme))  
(db:swissprot) ATOC\_ECOLI\_Q06065 ESCHERICHIA COLI 562 -11532990 7000684659  
atoc acetoacetate metabolism regulatory protein atoc:ornithine decarboxylase  
antizyme (cl:nitrogen assimilation regulatory protein ntrc:response  
regulator homology:rna polymerase sigma factor interaction domain homology)  
(db:pir2.dat) B64992 B64992 Escherichia coli 562 -11532990 224700 atoc:az  
acetoacetate metabolism regulatory protein atoc (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #374(49.8-50.1 min.))  
(nt:orf\_id:o374#3; similar to (swissprot accession) (le:7774) (re:9159)  
(di:direct) D90851 D90851 g1736875 Escherichia coli 562 -11532990 301340  
atoc ntrc/nifa-like protein regulator (fn:transactivating positive  
regulatory protein) (db:genpept-bct1) (de:escherichia coli ntrc/nifa-like  
protein regulator (atoc) gene,complete cds.) (nt:product binds to dna, s54,  
sensor kinase, and) (le:1) (re:1386) (di:direct) ECU17902 U17902 g619917  
Escherichia coli 562 -11532990 238731 atoc response regulator of  
ato:ornithine (fn:regulator; degradation of small molecules:)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 201 of 400 of the  
completegenome.) (nt:o461; 100 pct identical to atoc\_ecoli sw: q06065)  
(le:4969) (re:6354) (di:direct) AE000311 AE000311 g1788550 Escherichia coli  
562 -11532990 5000690239 (de:(ecoli\_2169) (pn:regulator of ato, ornithine  
decarboxylase antizyme, formerly ordi) (gn:atoc) (gtcfc:3.3) (ec:)  
(atoc\_ecoli) (keggfc:11.2) (rileyfc:1.1.3) (db:gtc-escherichia coli))  
ECOLI\_2169 ECOLI\_2169 Escherichia coli 562 10003330

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825606	7742	29898	753	250

Description

6500729133 caia:b0039 probable carnitine operon oxidoreductase caia  
(gtcf:8.1:3.4:3.5:9.13) (ec:1.3.99.-) (keggfc:3.4:3.5:5.13) (rileyfc:5.8.0)  
(db:gtc-escherichia coli) b0039 b0039 Escherichia coli 562 -11532991 232473  
caia (ec:1.3.99.-) (de:probable carnitine operon oxidoreductase caia,  
(db:swissprot) CAIA\_ECOLI P31571 ESCHERICHIA COLI 562 -11532991 163101 caia  
carnitine operon oxidoreductase caia (cl:acyl-coa dehydrogenase)  
(ec:1.3.99.-) (db:pir2.dat) I41011 G64724 Escherichia coli 562 -11532991  
5000690240 caia (db:genpept-bct1) (de:e.coli dna sequence of cai locus.)  
(le:2337) (re:3479) (di:direct) ECCAI X73904 g563862 Escherichia coli 562  
-11532991 7500878113 caia probable carnitine operon oxidoreductase  
(fn:putative regulator; central intermediary) (db:genpept-bct2)  
(ec:1.3.99.-) (de:escherichia coli k-12 mg1655 section 4 of 400 of the  
completegenome.) (nt:f380; 99 pct identical to caia\_ecoli sw: p31571)  
(le:5158) (re:6300) (di:complement) AE000114 AE000114 g1786223 Escherichia  
coli 562 -11532991 62520 caia (ec:1.3.99.-) (de:probable carnitine operon  
oxidoreductase caia,) (db:swissprot) CAIA\_ECOLI P31571 ESCHERICHIA COLI 562  
-11532991 7000684743 caia carnitine operon oxidoreductase caia (cl:acyl-coa  
dehydrogenase) (ec:1.3.99.-) (db:pir) I41011 I41011 Escherichia coli 562  
-11532991

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825607	7743	29899	828	275

Description

6500729134 ispa:b0421 geranyltranstransferase:farnesyl-diphosphate synthase:fpp synthase (gtcfc:3.4:9.12:9.13:12.10) (ec:2.5.1.10) (keggfc:3.4:9.11) (rileyfc:1.7.11:4.5.0) (db:gtc-escherichia coli) b0421 b0421 Escherichia coli 562 -11532992 79992 ispa (ec:2.5.1.10) (de:(fpp synthase)) (db:swissprot) ISPA\_ECOLI P22939 ESCHERICHIA COLI 562 -11532992 162929 ispa geranyltranstransferase (cl:dimethylallyltranstransferase) (ec:2.5.1.10) (db:pir2.dat) (mp:10 min) JQ0665 JQ0665 Escherichia coli 562 -11532992 240198 (sr:e.coli (strain k12) genomic dna, clone lambda2h5) (db:genpept-bct1) (de:e.coli ispa gene for farnesyl diphosphate synthase (ec 2.5.1.1).) (nt:orf2 for farnesyl diphosphate synthase) (le:484) (re:1383) (di:direct) ECOISPA D00694 g216584 Escherichia coli 562 -11532992 7500884296 ispa geranyltransperase (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:19652) (re:20551) (di:complement) ECU82664 U82664 g1773105 Escherichia coli 562 -11532992 234885 ispa geranyltranstransferase farnesyldiphosphate (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:2.5.1.10) (de:escherichia coli k-12 mg1655 section 38 of 400 of the completegenome.) (nt:f299; 100 pct identical to ispa\_ecoli sw: p22939) (le:7276) (re:8175) (di:complement) AE000148 AE000148 g1786623 Escherichia coli 562 -11532992 5000690241 (de:(ecoli\_405) (pn:geranyltranstransferase:farnesyldiphosphate synthase) (gn:ispa) (gtcfc:3.4:9.13) (ec:2.5.1.10) (ispa\_ecoli) (keggfc:3.4:9.11) (rileyfc:1.7.11:4.5.0) (db:gtc-escherichia coli)) ECOLI\_405 ECOLI\_405 Escherichia coli 562 10022242

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501825608	7744	29900	1200	399

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501825615	7745	29901	1221	406

#### Description

6500729135 ksga:b0051 dimethyladenosine transferase:s-adenosylmethionine-6-n:n-adenosyl rrna dimethyltransferase:16s rrna dimethylase:high level kasugamycin resistance protein ksga:kasugamycin dimethyltransferase (gtcfc:13.3:3.7:5.11:5.14:9.12) (ec:2.1.1.-) (keggfc:3.7:5.11:5.14:9.13) (rileyfc:5.4.0) (db:gtc-escherichia coli) b0051 b0051 Escherichia coli 562 -11532993 233586 ksga:rsma (ec:2.1.1.-) (de:dimethyltransferase)) (db:swissprot) KSGA\_ECOLI P06992 ESCHERICHIA COLI 562 -11532993 123249 ksga rrna adenine-n6:n6--dimethyltransferase::dimethyladenosine (cl:rrna (adenine-n6-)-methyltransferase) (ec:2.1.1.-) (db:pir1.dat) (mp:1 min) XYECCRO A24527 Escherichia coli 562 -11532993 5000690242 (db:genpept-bct1) (de:e. coli apah gene for diadenosine tetraphosphatase.) (nt:put. 16s rrna methyltransferase (ksga) (aa 1-273)) (le:203) (re:1024) (di:direct) ECAPAH X04711 g40917 Escherichia coli 562 -11532993 234943 ksga rrna adenosine-n6:n6--dimethyltransferase (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (ec:2.1.1.-) (de:e.coli k12 genome, 0-2.4min. region.) (le:51268) (re:52089) (di:complement) ECO110K D10483 g216476 Escherichia coli 562 -11532993 7500884747 (sr:e.coli dna, clone puc9ksga7) (db:genpept-bct1) (de:e.coli ksga gene coding for methyltransferase (met) conferringkasugamycin resistance.) (nt:methyltransferase (ksga)) (le:11) (re:832) (di:direct) ECOKSGA M11054 g146571 Escherichia coli 562 -11532993 232359 ksga s-adenosylmethionine-6-n:n-adenosyl rrna (fn:enzyme; drug/analog sensitivity) (db:genpept-bct2) (ec:2.1.1.-) (de:escherichia coli k-12 mg1655 section 5 of 400 of the completegenome.) (nt:f273; 100 pct identical to ksga\_ecoli sw:) (le:4447) (re:5268) (di:complement) AE000115 AE000115 g1786236 Escherichia coli 562 -11532993 7502851867 (db:genpept) (de:e. coli apah gene for diadenosine tetraphosphatase.) (nt:put. 16s rrna methyltransferase (ksga) (aa 1-273)) (le:203) (re:1024) (di:direct) ECAPAH X04711 g40917 Escherichia coli 562 -11532993 81177 ksga (ec:2.1.1.-) (de:dimethyltransferase)) (db:swissprot) KSGA\_ECOLI P06992 ESCHERICHIA COLI 562 -11532993

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501825621	7746	29902	267	88

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825624	7747	29903	1152	384

Description

6500729136 ybjf:b0859 hypothetical protein:hypothetical rna methyltransferase in poti-artj intergenic region (gtcfc:14.3:10.2) (ec:2.1.1.-) (keggfc:3.7:5.11:5.14:9.13) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0859 b0859 Escherichia coli 562 -11532994 4000709909 ybjf (ec:2.1.1.-) (de:(ec 2.1.1.-)) (db:swissprot) YBJF\_ECOLI P75817 ESCHERICHIA COLI 562 -11532994 7000687384 ybjf probable rna methyltransferase ybjf (db:pir2.dat) C64824 C64824 Escherichia coli 562 -11532994 7500896857 ybjf putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 77 of 400 of the completegenome.) (nt:o375; this 375 aa orf is 56 pct identical (13 gaps)) (le:10502) (re:11629) (di:direct) AE000187 AE000187 g1787083 Escherichia coli 562 -11532994 5000691843 hypothetical rna methyltransferase hi0958 ec (sr:escherichia coli(strain:k12) dna, clone:kohara clone #211) (db:genpept) (de:escherichia coli genomic dna. (19.4 - 19.8 min).) (nt:orf\_id:o211#2; similar to pir accession number) (le:797) (re:1924) (di:direct) D90724 D90724 g4062444 Escherichia coli 562 -11532994

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825642	7748	29904	1041	346

Description

6500729137 ygca:b2785 hypothetical rna methyltransferase in rela-bara intergenic region (gtcfc:14.3:10.2) (ec:2.1.1.-) (keggfc:3.7:5.11:5.14:9.13) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2785 b2785 Escherichia coli 562 -11532995 112278 ygca (ec:2.1.1.-) (de:(ec 2.1.1.-)) (db:swissprot) YGCA\_ECOLI P55135 ESCHERICHIA COLI 562 -11532995 7000687779 ygca ygca protein (cl:hypothetical protein hi0333) (db:pir2.dat) E65060 E65060 Escherichia coli 562 -11532995 7500924057 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 62 minute region.) (nt:alternate gene name ygca; orf\_f433) (le:11564) (re:12865) (di:complement) ECU29580 U29580 g882679 Escherichia coli 562 -11532995 239359 ygca putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 252 of 400 of the completegenome.) (nt:f433; this 433 aa orf is 26 pct identical (48 gaps)) (le:3949) (re:5250) (di:complement) AE000362 AE000362 g1789148 Escherichia coli 562 -11532995 5000690243 (de:(ecoli\_2716) (pn:hypothetical rna methyltransferase in rela-bara intergenic region) (gn:ygca) (gtcfc:3.7:5.13:5.14:9.12) (ec:2.1.1.-) (ygca\_ecoli) (keggfc:3.7:5.13:5.14:9.13) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2716 ECOLI\_2716 Escherichia coli 562 10054006

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825648	7749	29905	687	228

#### Description

6500729138 prma:b3259 ribosomal protein l11 methyltransferase  
 (gtcfc:14.3:10.4:10.2) (ec:2.1.1.-) (keggfc:3.7:5.11:5.14:9.13)  
 (rileyfc:3.1.2:5.8.0) (db:gtc-escherichia coli) b3259 b3259 Escherichia coli  
 562 -11532996 7000691910 prma ribosomal protein l11 methyltransferase  
 (cl:ribosomal protein l11 methyltransferase:bioc homology) (ec:2.1.1.-)  
 (db:pir2.dat) (mp:72 min) E65118 E65118 Escherichia coli 562 -11532996  
 7500953974 prma methylase for 50s ribosomal subunit protein l11 (fn:enzyme;  
 ribosomal proteins - synthesis,) (db:genpept-bct2) (ec:2.1.1.-)  
 (de:escherichia coli k-12 mg1655 section 294 of 400 of the completegenome.)  
 (nt:o293; sequence change joins 2 orfs from) (le:12808) (re:13689)  
 (di:direct) AE000404 AE000404 g2367208 Escherichia coli 562 -11532996

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825661	7750	29906	372	124

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825673	7751	29907	315	104

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825696	7752	29908	450	149

#### Description

6500729139 yigo:ubie:b3833 hypothetical 28.1 kd protein in udp-rfah  
 intergenic region:ubiquinone/menaquinone biosynthesis methlytransferase ubie  
 (gtcfc:3.7:5.11:5.14:9.12) (ec:2.1.1.-) (keggfc:3.7:5.11:5.14:9.13)  
 (rileyfc:5.7.0) (db:gtc-escherichia coli) b3833 b3833 Escherichia coli 562  
 -11532997 7500893666 ubie (ec:2.1.1.-) (de:(ec 2.1.1.-)) (db:swissprot)  
 UBIE\_ECOLI P27851 ESCHERICHIA COLI 562 -11532997 7000690932 yigo  
 hypothetical 28.1 kd protein in udp-rfah intergenic region:hypothetical  
 protein o251 (cl:spore germination protein c2:bioc homology) (db:pir2.dat)  
 B65188 B65188 Escherichia coli 562 -11532997 7500893668 ubie  
 2-octaprenyl-6-methoxy-1:4-benzoquinone -- (fn:enzyme; biosynthesis of  
 cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655  
 section 349 of 400 of the completegenome.) (nt:o251; 100 pct identical to  
 yigo\_ecoli sw: p27851) (le:2592) (re:3347) (di:direct) AE000459 AE000459  
 g2367307 Escherichia coli 562 -11532997

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825698	7753	29909	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825708	7754	29910	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825709	7755	29911	1029	342

Description

6500729140 apah:b0049

bis:5-nucleosyl-tetraphosphatase:symmetrical:diadenosine tetraphosphatase  
(gtcfc:4.1:4.4) (ec:3.6.1.41) (keggfc:4.1) (rileyfc:1.6.4)  
(db:gtc-escherichia coli) b0049 b0049 Escherichia coli 562 -11532998 59781  
apah (ec:3.6.1.41) (de:(diadenosine tetraphosphatase)) (db:swissprot)  
APAH\_ECOLI P05637 ESCHERICHIA COLI 562 -11532998 7000684586 apah bis  
5-nucleosyl -tetraphosphatase symmetrical::diadenosine tetraphosphatase  
symmetrical (cl:bis(5'-nucleosyl)-tetraphosphatase  
(symmetrical):phosphoesterase core homology) (ec:3.6.1.41) (db:pir1.dat)  
(mp:1 min) A64726 A64726 Escherichia coli 562 -11532998 7500876979 apah  
diadenosine tetraphosphatase (fn:enzyme; salvage of nucleosides and  
nucleotides) (db:genpept-bct2) (ec:3.6.1.41) (de:escherichia coli k-12  
mg1655 section 5 of 400 of the completegenome.) (nt:f280; 99 pct identical  
to apah\_ecoli sw: p05637) (le:3218) (re:4060) (di:complement) AE000115  
AE000115 g1786234 Escherichia coli 562 -11532998 5000690253 (de:(ecoli\_49)  
(pn:diadenosine tetraphosphatase) (gn:apah) (gtcfc:4.1) (ec:3.6.1.41)  
(apah\_ecoli) (keggfc:4.1) (rileyfc:1.6.4) (db:gtc-escherichia coli))  
ECOLI\_49 ECOLI\_49 Escherichia coli 562 10122632

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825729	7756	29912	660	219

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825738	7757	29913	441	147

Description

6500729141 polb:dina:b0060 dna polymerase ii:pol ii (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b0060 b0060 Escherichia coli 562 -11532999 124034 polb dna-directed dna polymerase:ii (cl:escherichia coli dna-directed dna polymerase ii) (ec:2.7.7.7) (db:pir1.dat) (mp:2 min) JDEC22 S15943 Escherichia coli 562 -11532999 237859 polb dna polymerase ii (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (le:63089) (re:65440) (di:complement) ECO110K D10483 g285766 Escherichia coli 562 -11532999 7500953271 polb dna polymerase ii (db:genpept-bct1) (de:e. coli polb gene for dna polymerase ii, and open reading frame(partial).) (le:300) (re:2651) (di:direct) ECPOLB X54847 g581193 Escherichia coli 562 -11532999 233590 polb dna polymerase ii (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:2.7.7.7) (de:escherichia coli k-12 mg1655 section 6 of 400 of the completgenome.) (nt:f783; 100 pct identical to dpo2\_ecoli sw: p21189;) (le:6223) (re:8574) (di:complement) AE000116 AE000116 g1786246 Escherichia coli 562 -11532999 5000690254 (de:(ecoli\_60) (pn:dna polymerase ii) (gn:polb) (gtcfc:4.1:4.2) (ec:2.7.7.7) (dpo2\_ecoli) (keggfc:4.1:4.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_60 ECOLI\_60 Escherichia coli 562 10066011

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825774	7758	29914	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825776	7759	29915	348	116

Description

6500729142 guac:b0104 gmp reductase:guanosine 5-monophosphate oxidoreductase (gtcfc:4.1) (ec:1.6.6.8) (keggfc:4.1) (rileyfc:1.6.1) (db:gtc-escherichia coli) b0104 b0104 Escherichia coli 562 -11533000 7000690897 guac gmp reductase (ec:1.6.6.8) (db:pir2.dat) (mp:3 min) H64732 H64732 Escherichia coli 562 -11533000 7500959754 guac gmp reductase (fn:enzyme; purine ribonucleotide biosynthesis) (db:genpept-bct2) (ec:1.6.6.8) (de:escherichia coli k-12 mg1655 section 9 of 400 of the completgenome.) (nt:o347; 99 pct identical (1 gap) to guac\_ecoli) (le:8200) (re:9243) (di:direct) AE000119 AE000119 g1786293 Escherichia coli 562 -11533000 5000690255 (de:(ecoli\_104) (pn:gmp reductase) (gn:guac) (gtcfc:4.1) (ec:1.6.6.8) (guac\_ecoli) (keggfc:4.1) (rileyfc:1.6.1) (db:gtc-escherichia coli)) ECOLI\_104 ECOLI\_104 Escherichia coli 562 10122659



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825786	7760	29916	327	108

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825787	7761	29917	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825788	7762	29918	516	171

Description

6500729143 hpt:b0125 hypoxanthine phosphoribosyltransferase:hprt  
(gtcfc:4.1:4.4) (ec:2.4.2.8) (keggfc:4.1) (rileyfc:1.6.4)  
(db:gtc-escherichia coli) b0125 b0125 Escherichia coli 562 -11533001 77557  
hpt (ec:2.4.2.8) (de:hypoxanthine phosphoribosyltransferase, (hprt))  
(db:swissprot) HPRT\_ECOLI P36766 ESCHERICHIA COLI 562 -11533001 138134 hpt  
hypoxanthine phosphoribosyltransferase (cl:hypoxanthine  
phosphoribosyltransferase) (ec:2.4.2.8) (db:pir2.dat) S45202 S45202  
Escherichia coli 562 -11533001 301603 orf (sr:escherichia coli (sub\_strain  
w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:escherichia  
coli genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0 min).)  
(nt:'hypoxanthine phosphoribosyltransferase (hpt)) (le:30028) (re:30576)  
(di:direct) ECO82K D26562 g473792 Escherichia coli 562 -11533001 233665 hpt  
hypoxanthine phosphoribosyltransferase (fn:enzyme; salvage of nucleosides  
and nucleotides) (db:genpept-bct2) (ec:2.4.2.8) (de:escherichia coli k-12  
mg1655 section 12 of 400 of the completegenome.) (nt:o182; 100 pct identical  
to hprt\_ecoli sw: p36766) (le:2715) (re:3263) (di:direct) AE000122 AE000122  
g1786317 Escherichia coli 562 -11533001 5000690256 (de:(ecoli\_125)  
(pn:hypoxanthine phosphoribosyltransferase) (gn:hpt) (gtcfc:4.1)  
(ec:2.4.2.8) (hprt\_ecoli) (keggfc:4.1) (rileyfc:1.6.4) (db:gtc-escherichia  
coli)) ECOLI\_125 ECOLI\_125 Escherichia coli 562 10019917

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825800	7763	29919	1797	599

Description

GTC ORF with score 137 to: (sr:thale cress) (db:genpept-pln2)  
(de:arabidopsis thaliana chromosome ii bac f13m22 genomic sequence,complete  
sequence.) (nt:hypothetical protein) (le:57887:59719:60078)  
(re:58388:59846:60132) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825838	7764	29920	273	90

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825843	7765	29921	354	118

Description

6500729144 dnae:polc:b0184 dna polymerase iii:alpha chain  
(gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (rileyfc:3.1.7)  
(db:gtc-escherichia coli) b0184 b0184 Escherichia coli 562 -11533002 69043  
dnae:polc (ec:2.7.7.7) (de:dna polymerase iii, alpha chain,) (db:swissprot)  
DP3A\_ECOLI P10443 ESCHERICHIA COLI 562 -11533002 124035 dnae:polc  
dna-directed dna polymerase:iii alpha chain (cl:dna-directed dna polymerase  
iii alpha chain) (ec:2.7.7.7) (db:pir1.dat) (mp:4 min) DJEC3A C28390  
Escherichia coli 562 -11533002 236173 dnae dna polymerase iii:alpha chain  
(sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (ec:2.7.7.7)  
(de:escherichia coli genome, 4.0 - 6.0 min region.) (le:14685) (re:18167)  
(di:direct) ECOTSF D83536 g1208955 Escherichia coli 562 -11533002 239812  
dnae dna polymerase iii alpha chain (db:genpept-bct1) (de:escherichia coli  
chromosome minutes 4-6.) (le:36201) (re:39683) (di:direct) ECU70214 U70214  
g1552761 Escherichia coli 562 -11533002 235017 dnae dna polymerase  
iii:alpha subunit (fn:enzyme; dna - replication, repair,) (db:genpept-bct2)  
(ec:2.7.7.7) (de:escherichia coli k-12 mg1655 section 17 of 400 of the  
completegenome.) (nt:ol160; 100 pct identical to dp3a\_ecoli sw: p10443)  
(le:10346) (re:13828) (di:direct) AE000127 AE000127 g1786381 Escherichia  
coli 562 -11533002 303250 dnae dna polymerase iii holoenzyme:alpha subunit  
(sr:escherichia coli k12 dna, clone plc26-43) (db:genpept-bct2) (ec:2.7.7.7)  
(de:escherichia coli lipid a biosynthesis (lpxa) gene, lipid adisaccharide  
synthase (lpxb) gene, (3r)-hydroxymyristol acylcarrier protein dehydrase  
(fabz) gene, and alpha subu... ECOLPXA M19334 g146663 Escherichia coli 562  
-11533002 5000690257 (de:(ecoli\_184) (pn:dna polymerase iii, alpha subunit)  
(gn:dnae) (gtcfc:4.1:4.2) (ec:2.7.7.7) (dp3a\_ecoli) (keggfc:4.1:4.2)  
(rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_184 ECOLI\_184 Escherichia  
coli 562 10011626

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825844	7766	29922	639	212

Description

GTC ORF with score 155 to: (db:genpept-bct2) (de:acinetobacter sp. adp1  
vanillate demethylase region, vanillatedemethylase (vanb) and vanillate  
demethylase (vana) genes, completeds.) (nt:similar to salicylate  
hydroxylase; orf7) (le:10288) (re:11433) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825845	7767	29923	501	166

Description

GTC ORF with score 108 to: (db:genpept-bct2) (de:bordetella pertussis d-3-phosphoglycerate dehydrogenase homolog(sera) and brg1 (brg1) genes, complete cds.) (nt:orf4; similar to salicylate hydroxylase) (le:7172) (re:8392) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825850	7768	29924	480	159

Description

6500729145 dnaq:mutd:b0215 dna polymerase iii epsilon subunit:dna polymerase iii:epsilon chain (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b0215 b0215 Escherichia coli 562 -11533003 235849 dnaq:mutd (ec:2.7.7.7) (de:dna polymerase iii, epsilon chain,) (db:swissprot) DP3E\_ECOLI P03007 ESCHERICHIA COLI 562 -11533003 7000685086 dnaq dna-directed dna polymerase:iii epsilon chain (cl:dnaq protein) (ec:2.7.7.7) (db:pir1.dat) (mp:5 min) IQECQ A64746 Escherichia coli 562 -11533003 5000690258 (db:genpept-bct1) (de:e. coli mutd(dnaq)-rnh region for dna polymerase iii epsilon subunit and rnaase h.) (nt:mutd polypeptide (aa 1-243)) (le:581) (re:1312) (di:direct) ECMUTD X04027 g42063 Escherichia coli 562 -11533003 236193 dnaq dna polymerase iii epsilon subunit (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli dnaq (mutd) gene encoding dna polymerase iii epsilon subunitand ribonuclease h (rnh) gene, complete cds.) (le:280) (re:1011) (di:complement) ECORNHQ K00985 g147679 Escherichia coli 562 -11533003 303270 dnaq dna polymerase iii:epsilon chain (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (ec:2.7.7.7) (de:escherichia coli genome, 4.0 - 6.0 min region.) (le:45608) (re:46339) (di:direct) ECOTSF D83536 g1208975 Escherichia coli 562 -11533003 233434 dnaq dna polymerase iii:epsilon subunit (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:2.7.7.7) (de:escherichia coli k-12 mg1655 section 20 of 400 of the completegenome.) (nt:o243; 100 pct identical to dp3e\_ecoli sw: p03007) (le:5096) (re:5827) (di:direct) AE000130 AE000130 g1786409 Escherichia coli 562 -11533003 69074 dnaq:mutd (ec:2.7.7.7) (de:dna polymerase iii, epsilon chain,) (db:swissprot) DP3E\_ECOLI P03007 ESCHERICHIA COLI 562 -11533003

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825855	7769	29925	378	125

Description

6500729146 apt:b0469 adenine phosphoribosyltransferase:aprt (gtcfc:4.1:4.4) (ec:2.4.2.7) (keggfc:4.1) (rileyfc:1.6.4) (db:gtc-escherichia coli) b0469 b0469 Escherichia coli 562 -11533004 59899 apt (ec:2.4.2.7) (de:adenine phosphoribosyltransferase, (aprt)) (db:swissprot) APT\_ECOLI P07672 ESCHERICHIA COLI 562 -11533004 123433 apt adenine phosphoribosyltransferase::amp pyrophosphorylase:transphosphoribosidase (cl:adenine phosphoribosyltransferase) (ec:2.4.2.7) (db:pir1.dat) (mp:11 min) RTECA A25635 Escherichia coli 562 -11533004 233815 apt (sr:e.coli dna) (db:genpept-bct1) (de:e.coli apt gene encoding adenine phosphoribosyl-transferase (aprt), complete cds.) (nt:adenine phosphoribosyl-transferase) (le:191) (re:742) (di:direct) ECOAPT M14040 g145294 Escherichia coli 562 -11533004 7500877004 (sr:e.coli dna) (db:genpept-bct1) (de:e.coli sequence of the apt-adk region.) (nt:apt orf) (le:190) (re:741) (di:direct) ECOAPTADK M38777 g145296 Escherichia coli 562 -11533004 233814 apt adenine phosphoribosyltransferase (fn:enzyme; salvage of nucleosides and nucleotides) (db:genpept-bct2) (ec:2.4.2.7) (de:escherichia coli k-12 mg1655 section 43 of 400 of the completegenome.) (nt:o183; 100 pct identical to apt\_ecoli sw: p07672) (le:1438) (re:1989) (di:direct) AE000153 AE000153 g1786675 Escherichia coli 562 -11533004 5000690259 (de:(ecoli\_452) (pn:adenine phosphoribosyltransferase) (gn:apt) (gtcfc:4.1) (ec:2.4.2.7) (apt\_ecoli) (keggfc:4.1) (rileyfc:1.6.4) (db:gtc-escherichia coli)) ECOLI\_452 ECOLI\_452 Escherichia coli 562 10002632

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825880	7770	29926	612	203

Description

6500729147 dnax:dnaz:b0470 dna polymerase iii subunits gamma and tau  
(gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (rileyfc:3.1.7)  
(db:gtc-escherichia coli) b0470 b0470 Escherichia coli 562 -11533005  
7500880556 dnax:dnaz (ec:2.7.7.7) (de:dna polymerase iii subunits gamma and  
tau,) (db:swissprot) DP3X\_ECOLI P06710 ESCHERICHIA COLI 562 -11533005  
124036 dnax:dnazx dna-directed dna polymerase:iii gamma/tau chain  
precursor:replication elongation factor ii-iii (cl:dna-directed dna  
polymerase iii gamma chain) (ec:2.7.7.7) (db:pir1.dat) (mp:10.4 min) DJEC3G  
A25549 Escherichia coli 562 -11533005 233816 (db:genpept-bct1) (de:e. coli  
dnazx replication gene.) (nt:dnazx gene product (aa 1-643)) (le:142)  
(re:2073) (di:direct) ECDNAZX X04275 g41291 Escherichia coli 562 -11533005  
240245 (sr:e.coli dna) (db:genpept-bct1) (de:e.coli sequence of the apt-adk  
region.) (nt:dnax orf) (le:870) (re:2801) (di:direct) ECOAPTADK M38777  
g145297 Escherichia coli 562 -11533005 240397 dnax dna polymerase iii  
subunits gamma and tau (db:genpept-bct1) (de:escherichia coli minutes 9 to  
11 genomic sequence.) (le:71540) (re:73471) (di:direct) ECU82664 U82664  
g1773152 Escherichia coli 562 -11533005 5000690260 dnazx protein aa 1-643  
(db:genpept-bct1) (de:e.coli dnazx gene for dna polymerase iii subunits  
gamma (dnaz) andtau (dnax).) (le:566) (re:2497) (di:direct) ECZXPIII X04487  
g43320 Escherichia coli 562 -11533005 232701 dnax dna polymerase iii:tau  
and gamma subunits:dna (fn:enzyme; dna - replication, repair,)  
(db:genpept-bct2) (ec:2.7.7.7) (de:escherichia coli k-12 mg1655 section 43  
of 400 of the completegenome.) (nt:o643; 100 pct identical to dp3x\_ecoli sw:  
p06710;) (le:2118) (re:4049) (di:direct) AE000153 AE000153 g1786676  
Escherichia coli 562 -11533005 69078 dnax:dnaz (ec:2.7.7.7) (de:dna  
polymerase iii subunits gamma and tau,) (db:swissprot) DP3X\_ECOLI P06710  
ESCHERICHIA COLI 562 -11533005

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825886	7771	29927	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825902	7772	29928	912	303

Description

6500729148 adk:plsa:dnaw:b0474 adenylate kinase:atp-amp transphosphorylase (gtcfc:4.1) (ec:2.7.4.3) (keggfc:4.1) (rileyfc:1.6.1) (db:gtc-escherichia coli) b0474 b0474 Escherichia coli 562 -11533006 228047 adk:plsa:dnaw (ec:2.7.4.3) (de:adenylate kinase, (atp-amp transphosphorylase)) (db:swissprot) KAD\_ECOLI P05082 ESCHERICHIA COLI 562 -11533006 123892 adk:plsa:dnaw adenylate kinase::atp-amp transphosphorylase (cl:adenylate kinase) (ec:2.7.4.3) (db:pir1.dat) (mp:11 min) KIECA A24275 Escherichia coli 562 -11533006 5000690261 (db:genpept-bct1) (de:e. coli adk gene for adenylate kinase.) (nt:adenylate kinase (adk) (aa 1-214)) (le:194) (re:838) (di:direct) ECADK X03038 g40904 Escherichia coli 562 -11533006 7500884458 (sr:e.coli dna) (db:genpept-bct1) (de:e.coli sequence of the apt-adk region.) (nt:adk orf) (le:5953) (re:6597) (di:direct) ECOAPTADK M38777 g145301 Escherichia coli 562 -11533006 233820 adk adenylate kinase activity:pleiotropic effects (fn:enzyme; purine ribonucleotide biosynthesis) (db:genpept-bct2) (ec:2.7.4.3) (de:escherichia coli k-12 mg1655 section 43 of 400 of the completegenome.) (nt:o214; 100 pct identical to kad\_ecoli sw: p05082;) (le:7201) (re:7845) (di:direct) AE000153 AE000153 g1786680 Escherichia coli 562 -11533006 80327 adk:plsa:dnaw (ec:2.7.4.3) (de:adenylate kinase, (atp-amp transphosphorylase)) (db:swissprot) KAD\_ECOLI P05082 ESCHERICHIA COLI 562 -11533006

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825915	7773	29929	282	93

Description

6500729149 gsk:b0477 inosine-guanosine kinase (gtcfc:4.1:4.4) (ec:2.7.1.73) (keggfc:4.1) (rileyfc:1.6.4) (db:gtc-escherichia coli) b0477 b0477  
Escherichia coli 562 -11533007 79412 gsk (ec:2.7.1.73)  
(de:inosine-guanosine kinase,) (db:swissprot) INKG\_ECOLI P22937 ESCHERICHIA COLI 562 -11533007 163917 gsk inosine kinase::inosine-guanosine kinase (ec:2.7.1.73) (db:pir2.dat) (mp:11 min) JQ0812 JQ0812 Escherichia coli 562 -11533007 240252 gsk inosine-guanosine kinase (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (ec:2.7.1.73) (de:escherichia coli gsk gene for inosine-guanosine kinase, completecds.) (le:217) (re:1521) (di:direct) ECOGSK D00798 g216562 Escherichia coli 562 -11533007 7500884158 gsk inosine kinase (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:79573) (re:80877) (di:direct) ECU82664 U82664 g1773159 Escherichia coli 562 -11533007 234582 gsk inosine-guanosine kinase (fn:enzyme; salvage of nucleosides and nucleotides) (db:genpept-bct2) (ec:2.7.1.73) (de:escherichia coli k-12 mg1655 section 44 of 400 of the completegenome.) (nt:o434; 100 pct identical to gb: ecogsk\_1) (le:106) (re:1410) (di:direct) AE000154 AE000154 g1786684 Escherichia coli 562 -11533007 5000690262 (de:(ecoli\_460) (pn:inosine-guanosine kinase) (gn:gsk) (gtcfc:4.1) (ec:2.7.1.73) (ingk\_ecoli) (keggfc:4.1) (rileyfc:1.6.4) (db:gtc-escherichia coli)) ECOLI\_460 ECOLI\_460 Escherichia coli 562 10087084

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825916	7774	29930	240	79
<u>Description</u>				
6500729150 usha:b0480 udp-sugar hydrolase precursor:udp-sugar diphosphatase:udp-sugar pyrophosphatase 5-nucleotidase (gtcfc:4.3:7.1:9.4) (keggfc:4.1:4.2:4.4:9.4) (rileyfc:1.3.3) (db:gtc-escherichia coli) b0480 b0480 Escherichia coli 562 -11533008 104006 usha (ec:3.6.1.45:3.1.3.5) (de:(udp-sugar pyrophosphatase) (5'-nucleotidase,)) (db:swissprot) USHA_ECOLI P07024 ESCHERICHIA COLI 562 -11533008 7000686912 usha udp-sugar hydrolase:precursor:udp-sugar diphosphatase:udpglucose hydrolase (cl:5'-nucleotidase:5'-nucleotidase homology:phosphoesterase core homology) (ec:3.6.1.45) (db:pir1.dat) (mp:11 min) YXECUG G64778 Escherichia coli 562 -11533008 7500893869 usha udp-sugar hydrolase precursor (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:84362) (re:86014) (di:direct) ECU82664 U82664 g1773162 Escherichia coli 562 -11533008 240255 usha udp-sugar hydrolase 5-nucleotidase (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:3.6.1.45) (de:escherichia coli k-12 mg1655 section 44 of 400 of the completegenome.) (nt:o550; 99 pct identical to usha_ecoli sw: p07024) (le:4895) (re:6547) (di:direct) AE000154 AE000154 g1786687 Escherichia coli 562 -11533008 5000690263 (de:(ecoli_463) (pn:udp-sugar hydrolase:5"-nucleotidase) (gn:usha) (gtcfc:4.1:4.2:7.1:9.4) (ec:3.6.1.45) (usha_ecoli) (keggfc:4.1:4.2:4.4:9.4) (rileyfc:1.3.3) (db:gtc-escherichia coli)) ECOLI_463 ECOLI_463 Escherichia coli 562 10122843				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825918	7775	29931	363	120

Description

6500729151 ybbx:b0512 hypothetical protein:putative allantoinase  
 (gtcfc:4.1:14.1) (ec:3.5.2.5) (keggfc:4.1) (rileyfc:5.7.0)  
 (db:gtc-escherichia coli) b0512 b0512 Escherichia coli 562 -11533009  
 4000709551 ybbx:glxb3 (ec:3.5.2.5) (de:putative allantoinase,)  
 (db:swissprot) ALLA\_ECOLI P77671 ESCHERICHIA COLI 562 -11533009 7000684559  
 ybbx probable allantoinase::protein b0512 (cl:allantoinase:bacillus  
 dihydroorotase homology) (ec:3.5.2.5) (db:pir2.dat) G64782 G64782  
 Escherichia coli 562 -11533009 7000684560 (db:genpept-bct1) (de:escherichia  
 coli minutes 9 to 11 genomic sequence.) (nt:similar to s. cerevisiae dal1)  
 (le:118595) (re:119956) (di:direct) ECU82664 U82664 g1773192 Escherichia  
 coli 562 -11533009 7500876770 glxb3 glxb3 (db:genpept-bct1) (de:escherichia  
 coli glyoxylate induced proteins glxb1, glxb2, glxb3,glxb4, glxb6, glxb7 and  
 glxb8, and glycerate kinase glxb5 genes,complete cds.) (nt:similar to  
 saccharomyces cerevisiae allantoinase,) (le:2677) (re:4038) (di:direct)  
 ECU89279 U89279 g2735238 Escherichia coli 562 -11533009 240285 ybbx  
 putative hydrolase (fn:putative enzyme; not classified) (db:genpept-bct2)  
 (de:escherichia coli k-12 mg1655 section 47 of 400 of the completegenome.)  
 (nt:o453; this 453 aa orf is 33 pct identical (19 gaps)) (le:5306) (re:6667)  
 (di:direct) AE000157 AE000157 g1786722 Escherichia coli 562 -11533009  
 5000691633 (de:(ecoli\_495) (pn:function not assigned) (gtcfc:13.7:14.1)  
 (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_495  
 ECOLI\_495 Escherichia coli 562 10122870

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825936	7776	29932	381	127

#### Description

6500729152 purk:b0522 phosphoribosylaminoimidazole carboxylase atpase subunit:air carboxylase:airc (gtcfc:4.1) (ec:4.1.1.21) (keggfc:4.1) (rileyfc:1.6.1) (db:gtc-escherichia coli) b0522 b0522 Escherichia coli 562 -11533010 92464 purk (ec:4.1.1.21) (de:(air carboxylase) (airc)) (db:swissprot) PURK\_ECOLI P09029 ESCHERICHIA COLI 562 -11533010 125308 purk phosphoribosylaminoimidazole carboxylase:carbon dioxide-fixation chain (cl:phosphoribosylaminoimidazole carboxylase carbon dioxide-fixation chain:phosphoribosylaminoimidazole carboxylase carbon dioxide-fixation chain homology) (ec:4.1.1.21) (db:pir1.dat) (mp:12 min) DCECPK JU0001 Escherichia coli 562 -11533010 240296 (sr:e.coli (k12) dna, (library of clarke-carbon), clone plc8) (db:genpept-bct1) (de:e.coli 5'-phosphoribosyl-5-amino-4-imidazole carboxylase i and ii(pure and purk) genes, complete cds.) (nt:5'-phosphoribosyl-5-amino-4-imidazole carboxylase) (le:899) (... ECOPUREK M19657 g147413 Escherichia coli 562 -11533010 7500889085 purk 5-phosphoribosyl-5-amino-4-imidazole (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:130976) (re:132043) (di:complement) ECU82664 U82664 g1773203 Escherichia coli 562 -11533010 235603 purk phosphoribosylaminoimidazole carboxylase = air (fn:enzyme; purine ribonucleotide biosynthesis) (db:genpept-bct2) (ec:4.1.1.21) (de:escherichia coli k-12 mg1655 section 48 of 400 of the completegenome.) (nt:f355; 99 pct identical to purk\_ecoli sw: p09029) (le:5035) (re:6102) (di:complement) AE000158 AE000158 g1786733 Escherichia coli 562 -11533010 5000690264 (de:(ecoli\_505) (pn:phosphoribosylaminoimidazole carboxylase , air carboxylase, co:2-fixing subunit:phosphoribosylaminoimidazole carboxylase ) (gn:purk) (gtcfc:4.1) (ec:4.1.1.21) (purk\_ecoli) (keggfc:4.1) (rileyfc:1.6.1) (db:gtc) ECOLI\_505 ECOLI\_505 Escherichia coli 562 10066303

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825937	7777	29933	261	86

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825947	7778	29934	204	67

#### Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501825948	7779	29935	1227	408

#### Description

6500729153 pure:b0523 phosphoribosylaminoimidazole carboxylase catalytic subunit:air carboxylase:airc (gtcfc:4.1) (ec:4.1.1.21) (keggfc:4.1) (rileyfc:1.6.1) (db:gtc-escherichia coli) b0523 b0523 Escherichia coli 562 -11533011 125306 pure phosphoribosylaminoimidazole carboxylase:catalytic chain (cl:phosphoribosylaminoimidazole carboxylase catalytic chain:phosphoribosylaminoimidazole carboxylase catalytic chain homology) (ec:4.1.1.21) (db:pir1.dat) (mp:12 min) DEECPE JT0499 Escherichia coli 562 -11533011 237962 (sr:e.coli (k12) dna, (library of clarke-carbon), clone plc8) (db:genpept-bct1) (de:e.coli 5'-phosphoribosyl-5-amino-4-imidazole carboxylase i and ii(pure and purk) genes, complete cds.) (nt:5'-phosphoribosyl-5-amino-4-imidazole carboxylase i) (le:393)...  
 ECOPUREK M19657 g147412 Escherichia coli 562 -11533011 240297 (db:genpept-bct1) (de:e. coli purek genes for air carboxylase(5'-phosphoribosyl-5-aminoimidazole carboxylase (ec 4.1.1.21))). (nt:pure gene product (catalytic subunit) (aa 1- 169)) (le:322) (re:831) (di:direct) ECPUREK X12982 g42588 Escherichia coli 562 -11533011 7500953323 pur6 phosphoribosylaminoimidazole carboxylase (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:132040) (re:132549) (di:complement) ECU82664 U82664 g1773204 Escherichia coli 562 -11533011 235602 pure phosphoribosylaminoimidazole carboxylase = air (fn:enzyme; purine ribonucleotide biosynthesis) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 48 of 400 of the completegenome.) (nt:fl69; 100 pct identical to pur6\_ecoli sw: p09028) (le:6099) (re:6608) (di:complement) AE000158 AE000158 g1786734 Escherichia coli 562 -11533011 5000690265 (de:(ecoli\_506) (pn:phosphoribosylaminoimidazole carboxylase , air carboxylase, catalytic subunit:phosphoribosylaminoimidazole carboxylase ) (gn:pure) (gtcfc:4.1) (ec:4.1.1.21) (pur6\_ecoli) (keggfc:4.1) (rileyfc:1.6.1) (db:gtc-e) ECOLI\_506 ECOLI\_506 Escherichia coli 562 10066302

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501825953	7780	29936	1632	544

#### Description

GTC ORF with score 891 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501825968	7781	29937	327	109

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825969	7782	29938	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825980	7783	29939	2265	755

Description

6500729154 hola:b0640 dna polymerase iii:delta subunit (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b0640 b0640 Escherichia coli 562 -11533012 77461 hola (ec:2.7.7.7) (de:dna polymerase iii, delta subunit,) (db:swissprot) HOLA ECOLI P28630 ESCHERICHIA COLI 562 -11533012 162955 hola dna-directed dna polymerase:iii delta chain (ec:2.7.7.7) (db:pir2.dat) A45251 A45251 Escherichia coli 562 -11533012 223126 hola dna-directed dna polymerase iii delta chain (sr:escherichia coli(strain:k12) dna, clone:kohara clone #169) (db:genpept-bct1) (de:escherichia coli genomic dna. (14.3 - 14.7 min).) (le:6822) (re:7853) (di:complement) D90704 D90704 g1651267 Escherichia coli 562 -11533012 234190 hola dna polymerase iii delta subunit (sr:escherichia coli (strain k-12) (library: lamda-phage of y. kohara) (db:genpept-bct1) (de:escherichia coli (clone puc-delta) dna polymerase iii delta subunit(hola) gene, complete cds.) (le:128) (re:1159) (di:direct) ECODELTA L04576 g145729 Escherichia coli 562 -11533012 240154 hola dna polymerase iii delta subunit (fn:accessory protein involved in replication) (sr:escherichia coli (strain maf102) dna) (db:genpept-bct1) (de:e. coli dna polymerase iii delta subunit (hola) gene, complete cds.) (le:55) (re:1086) (di:direct) ECODNAPDS M94267 g145785 Escherichia coli 562 -11533012 7500883457 hola dna-directed dna polymeraseiii delta chain (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (le:111204) (re:112235) (di:complement) ECU82598 U82598 g1778558 Escherichia coli 562 -11533012 234138 hola dna polymerase iii:delta subunit (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:2.7.7.7) (de:escherichia coli k-12 mg1655 section 58 of 400 of the completegenome.) (nt:f343; 100 pct identical to hola\_ecoli sw: p28630) (le:8309) (re:9340) (di:complement) AE000168 AE000168 g1786859 Escherichia coli 562 -11533012 5000690266 hola dna-directed dna polymerase ec 2.7.7.7 iii (sr:escherichia coli(strain:k12) dna, clone:kohara clone #169) (db:genpept) (de:escherichia coli genomic dna. (14.3 - 14.7 min).) (nt:orf\_id:o169#8; similar to pir accession number) (le:6822) (re:7853) (di:complement) D90704 D90704 g1651267 Escherichia coli 562 -11533012

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825993	7784	29940	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825994	7785	29941	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501825995	7786	29942	561	186

Description

6500729155 holb:b1099 dna polymerase iii:delta subunit (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b1099 b1099 Escherichia coli 562 -11533013 77463 holb (ec:2.7.7.7) (de:dna polymerase iii, delta' subunit,) (db:swissprot) HOLB\_ECOLI P28631 ESCHERICHIA COLI 562 -11533013 162956 holb dna-directed dna polymerase:iii delta chain (cl:dna-directed dna polymerase iii delta' chain) (ec:2.7.7.7) (db:pir2.dat) (mp:24 min) S35523 S35523 Escherichia coli 562 -11533013 223361 holb dna-directed dna polymerase iii delta chain (sr:escherichia coli(strain:k12) dna, clone:kohara clone #236) (db:genpept-bct1) (de:escherichia coli genomic dna.(24.7 - 25.1 min).) (le:6404) (re:7408) (di:direct) D90745 D90745 g1651540 Escherichia coli 562 -11533013 7500883460 holb dna polymerase iii delta prime subunit (fn:accessory protein involved in replication) (sr:escherichia coli (strain maf102) dna) (db:genpept-bct1) (de:e. coli dna polymerase iii delta prime subunit (holb) gene,complete cds.) (le:385) (re:1389) (di:direct) ECODNAPDPS L01483 g145783 Escherichia coli 562 -11533013 234189 holb dna polymerase iii:delta prime subunit (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:2.7.7.7) (de:escherichia coli k-12 mg1655 section 100 of 400 of the completegenome.) (nt:o334; 99 pct identical to holb\_ecoli sw: p28631) (le:7067) (re:8071) (di:direct) AE000210 AE000210 g1787341 Escherichia coli 562 -11533013 5000690267 holb dna-directed dna polymerase ec 2.7.7.7 iii (sr:escherichia coli(strain:k12) dna, clone:kohara clone #236) (db:genpept) (de:escherichia coli genomic dna. (24.8 - 25.2 min).) (nt:orf\_id:o236#8; similar to pir accession number) (le:6404) (re:7408) (di:direct) D90745 D90745 g1651540 Escherichia coli 562 -11533013

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826006	7787	29943	2058	685

Description

6500729156 purb:b1131 adenylosuccinate lyase:adenylosuccinase:asl  
 (gtcfc:4.1:5.2) (ec:4.3.2.2) (keggfc:4.1:5.2) (rileyfc:1.6.1)  
 (db:gtc-escherichia coli) b1131 b1131 Escherichia coli 562 -11533014  
 7500889066 purb (ec:4.3.2.2) (de:adenylosuccinate lyase, (adenylosuccinase)  
 (asl)) (db:swissprot) PUR8\_ECOLI P25739 ESCHERICHIA COLI 562 -11533014  
 162671 purb adenylosuccinate lyase::adenylosuccinase (ec:4.3.2.2)  
 (db:pir2.dat) S19212 S19212 Escherichia coli 562 -11533014 223378 purb  
 adenylosuccinate lyase (sr:escherichia coli(strain:k12) dna, clone:kohara  
 clone #239) (db:genpept-bct1) (de:escherichia coli genomic dna.(25.6 - 26.0  
 min).) (le:6850) (re:8220) (di:complement) D90748 D90748 g1651559  
 Escherichia coli 562 -11533014 223383 purb adenylosuccinate lyase  
 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #240)  
 (db:genpept-bct1) (de:escherichia coli genomic dna.(25.6 - 26.0 min).)  
 (le:1167) (re:2537) (di:complement) D90749 D90749 g1651565 Escherichia coli  
 562 -11533014 5000690268 purb succinyl-amp lyase (db:genpept-bct1)  
 (ec:4.3.2.2) (de:e.coli orf-15, orf-23, purb and phop (5'end) genes.)  
 (nt:adenylosuccinate lyase) (le:1376) (re:2746) (di:direct) ECPURB X59307  
 g42585 Escherichia coli 562 -11533014 237960 purb adenylosuccinate lyase  
 (fn:enzyme; purine ribonucleotide biosynthesis) (db:genpept-bct2)  
 (ec:4.3.2.2) (de:escherichia coli k-12 mg1655 section 103 of 400 of the  
 completegenome.) (nt:f456; 99 pct identical to pur8\_ecoli sw: p25739)  
 (le:4927) (re:6297) (di:complement) AE000213 AE000213 g1787376 Escherichia  
 coli 562 -11533014 7502851868 purb adenylosuccinate lyase ec 4.3.2.2  
 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #239) (db:genpept)  
 (de:escherichia coli genomic dna. (25.6 - 25.9 min).) (nt:orf\_id:o240#2;  
 similar to pir accession number) (le:6850) (re:8220) (di:complement) D90748  
 D90748 g1651559 Escherichia coli 562 -11533014 7502851869 purb  
 adenylosuccinate lyase ec 4.3.2.2 (sr:escherichia coli(strain:k12) dna,  
 clone:kohara clone #240) (db:genpept) (de:escherichia coli genomic dna.  
 (25.7 - 26.1 min).) (nt:orf\_id:o240#2; similar to pir accession number)  
 (le:1167) (re:2537) (di:complement) D90749 D90749 g1651565 Escherichia coli  
 562 -11533014 92439 purb (ec:4.3.2.2) (de:adenylosuccinate lyase,  
 (adenylosuccinase) (asl)) (db:swissprot) PUR8\_ECOLI P25739 ESCHERICHIA COLI  
 562 -11533014

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826017	7788	29944	207	68

# Description

6500729157 add:b1623 adenosine deaminase:adenosine aminohydrolase  
(gtcf:4.1:4.4) (ec:3.5.4.4) (keggfc:4.1) (rileyfc:1.6.4)  
(db:gtc-escherichia coli) b1623 b1623 Escherichia coli 562 -11533015 58616  
add (ec:3.5.4.4) (de:adenosine deaminase, (adenosine aminohydrolase))  
(db:swissprot) ADD\_ECOLI P22333 ESCHERICHIA COLI 562 -11533015 7000684525  
add adenosine deaminase (cl:adenosine deaminase) (ec:3.5.4.4) (db:pir2.dat)  
A64919 A64919 Escherichia coli 562 -11533015 224052 add adenosine deaminase  
ec 3.5.4.4 adenosine (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara  
lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#314(36.3-36.7 min.)) (nt:orf\_id:o314#9; similar to (swissprot accession)  
(le:16917) (re:17918) (di:direct) D90805 D90805 g1742677 Escherichia coli  
562 -11533015 224059 add adenosine deaminase ec 3.5.4.4 adenosine  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #315(36.6-36.9  
min.)) (nt:orf\_id:o314#9; similar to (swissprot accession) (le:5229)  
(re:6230) (di:direct) D90806 D90806 g1742685 Escherichia coli 562 -11533015  
300772 add adenosine deaminase ec 3.5.4.4 adenosine (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #317(36.6-36.9 min.))  
(nt:orf\_id:o314#9; similar to (swissprot accession) (le:5330) (re:6331)  
(di:direct) D90808 D90808 g1742717 Escherichia coli 562 -11533015 300747  
add adenosine deaminase (fn:enzyme; salvage of nucleosides and nucleotides)  
(db:genpept-bct2) (ec:3.5.4.4) (de:escherichia coli k-12 mg1655 section 148  
of 400 of the completegenome.) (nt:o333; this 333 aa orf is 99 pct identical  
(1 gap)) (le:2954) (re:3955) (di:direct) AE000258 AE000258 g1787910  
Escherichia coli 562 -11533015 224089 add adenosine deaminase ec 3.5.4.4  
adenosine (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda  
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#317(36.6-36.9 min.)) (nt:orf\_id:o314#9; similar to (swissprot accession)  
(le:5330) (re:6331) (di:direct) D90808 D90808 g1742717 Escherichia coli 562  
-11533015 5000690269 (de:(ecoli\_1582) (pn:adenosine deaminase) (gn:add)  
(gtcf:4.1) (ec:3.5.4.4) (add\_ecoli) (keggfc:4.1) (rileyfc:1.6.4)  
(db:gtc-escherichia coli)) ECOLI\_1582 ECOLI\_1582 Escherichia coli 562  
10119737

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826018	7789	29945	624	207

Description

6500729158 hole:b1842 dna polymerase iii:theta subunit (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b1842 b1842 Escherichia coli 562 -11533016 77470 hole (ec:2.7.7.7) (de:dna polymerase iii, theta subunit,) (db:swissprot) HOLE\_ECOLI P28689 ESCHERICHIA COLI 562 -11533016 162958 hole dna-directed dna polymerase:iii theta chain:dna polymerase iii holoenzyme theta chain (ec:2.7.7.7) (db:pir2.dat) S34951 S34951 Escherichia coli 562 -11533016 224333 hole dna-directed dna polymerase ec 2.7.7.7 iii q (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #336(41.2-41.6 min.)) (nt:orf\_id:o336#9; similar to (pir accession number) (le:12225) (re:12455) (di:direct) D90827 D90827 g1736484 Escherichia coli 562 -11533016 234679 hole dna polymerase iii theta subunit (sr:escherichia coli (strain k-12) (library: lambda phage (from y) (db:genpept-bct1) (de:e. coli dna polymerase iii theta subunit (hole) gene, complete cds.) (le:173) (re:403) (di:direct) ECODNAPOLY L04572 g145787 Escherichia coli 562 -11533016 300973 hole dna polymerase iii theta subunit (sr:escherichia coli (strain maf102) dna) (db:genpept-bct1) (de:escherichia coli dna polymerase iii theta subunit (hole) gene,complete cds.) (le:165) (re:395) (di:direct) ECOHOLETTA L05381 g146393 Escherichia coli 562 -11533016 234191 hole dna polymerase iii:theta subunit (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:2.7.7.7) (de:escherichia coli k-12 mgl655 section 168 of 400 of the completegenome.) (nt:o76; 100 pct identical to hole\_ecoli sw: p28689; cg) (le:4958) (re:5188) (di:direct) AE000278 AE000278 g1788147 Escherichia coli 562 -11533016 5000690270 (de:(ecoli\_1799) (pn:dna polymerase iii, theta subunit) (gn:hole) (gtcfc:4.1:4.2) (ec:2.7.7.7) (hole\_ecoli) (keggfc:4.1:4.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_1799 ECOLI\_1799 Escherichia coli 562 10019830

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826027	7790	29946	555	184

Description

6500729159 amn:b1982 amp nucleosidase (gtcfc:4.1:4.4) (ec:3.2.2.4) (keggfc:4.1) (rileyfc:1.6.4) (db:gtc-escherichia coli) b1982 b1982 Escherichia coli 562 -11533017 59324 amn (ec:3.2.2.4) (de:amp nucleosidase,) (db:swissprot) AMN\_ECOLI P15272 ESCHERICHIA COLI 562 -11533017 7000684572 amn amp nucleosidase (ec:3.2.2.4) (db:pir2.dat) H64962 H64962 Escherichia coli 562 -11533017 224485 amn amp nucleosidase ec 3.2.2.4 . (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #347(44.2-44.5 min.)) (nt:orf\_id:o347#3; similar to (swissprot accession) (le:3849) (re:5303) (di:direct) D90837 D90837 g1736646 Escherichia coli 562 -11533017 301125 amn amp nucleosidase (fn:enzyme; salvage of nucleosides and nucleotides) (db:genpept-bct2) (ec:3.2.2.4) (de:escherichia coli k-12 mg1655 section 180 of 400 of the completegenome.) (nt:o484; 98 pct identical (1 gap) to amn\_ecoli) (le:2946) (re:4400) (di:direct) AE000290 AE000290 g1788293 Escherichia coli 562 -11533017 5000690271 (de:(ecoli\_1933) (pn:amp nucleosidase) (gn:amn) (gtcfc:4.1) (ec:3.2.2.4) (amn\_ecoli) (keggfc:4.1) (rileyfc:1.6.4) (db:gtc-escherichia coli)) ECOLI\_1933 ECOLI\_1933 Escherichia coli 562 10119937

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826031	7791	29947	1395	464

Description

6500729160 nrda:dna:b2234 ribonucleoside-diphosphate reductase 1 alpha chain:ribonucleotide reductase 1:b1 protein:r1 protein (gtcfc:4.1:4.2) (ec:1.17.4.1) (keggfc:4.1:4.2) (rileyfc:1.6.3) (db:gtc-escherichia coli) (rileyfc:small-molecule metabolism, 2'-deoxyribonucleotide metabolism) b2234 b2234 Escherichia coli 562 -11533018 94409 nrda:dna (ec:1.17.4.1) (de:(ribonucleotide reductase 1) (b1 protein) (r1 protein)) (db:swissprot) RIR1\_ECOLI P00452 ESCHERICHIA COLI 562 -11533018 7000686335 nrda ribonucleoside-diphosphate reductase:1 alpha chain:ribonucleotide reductase b1 protein:ribonucleotide reductase r1 protein (cl:herpesvirus ribonucleoside-diphosphate reductase large chain) (ec:1.17.4.1) (db:pir1.dat) (mp:49) RDEC1R H64993 Escherichia coli 562 -11533018 224740 dna ribonucleoside-diphosphate reductase 1 alpha (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #377(50.5-50.9 min.)) (nt:similar to (swissprot accession number p00452)) (le:5149) (re:7434) (di:direct) D90855 D90855 g1799581 Escherichia coli 562 -11533018 7500889798 nrda ribonucleoside diphosphate reductase 1:alpha (fn:enzyme; 2'-deoxyribonucleotide metabolism) (db:genpept-bct2) (ec:1.17.4.1) (de:escherichia coli k-12 mg1655 section 203 of 400 of the completegenome.) (nt:o761; 99 pct identical to rir1\_ecoli sw: p00452;) (le:5402) (re:7687) (di:direct) AE000313 AE000313 g2367133 Escherichia coli 562 -11533018

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826065	7792	29948	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826103	7793	29949	1203	400

Description

GTC ORF with score 295 to: (sr:coprinus cinereus strain=okayama-7)  
(db:genpept-pln2) (de:coprinus cinereus dna repair and meiosis gene (rad9),  
complete cds.) (nt:dna repair and meiosis) (le:300:542:851:1758:1925)  
(re:492:800:1697:1872:2565) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826118	7794	29950	390	129

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826125	7795	29951	1119	373

Description

6500729161 nrdb:ftsb:b2235 ribonucleoside-diphosphate reductase 1 beta chain:ribonucleotide reductase 1:b2 protein:r2 protein (gtcfc:4.1:4.2) (ec:1.17.4.1) (keggfc:4.1:4.2) (rileyfc:1.6.3) (db:gtc-escherichia coli) (rileyfc:small-molecule metabolism, 2'-deoxyribonucleotide metabolism) b2235 b2235 Escherichia coli 562 -11533019 123166 nrdb ribonucleoside-diphosphate reductase:1 beta chain:ribonucleotide reductase b2 protein (cl:herpesvirus ribonucleoside-diphosphate reductase small chain) (ec:1.17.4.1) (db:pir1.dat) (mp:49) RDEC2R A00527 Escherichia coli 562 -11533019 224741 nrdb ribonucleoside-diphosphate reductase ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #377(50.5-50.9 min.)) (nt:similar to (pir accession number a00527)) (le:7668) (re:8798) (di:direct) D90855 D90855 g1799582 Escherichia coli 562 -11533019 7500953219 nrdb (sr:escherichia coli k-12 dna, clone pps2) (db:genpept-bct1) (de:e.coli ribonucleoside diphosphate reductase operon: nrda and nrdbgenes encoding subunits b1 and b2.) (nt:ribonucleoside diphosphate reductase b2 subunit) (le:6010) (re:7140) (di:direct) ECONRDA K02672 g146967 Escherichia coli 562 -11533019 235249 nrdb ribonucleoside-diphosphate reductase 1:beta (fn:enzyme; 2'-deoxyribonucleotide metabolism) (db:genpept-bct2) (ec:1.17.4.1) (de:escherichia coli k-12 mg1655 section 203 of 400 of the completegenome.) (nt:o376; 100 pct identical to rir2\_ecoli sw: p00453) (le:7921) (re:9051) (di:direct) AE000313 AE000313 g1788567 Escherichia coli 562 -11533019 5000690273 (de:(ecoli\_2184) (pn:ribonucleoside-diphosphate reductase 1, beta subunit, b2) (gn:nrdb) (gtcfc:4.1:4.2) (ec:1.17.4.1) (rir2\_ecoli) (keggfc:4.1:4.2) (rileyfc:1.6.3) (db:gtc-escherichia coli)) ECOLI\_2184 ECOLI\_2184 Escherichia coli 562 10065744

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826142	7796	29952	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826147	7797	29953	519	172
<u>Description</u>				
6500729162 purf:b2312 amidophosphoribosyltransferase:glutamine phosphoribosylpyrophosphate amidotransferase:atase (gtcfc:4.1:5.1) (ec:2.4.2.14) (keggfc:4.1:5.1) (rileyfc:1.6.1) (db:gtc-escherichia coli) b2312 b2312 Escherichia coli 562 -11533020 7000688860 purf amidophosphoribosyltransferase (cl:amidophosphoribosyltransferase) (ec:2.4.2.14) (db:pir1.dat) (mp:49 min) XQEC F65003 Escherichia coli 562 -11533020 7500953241 purf amidophosphoribosyltransferase = prpp (fn:enzyme; purine ribonucleotide biosynthesis) (db:genpept-bct2) (ec:2.4.2.14) (de:escherichia coli k-12 mg1655 section 210 of 400 of the completegenome.) (nt:f505; 99 pct identical to pur1_ecoli sw: p00496) (le:2790) (re:4307) (di:complement) AE000320 AE000320 g1788651 Escherichia coli 562 -11533020 5000690274 (de:(ecoli_2261) (pn:amidophosphoribosyltransferase , prpp amidotransferase:amidophosphoribosyltransferase ) (gn:purf) (gtcfc:4.1:5.1) (ec:2.4.2.14) (pur1_ecoli) (keggfc:4.1:5.1) (rileyfc:1.6.1) (db:gtc-escherichia coli)) ECOLI_2261 ECOLI_2261 Escherichia coli 562 10123636				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826164	7798	29954	2241	746

#### Description

6500729163 purc:b2476 phosphoribosylaminoimidazole-succinocarboxamide synthase:saicar synthetase (gtcfc:4.1) (ec:6.3.2.6) (keggfc:4.1) (rileyfc:1.6.1) (db:gtc-escherichia coli) b2476 b2476 Escherichia coli 562 -11533021 92431 purc (ec:6.3.2.6) (de:(saicar synthetase)) (db:swissprot) PUR7\_ECOLI P21155 ESCHERICHIA COLI 562 -11533021 126005 purc phosphoribosylaminoimidazolesuccinocarboxamide synthase::saicar synthetase (cl:phosphoribosylaminoimidazolesuccinocarboxamide synthase) (ec:6.3.2.6) (db:pir1.dat) C36146 C36146 Escherichia coli 562 -11533021 225041 phosphoribosylaminoimidazolesuccinocarboxamide (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #423(55.7-56.1 min.)) (nt:similar to (pir accession number c36146)) (le:7855) (re:8568) (di:complement) D90876 D90876 g1799903 Escherichia coli 562 -11533021 225051 phosphoribosylaminoimidazolesuccinocarboxamide (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #424(55.9-56.3 min.)) (nt:similar to (pir accession number c36146)) (le:595) (re:1308) (di:complement) D90877 D90877 g1805534 Escherichia coli 562 -11533021 7500889063 purc (sr:e.coli (strain k12) dna) (db:genpept-bct1) (de:e.coli 5-phosphoribosyl 5-aminoimidazole 4-n-succinocarboxamidesynthetase (saicar) and dapx gene, complete cds.) (nt:5'-phosphoribosyl-5-aminoimidazole-4-) (le:1281) (re:1994) (di:direct) ECOPURCA M33928 g147410 Escherichia coli 562 -11533021 235601 purc phosphoribosylaminoimidazole-succinocarboxamide (fn:enzyme; purine ribonucleotide biosynthesis) (db:genpept-bct2) (ec:6.3.2.6) (de:escherichia coli k-12 mg1655 section 224 of 400 of the completegenome.) (nt:f237; 100 pct identical to pur7\_ecoli sw: p21155) (le:9422) (re:10135) (di:complement) AE000334 AE000334 g1788820 Escherichia coli 562 -11533021 5000690276 (de:(ecoli\_2416) (pn:phosphoribosylaminoimidazole-succinocarboxamide synthetase , saicar synthetase:phosphoribosylaminoimidazole-succinocarboxamide synthetase ) (gn:purc) (gtcfc:4.1) (ec:6.3.2.6) (pur7\_ecoli) (keggfc:4.1) (riley) ECOLI\_2416 ECOLI\_2416 Escherichia coli 562 10034463

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826180	7799	29955	264	87

#### Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826181	7800	29956	2268	755

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826189	7801	29957	348	115

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826190	7802	29958	351	116

Description

6500729164 purm:purg:b2499 phosphoribosylformylglycinamide  
cyclo-ligase:airs:phosphoribosyl-aminoimidazole synthetase:air synthase  
(gtcfc:4.1) (ec:6.3.3.1) (keggfc:4.1) (rileyfc:1.6.1) (db:gtc-escherichia  
coli) b2499 b2499 Escherichia coli 562 -11533022 126011 purm  
phosphoribosylformylglycinamide  
cyclo-ligase::5-phosphoribosyl-5-aminoimidazole synthetase  
(cl:phosphoribosylformylglycinamide  
cyclo-ligase:phosphoribosylformylglycinamide cyclo-ligase homology)  
(ec:6.3.3.1) (db:pir1.dat) (mp:54 min) AJECPC A25955 Escherichia coli 562  
-11533022 225075 purg phosphoribosylformylglycinamide cyclo-ligase  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #425(56.2-56.5  
min.)) (nt:similar to (swissprot accession number p08178)) (le:9118)  
(re:10155) (di:direct) D90878 D90878 g1805559 Escherichia coli 562 -11533022  
7500953383 purm 5-phosphoribosyl-5-aminoimidazole synthetase  
(sr:escherichia coli (strain k-12) (clone: plc1-41 and pjs16) dna)  
(db:genpept-bct1) (ec:6.3.3.1) (de:e.coli purm gene encoding  
5'-phosphoribosyl-5-aminoimidazolesynthetase, and purn gene, complete cds.)  
(le:780) (re:1817) (di:direct) ECOPURMN M13747 g147425 Escherichia coli 562  
-11533022 235610 purm phosphoribosylaminoimidazole synthetase = air  
(fn:enzyme; purine ribonucleotide biosynthesis) (db:genpept-bct2)  
(ec:6.3.3.1) (de:escherichia coli k-12 mg1655 section 226 of 400 of the  
completegenome.) (nt:o345; 99 pct identical to pur5\_ecoli sw: p08178)  
(le:5240) (re:6277) (di:direct) AE000336 AE000336 g1788845 Escherichia coli  
562 -11533022 5000690277 (de:(ecoli\_2439) (pn:phosphoribosylaminoimidazole  
synthetase , air synthetase:phosphoribosylaminoimidazole synthetase )  
(gn:purm) (gtcfc:4.1) (ec:6.3.3.1) (pur5\_ecoli) (keggfc:4.1) (rileyfc:1.6.1)  
(db:gtc-escherichia coli)) ECOLI\_2439 ECOLI\_2439 Escherichia coli 562  
10034440

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826191	7803	29959	555	184

# Description

6500729165 purn:b2500 phosphoribosylglycinamide  
myltransferase:phosphoribosylglycinamide formyltransferase:gart:gar  
transformylase:5-phosphoribosylglycinamide transformylase (gtcfc:4.1:9.6)  
(ec:2.1.2.2) (keggfc:4.1:9.8) (rileyfc:1.6.1) (db:gtc-escherichia coli)  
(gtcfc:nucleotide metabolism-purine metabolism:metabolism of cofactors and  
vitamins-biotin metabolism (b8) and folate biosynthesis) b2500 b2500  
Escherichia coli 562 -11533023 92400 purn (ec:2.1.2.2) (de:transformylase)  
(5'-phosphoribosylglycinamide transformylase)) (db:swissprot) PUR3\_ECOLI  
P08179 ESCHERICHIA COLI 562 -11533023 123291 purn phosphoribosylglycinamide  
formyltransferase (cl:phosphoribosylglycinamide  
formyltransferase:phosphoribosylglycinamide formyltransferase homology)  
(ec:2.1.2.2) (db:pir1.dat) (mp:54 min) XYECGF A28486 Escherichia coli 562  
-11533023 225076 purn phosphoribosylglycinamide formyltransferase ec  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #425(56.2-56.5  
min.)) (nt:similar to (pir accession number a28486)) (le:10155) (re:10793)  
(di:direct) D90878 D90878 g1805560 Escherichia coli 562 -11533023  
7500889050 purn (sr:escherichia coli (strain k-12) (clone: plc1-41 and  
pjs16) dna) (db:genpept-bct1) (de:e.coli purm gene encoding  
5'-phosphoribosyl-5-aminoimidazolesynthetase, and purn gene, complete cds.)  
(le:1817) (re:2455) (di:direct) ECOPURMN M13747 g147426 Escherichia coli 562  
-11533023 235611 purn phosphoribosylglycinamide formyltransferase 1  
(fn:enzyme; purine ribonucleotide biosynthesis) (db:genpept-bct2)  
(ec:2.1.2.2) (de:escherichia coli k-12 mg1655 section 226 of 400 of the  
completegenome.) (nt:o212; 99 pct identical to pur3\_ecoli sw: p08179)  
(le:6277) (re:6915) (di:direct) AE000336 AE000336 g1788846 Escherichia coli  
562 -11533023 5000690278 (de:(ecoli\_2440)  
(pn:5"-phosphoribosyl-glycinamide:gar transformylase 1) (gn:purn)  
(gtcfc:4.1:9.6) (ec:2.1.2.2) (pur3\_ecoli) (keggfc:4.1:9.8) (rileyfc:1.6.1)  
(db:gtc-escherichia coli)) ECOLI\_2440 ECOLI\_2440 Escherichia coli 562  
10034432

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826192	7804	29960	231	76

Description

6500729166 ppx:b2502 exopolyphosphatase:metaphosphatase (gtcfc:4.1:13.10) (ec:3.6.1.11) (keggfc:4.1) (rileyfc:1.1.4) (db:gtc-escherichia coli) b2502 b2502 Escherichia coli 562 -11533024 163005 ppx exopolyphosphatase:ppx (cl:exopolyphosphatase) (ec:3.6.1.11) (db:pir2.dat) A45333 A45333 Escherichia coli 562 -11533024 225078 exopolyphosphatase ppx (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #425(56.2-56.5 min.)) (nt:similar to (pir accession number a45333)) (le:13036) (re:14577) (di:direct) D90878 D90878 g1805562 Escherichia coli 562 -11533024 7500959734 ppx exopolyphosphatase (sr:escherichia coli (library:embl4-derivative of kohara) dna) (db:genpept-bct1) (de:escherichia coli exopolyphosphatase (ppx) gene, complete cds.) (le:40) (re:1581) (di:direct) ECOPPX L06129 g147343 Escherichia coli 562 -11533024 235543 ppx exopolyphosphatase (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:3.6.1.11) (de:escherichia coli k-12 mg1655 section 226 of 400 of the completegenome.) (nt:o513; 100 pct identical to ppx\_ecoli sw: p29014 but) (le:9158) (re:10699) (di:direct) AE000336 AE000336 g1788848 Escherichia coli 562 -11533024 5000690279 (de:(ecoli\_2442) (pn:exopolyphosphatase) (gn:ppx) (gtcfc:4.1) (ec:3.6.1.11) (ppx\_ecoli) (keggfc:4.1) (rileyfc:1.1.4) (db:gtc-escherichia coli)) ECOLI\_2442 ECOLI\_2442 Escherichia coli 562 10086721

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826195	7805	29961	366	121

Description

6500729167 guaa:b2507 gmp synthase:glutamine-hydrolyzing:glutamine  
amidotransferase:gmp synthetase (gtcfc:4.1:5.1) (ec:6.3.5.2)  
(keggfc:4.1:5.1) (rileyfc:1.6.1) (db:gtc-escherichia coli) b2507 b2507  
Escherichia coli 562 -11533025 74989 guaa (ec:6.3.5.2)  
(de:amidotransferase) (gmp synthetase)) (db:swissprot) GUAA\_ECOLI P04079  
ESCHERICHIA COLI 562 -11533025 126048 guaa gmp synthase  
glutamine-hydrolyzing (cl:gmp synthase (glutamine-hydrolyzing):trpg  
homology) (ec:6.3.5.2) (db:pir1.dat) (mp:54 min) SYECGU A24640 Escherichia  
coli 562 -11533025 225082 guaa gmp synthase glutamine-hydrolyzing ec  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #427(56.5-56.9  
min.)) (nt:similar to (pir accession number a24640)) (le:5796) (re:7373)  
(di:complement) D90880 D90880 g1805567 Escherichia coli 562 -11533025  
7500882839 guaa gmp synthetase (db:genpept-bct1) (ec:6.3.4.1) (de:e.coli  
guaba operon: imp dehydrogenase (guab) and gmp synthetase(guaa) genes,  
complete cds.) (le:1846) (re:3423) (di:direct) ECOGUABA M10101 g146276  
Escherichia coli 562 -11533025 234588 guaa gmp synthetase  
glutamine-hydrolyzing (fn:enzyme; purine ribonucleotide biosynthesis)  
(db:genpept-bct2) (ec:6.3.4.1) (de:escherichia coli k-12 mg1655 section 227  
of 400 of the completegenome.) (nt:f525; 100 pct identical to guaa\_ecoli sw:  
p04079) (le:1874) (re:3451) (di:complement) AE000337 AE000337 g1788854  
Escherichia coli 562 -11533025 5000690280 (de:(ecoli\_2447) (pn:gmp  
synthetase) (gn:guaa) (gtcfc:4.1:5.1) (ec:6.3.5.2) (guaa\_ecoli)  
(keggfc:4.1:5.1) (rileyfc:1.6.1) (db:gtc-escherichia coli)) ECOLI\_2447  
ECOLI\_2447 Escherichia coli 562 10017501

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826197	7806	29962	534	177

Description

6500729168 guab:b2508 inosine-5-monophosphate dehydrogenase:imp  
dehydrogenase:impdh:impd (gtcfc:4.1) (ec:1.1.1.205) (keggfc:4.1)  
(rileyfc:1.6.1) (db:gtc-escherichia coli) b2508 b2508 Escherichia coli 562  
-11533026 79298 guab:guar (ec:1.1.1.205) (de:dehydrogenase) (impdh) (impd))  
(db:swissprot) IMDH\_ECOLI P06981 ESCHERICHIA COLI 562 -11533026 7000685629  
guab imp dehydrogenase (cl:imp dehydrogenase:cbs homology) (ec:1.1.1.205)  
(db:pir1.dat) (mp:54 min) DEECIP C65027 Escherichia coli 562 -11533026  
7500884112 guab imp dehydrogenase (fn:enzyme; purine ribonucleotide  
biosynthesis) (db:genpept-bct2) (ec:1.2.1.14) (de:escherichia coli k-12  
mg1655 section 227 of 400 of the completegenome.) (nt:f488; 99 pct identical  
to imp\_ecoli sw: p06981) (le:3520) (re:4986) (di:complement) AE000337  
AE000337 g1788855 Escherichia coli 562 -11533026 5000690281  
(de:(ecoli\_2448) (pn:imp dehydrogenase) (gn:guab) (gtcfc:4.1) (ec:1.1.1.205)  
(imdh\_ecoli) (keggfc:4.1) (rileyfc:1.6.1) (db:gtc-escherichia coli))  
ECOLI\_2448 ECOLI\_2448 Escherichia coli 562 10123714

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826208	7807	29963	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826212	7808	29964	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826213	7809	29965	318	105

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826218	7810	29966	555	184

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826219	7811	29967	243	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826224	7812	29968	495	165

Description

6500729169 ndk:b2518 nucleoside diphosphate kinase:ndk:ndp kinase  
 (gtcfc:4.1:4.2) (ec:2.7.4.6) (keggfc:4.1:4.2) (rileyfc:1.6.1)  
 (db:gtc-escherichia coli) b2518 b2518 Escherichia coli 562 -11533027 164172  
 ndk nucleoside-diphosphate kinase (cl:nucleoside-diphosphate kinase)  
 (ec:2.7.4.6) (db:pir2.dat) (mp:54.2 min) JH0495 JH0495 Escherichia coli 562  
 -11533027 225094 ndk nucleoside-diphosphate kinase ec 2.7.4.6  
 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
 (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #428(56.8-57.0  
 min.)) (nt:similar to (pir accession number jh0495)) (le:3339) (re:3770)  
 (di:complement) D90881 D90881 g1799917 Escherichia coli 562 -11533027  
 225098 ndk nucleoside-diphosphate kinase ec 2.7.4.6 (sr:escherichia coli  
 (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
 (de:e.coli genomic dna, kohara clone #429(56.9-57.2 min.)) (nt:similar to  
 (pir accession number jh0495)) (le:2343) (re:2774) (di:complement) D90882  
 D90882 g1799922 Escherichia coli 562 -11533027 7500960400 ndk nucleoside  
 diphosphate kinase (db:genpept-bct1) (de:e.coli ndk gene for nucleoside  
 diphosphate kinase.) (nt:n-terminal sequence agrees with purified protein)  
 (le:181) (re:612) (di:direct) ECNDK X57555 g416172 Escherichia coli 562  
 -11533027 233474 ndk nucleoside diphosphate kinase (fn:enzyme; purine  
 ribonucleotide biosynthesis) (db:genpept-bct2) (ec:2.7.4.6) (de:escherichia  
 coli k-12 mg1655 section 228 of 400 of the completegenome.) (nt:f143; 100  
 pct identical to ndk\_ecoli sw: p24233) (le:3833) (re:4264) (di:complement)  
 AE000338 AE000338 g1788866 Escherichia coli 562 -11533027 5000690282  
 (de:(ecoli\_2458) (pn:nucleoside diphosphate kinase) (gn:ndk) (gtcfc:4.1:4.2)  
 (ec:2.7.4.6) (ndk\_ecoli) (keggfc:4.1:4.2) (rileyfc:1.6.1)  
 (db:gtc-escherichia coli)) ECOLI\_2458 ECOLI\_2458 Escherichia coli 562  
 10087208

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826227	7813	29969	669	222

#### Description

6500729170 purl:puri:b2557 phosphoribosylformylglycineamide synthetase:phosphoribosylformylglycinamidine synthetase:fgam synthetase:formylglycineamide ribotide amidotransferase:fgarat (gtcfc:4.1) (ec:6.3.5.3) (keggfc:4.1) (rileyfc:1.6.1) (db:gtc-escherichia coli) b2557 b2557 Escherichia coli 562 -11533028 7000688915 purl phosphoribosylformylglycinamidine synthetase::formylglycinamide ribonucleotide synthetase:phosphoribosylformylglycinamidine synthetase (cl:phosphoribosylformylglycinamidine synthetase) (ec:6.3.5.3) (db:pir1.dat) (mp:55 min) SYECPG D65033 Escherichia coli 562 -11533028 7500953388 purl phosphoribosylformyl-glycineamide synthetase = (fn:enzyme; purine ribonucleotide biosynthesis) (db:genpept-bct2) (ec:6.3.5.3) (de:escherichia coli k-12 mg1655 section 232 of 400 of the completegenome.) (nt:f1295; 100 pct identical to purl\_ecoli sw:) (le:2098) (re:5985) (di:complement) AE000342 AE000342 g1788909 Escherichia coli 562 -11533028 5000690283 (de:(ecoli\_2497) (pn:phosphoribosylformyl-glycineamide synthetase , fgam synthetase:phosphoribosylformyl-glycineamide synthetase ) (gn:pur1) (gtcfc:4.1) (ec:6.3.5.3) (pur1\_ecoli) (keggfc:4.1) (rileyfc:1.6.1) (db:gtc-escherichia) ECOLI\_2497 ECOLI\_2497 Escherichia coli 562 10123728

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826233	7814	29970	1023	340

#### Description

6500729171 nrde:b2675 ribonucleoside-diphosphate reductase 2 alpha chain:ribonucleotide reductase 2:rle protein (gtcfc:4.1:4.2:10.5) (ec:1.17.4.1) (keggfc:4.1:4.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2675 b2675 Escherichia coli 562 -11533029 7000691909 nrde ribonucleoside-diphosphate reductase:2 alpha chain (cl:salmonella typhimurium ribonucleoside-diphosphate reductase) (ec:1.17.4.1) (db:pir2.dat) D65047 D65047 Escherichia coli 562 -11533029 7500960452 nrde ribonucleoside-diphosphate reductase 2:alpha (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:1.17.4.1) (de:escherichia coli k-12 mg1655 section 242 of 400 of the completegenome.) (nt:o714; 100 pct identical to 310 bp fragment nrde) (le:2549) (re:4693) (di:direct) AE000352 AE000352 g1789030 Escherichia coli 562 -11533029 5000690284 (de:(ecoli\_2608) (pn:ribonucleoside diphosphate reductase 2, alpha subunit) (gn:nrde) (gtcfc:4.1:4.2) (ec:1.17.4.1) (rir3\_ecoli) (keggfc:4.1:4.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2608 ECOLI\_2608 Escherichia coli 562 10123776

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826236	7815	29971	213	70

Description

6500729172 nrdf:b2676 ribonucleoside-diphosphate reductase 2 beta chain:ribonucleotide reductase 2:r2f protein (gtcfc:4.1:4.2:10.5) (ec:1.17.4.1) (keggfc:4.1:4.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2676 b2676 Escherichia coli 562 -11533030 94473 nrdf (ec:1.17.4.1) (de:(ribonucleotide reductase 2) (r2f protein)) (db:swissprot) RIR4\_ECOLI P37146 ESCHERICHIA COLI 562 -11533030 7000686341 nrdf ribonucleoside-diphosphate reductase:2 beta chain (cl:ribonucleoside-diphosphate reductase beta) (ec:1.17.4.1) (db:pir2.dat) E65047 E65047 Escherichia coli 562 -11533030 225231 nrdf ribonucleoside-diphosphate reductase 2 beta (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #445(60.2-60.6 min.)) (nt:similar to (swissprot accession number p37146)) (le:6974) (re:7933) (di:direct) D90891 D90891 g1800064 Escherichia coli 562 -11533030 7500889810 nrdf ribonucleoside-diphosphate reductase 2:beta (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:1.17.4.1) (de:escherichia coli k-12 mg1655 section 242 of 400 of the completegenome.) (nt:o319; 100 pct identical to 110 aa) (le:4703) (re:5662) (di:direct) AE000352 AE000352 g1789031 Escherichia coli 562 -11533030 5000690285 (de:(ecoli\_2609) (pn:ribonucleotide-diphosphate reductase 2, beta chain, frag) (gn:nrdf) (gtcfc:4.1:4.2) (ec:1.17.4.1) (rir4\_ecoli) (keggfc:4.1:4.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2609 ECOLI\_2609 Escherichia coli 562 10120319

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826244	7816	29972	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826245	7817	29973	867	288

Description

6500729173 rela:b2784 gtp pyrophosphokinase:atp:gtp  
 3-pyrophosphotransferase:ppgpp synthetase i (gtcfc:4.1:10.2) (ec:2.7.6.5)  
 (keggfc:4.1) (rileyfc:2.0.0) (db:gtc-escherichia coli) b2784 b2784  
 Escherichia coli 562 -11533031 93880 rela (ec:2.7.6.5) (de:(ppgpp  
 synthetase i)) (db:swissprot) RELA\_ECOLI P11585 ESCHERICHIA COLI 562  
 -11533031 7000686295 rela gtp pyrophosphokinase::guanosine  
 3:5-polyphosphate synthase:stringent factor (cl:guanosine  
 3',5'-bis(diphosphate) 3'-pyrophosphatase) (ec:2.7.6.5) (db:pir1.dat) (mp:60  
 min) KIECG D65060 Escherichia coli 562 -11533031 7500889619 rela gtp  
 pyrophosphokinase (db:genpept-bct1) (ec:2.7.6.5) (de:escherichia coli k-12  
 genome; approximately 62 minute region.) (nt:cg site no. 306) (le:9282)  
 (re:11516) (di:complement) ECU29580 U29580 g882678 Escherichia coli 562  
 -11533031 239358 rela p ppgpp synthetase i gtp pyrophosphokinase  
 (fn:enzyme; global regulatory functions) (db:genpept-bct2) (ec:2.7.6.5)  
 (de:escherichia coli k-12 mg1655 section 252 of 400 of the completengenome.)  
 (nt:f744; 99 pct identical to rela\_ecoli sw: p11585; cg) (le:1667) (re:3901)  
 (di:complement) AE000362 AE000362 g1789147 Escherichia coli 562 -11533031  
 5000690286 (de:(ecoli\_2715) (pn:regulation of rna synthesis; stringent  
 factor;pppgpp synthetase i) (gn:rela) (gtcfc:4.1) (ec:2.7.6.5) (rela\_ecoli)  
 (keggfc:4.1) (rileyfc:2.0.0) (db:gtc-escherichia coli)) ECOLI\_2715  
 ECOLI\_2715 Escherichia coli 562 10035867

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826264	7818	29974	627	208

Description

6500729174 pnp:b3164 polynucleotide phosphorylase (gtcfc:4.1:4.2:10.2)  
 (ec:2.7.7.8) (keggfc:4.1:4.2) (rileyfc:3.1.9) (db:gtc-escherichia coli)  
 b3164 b3164 Escherichia coli 562 -11533032 236403 pnp polynucleotide  
 phosphorylase (db:genpept-bct1) (ec:2.7.7.8) (de:escherichia coli k-12  
 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no.217; different  
 start due to differences) (le:89785) (re:91989) (di:complement) ECOUW67  
 U18997 g606104 Escherichia coli 562 -11533032 7500974864 pnp polynucleotide  
 phosphorylase:cytidylate kinase (fn:enzyme; rna synthesis, modification,  
 dna) (db:genpept-bct2) (ec:2.7.7.8) (de:escherichia coli k-12 mg1655 section  
 287 of 400 of the completengenome.) (nt:f734; cg site no.217; different start  
 due) (le:5656) (re:7860) (di:complement) AE000397 AE000397 g1789555  
 Escherichia coli 562 -11533032 5000690287 (de:(ecoli\_3088)  
 (pn:polynucleotide phosphorylase) (gn:pnp) (gtcfc:4.1:4.2) (ec:2.7.7.8)  
 (pnp\_ecoli) (keggfc:4.1:4.2) (rileyfc:3.1.9) (db:gtc-escherichia coli))  
 ECOLI\_3088 ECOLI\_3088 Escherichia coli 562 -11533032 7000691889 h65106  
 (de:(pn:polyribonucleotide nucleotidyltransferase,) (gn:pnp) (ec:2.7.7.8)  
 (db:pir)) H65106 H65106 Escherichia coli 562 10123985

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826271	7819	29975	456	151

Description

6500729175 rpoa:pez:phs:sez:b3295 rpoa:dna-directed rna polymerase alpha chain:transcriptase alpha chain:rna polymerase alpha subunit (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (rileyfc:3.1.9) (db:gtc-escherichia coli) b3295 b3295 Escherichia coli 562 -11533033 238133 rpoa:pez:phs:sez (ec:2.7.7.6) (de:alpha chain) (rna polymerase alpha subunit)) (db:swissprot) RPOA\_ECOLI P00574 ESCHERICHIA COLI 562 -11533033 7502851870 rpoa:pez:phs:sez (ec:2.7.7.6) (de:alpha chain) (rna polymerase alpha subunit)) (db:swissprot) RPOA\_ECOLI P00574 SALMONELLA TYPHIMURIUM 602 -11533033 7500890598 rpoa dna-directed rna polymerase:alpha chain:transcriptase alpha chain (cl:dna-directed rna polymerase alpha chain) (ec:2.7.7.6) (db:pir1.dat) (mp:72 min) RNECA A22884 Escherichia coli 562 -11533033 139062 rpoa dna-directed rna polymerase:alpha chain (cl:dna-directed rna polymerase alpha chain) (ec:2.7.7.6) (db:pir2.dat) A41658 A41658 Salmonella typhimurium 602 -11533033 235879 rpoa (sr:escherichia coli dna, clones phr14 and phr15 (2)) (db:genpept-bct1) (de:e.coli alpha ribosomal protein operon (rpoa, rplq, and rpsd) genes coding for rna polymerase alpha subunit and ribosomal proteins l17 and s4.) (nt:rna polymerase alpha subunit) (... ECORPOA J01685 g147715 Escherichia coli 562 -11533033 236528 rpoa (fn:rna polymerase, alpha-subunit) (db:genpept-bct1) (ec:2.7.7.6) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 234) (le:220788) (re:221777) (di:complement) ECOUW67 U18997 g606229 Escherichia coli 562 -11533033 5000690288 (db:genpept-bct1) (de:e.coli rpoa-rplq dna for rna-polymerase alpha subunit and ribosomal component l17.) (nt:rna polymerase alpha subunit) (le:10) (re:999) (di:direct) ECRPOA X00766 g42807 Escherichia coli 562 -11533033 264471 rpoa rna polymerase alpha-subunit (sr:salmonella typhimurium (strain lt2) dna) (db:genpept-bct1) (de:salmonella typhimurium rna polymerase alpha subunit (rpoa) gene, complete cds.) (le:36) (re:1025) (di:direct) STYRPOA M77750 g154353 Salmonella typhimurium 602 -11533033 7500890599 rpoa rna polymerase:alpha subunit (fn:enzyme; rna synthesis, modification, dna) (db:genpept-bct2) (ec:2.7.7.6) (de:escherichia coli k-12 mg1655 section 297 of 400 of the complete genome.) (nt:f329; cg site no. 234; 100 pct identical amino) (le:8110) (re:9099) (di:complement) AE000407 AE000407 g1789690 Escherichia coli 562 -11533033 96168 rpoa:pez:phs:sez (ec:2.7.7.6) (de:alpha chain) (rna polymerase alpha subunit)) (db:swissprot) RPOA\_ECOLI P00574 ESCHERICHIA COLI 562 -11533033 7502851871 rpoa:pez:phs:sez (ec:2.7.7.6) (de:alpha chain) (rna polymerase alpha subunit)) (db:swissprot) RPOA\_ECOLI P00574 SALMONELLA TYPHIMURIUM 602 -11533033 96169 rpoa:pez:phs:sez (ec:2.7.7.6) (de:alpha chain) (rna polymerase alpha subunit)) (db:swissprot) RPOA\_ECOLI P00574 ESCHERICHIA COLI 562 -11533033 7502851872 rpoa:pez:phs:sez (ec:2.7.7.6) (de:alpha chain) (rna polymerase alpha subunit)) (db:swissprot) RPOA\_ECOLI P00574 SALMONELLA TYPHIMURIUM 602 -11533033 123918 rpoa dna-directed rna polymerase:alpha chain (cl:dna-directed rna polymerase alpha chain) (ec:2.7.7.6) (db:pir) A41658 A41658 Salmonella typhimurium 602 -11533033

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826279	7820	29976	2283	760
<u>Description</u>				
6500729176 rpoh:htpr:hin:fam:b3461 rna polymerase sigma-32 subunit:rna polymerase sigma-32 factor:heat shock regulatory protein f33.4 (gtcfc:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (rileyfc:2.0.0) (db:gtc-escherichia coli) b3461 b3461 Escherichia coli 562 -11533034 95942 rpoh:htpr:hin:fam (de:rna polymerase sigma-32 factor (heat shock regulatory protein f33.4)) (db:swissprot) RP32_ECOLI P00580 ESCHERICHIA COLI 562 -11533034 7000686441 rpoh:htpr transcription initiation factor sigma 32:heat shock regulatory protein (cl:transcription initiation factor sigma katf:transcription initiation factor sigma katf homology) (db:pir1.dat) (mp:76 min) RGECH H65142 Escherichia coli 562 -11533034 236696 (sr:e.coli k12 dna) (db:genpept-bct1) (de:e.coli rpoh gene encoding rna polymerase sigma-32 subunit, completecds.) (nt:rna polymerase sigma-32 subunit) (le:132) (re:986) (di:direct) ECORPOH M20668 g147732 Escherichia coli 562 -11533034 7500890503 rpoh rna polymerase sigma-32 subunit (sr:escherichia coli (sub_strain mgl655, strain k-12) (library: lambda) (db:genpept-bct1) (ec:2.7.7.6) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 618; alternate names fam, hin, htpr;) (le:14191) (re:15045) (di:complement) ECOUW76 U00039 g466597 Escherichia coli 562 -11533034 235889 rpoh rna polymerase:sigma 32 factor:regulation of (fn:factor; global regulatory functions) (db:genpept-bct2) (ec:2.7.7.6) (de:escherichia coli k-12 mgl655 section 312 of 400 of the completegenome.) (nt:f284; 100 pct identical to rp32_ecoli sw: p00580;) (le:2049) (re:2903) (di:complement) AE000422 AE000422 g1789871 Escherichia coli 562 -11533034 5000690289 (de:(ecoli_3379) (pn:rna polymerase, sigma:32 subunit; regulation of proteins induced at high temperatures) (gn:rpoh) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rp32_ecoli) (keggfc:4.1:4.2) (rileyfc:2.0.0) (db:gtc-escherichia coli)) ECOLI_3379 ECOLI_3379 Escherichia coli 562 10037888				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826285	7821	29977	429	142

Description

6500729177 gmk:spor:b3648 5guanylate kinase:guanylate kinase:gmp kinase  
 (gtcfc:4.1) (ec:2.7.4.8) (keggfc:4.1) (rileyfc:1.6.1) (db:gtc-escherichia  
 coli) b3648 b3648 Escherichia coli 562 -11533035 80655 gmk:spor  
 (ec:2.7.4.8) (de:guanylate kinase, (gmp kinase)) (db:swissprot) KGUA\_ECOLI  
 P24234 ESCHERICHIA COLI 562 -11533035 123898 gmk guanylate kinase  
 (cl:guanylate kinase:guanylate kinase homology) (ec:2.7.4.8) (db:pir1.dat)  
 KIECGU S43041 Escherichia coli 562 -11533035 236886 gmk gmp kinase  
 (db:genpept-bct1) (ec:2.7.4.8) (de:escherichia coli 5'guanylate kinase (gmk)  
 gene, complete cds.) (le:908) (re:1531) (di:direct) ECOGMK M84400 g146230  
 Escherichia coli 562 -11533035 7500884602 gmk 5guanylate kinase  
 (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52)  
 (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.)  
 (nt:alternate gene name spor) (le:10820) (re:11443) (di:direct) ECOUW82  
 L10328 g290498 Escherichia coli 562 -11533035 234555 gmk guanylate kinase  
 (fn:enzyme; purine ribonucleotide biosynthesis) (db:genpept-bct2)  
 (de:escherichia coli k-12 mg1655 section 332 of 400 of the completengenome.)  
 (nt:o207; alternate gene name spor) (le:2819) (re:3442) (di:direct) AE000442  
 AE000442 g1790080 Escherichia coli 562 -11533035 5000690290  
 (de:(ecoli\_3568) (pn:guanylate kinase) (gn:gmk) (gtcfc:4.1) (ec:2.7.4.8)  
 (kgua\_ecoli) (keggfc:4.1) (rileyfc:1.6.1) (db:gtc-escherichia coli))  
 ECOLI\_3568 ECOLI\_3568 Escherichia coli 562 10022896

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826302	7822	29978	237	78

Description

6500729178 rpoz:b3649 dna-directed rna polymerase omega chain:transcriptase omega chain:rna polymerase omega subunit (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (rileyfc:3.1.9) (db:gtc-escherichia coli) b3649 b3649 Escherichia coli 562 -11533036 96309 rpoz (ec:2.7.7.6) (de:omega chain) (rna polymerase omega subunit)) (db:swissprot) RPOZ\_ECOLI P08374 ESCHERICHIA COLI 562 -11533036 123965 rpoz dna-directed rna polymerase:omega chain:transcriptase omega chain (cl:dna-directed rna polymerase omega chain) (ec:2.7.7.6) (db:pir1.dat) (mp:82 min) RNECO A29038 Escherichia coli 562 -11533036 236024 (sr:e.coli dna, clone pdrg4) (db:genpept-bct1) (de:escherichia coli rpoz gene encoding omega protein, complete cds.) (nt:omega protein) (le:346) (re:621) (di:direct) ECOOMEGA M15266 g146978 Escherichia coli 562 -11533036 236887 rpoz omega protein (sr:e. coli (strain k-12) dna, clone pga1) (db:genpept-bct1) (de:e. coli spot gene encoding (p)ppgpp 3'-pyrophosphohydrolase, omega(rpoz) protein genes, complete cds.) (le:67) (re:342) (di:direct) ECOSPOT M24503 g147864 Escherichia coli 562 -11533036 7500890674 rpoz rna polymerase omega subunit (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:11498) (re:11773) (di:direct) ECOUW82 L10328 g290499 Escherichia coli 562 -11533036 235261 rpoz rna polymerase:omega subunit (fn:enzyme; rna synthesis, modification, dna) (db:genpept-bct2) (ec:2.7.7.6) (de:escherichia coli k-12 mg1655 section 332 of 400 of the completegenome.) (nt:o91; 100 pct identical amino acid sequence and) (le:3497) (re:3772) (di:direct) AE000442 AE000442 g1790081 Escherichia coli 562 -11533036 5000690291 (de:(ecoli\_3569) (pn:rna polymerase, omega subunit) (gn:rpoz) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rpoz\_ecoli) (keggfc:4.1:4.2) (rileyfc:3.1.9) (db:gtc-escherichia coli)) ECOLI\_3569 ECOLI\_3569 Escherichia coli 562 10038252

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826303	7823	29979	294	97

Description

GTC ORF with score 148 to: (sr:plasmid ptrab4) (db:genpept-bct1) (de:agrobacterium vitis plasmid ptrab4 putative lysr-type protein(ttua), putative tartrate transport protein (ttub), putativetartrate dehydrogenase (ttuc), putative hydroxypyruvate ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826305	7824	29980	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826309	7825	29981	201	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826327	7826	29982	630	209

Description

6500729179 spot:b3650 diphosphate 3-pyrophosphohydrolase:cg site no.  
156:guanosine-3:5-bis:diphosphate  
3-pyrophosphohydrolase:ppgppase:penta-phosphate  
guanosine-3-pyrophosphohydrolase (gtcfc:4.1:10.2) (ec:3.1.7.2) (keggfc:4.1)  
(rileyfc:2.0.0) (db:gtc-escherichia coli) b3650 b3650 Escherichia coli 562  
-11533037 99298 spot (ec:3.1.7.2) (de:((ppgpp)ase) (penta-phosphate  
guanosine-3'-pyrophosphohydrolase)) (db:swissprot) SPOT\_ECOLI P17580  
ESCHERICHIA COLI 562 -11533037 124357 spot guanosine 3:5-bis diphosphate  
3-pyrophosphatase::ppgpp ase (cl:guanosine 3',5'-bis(diphosphate)  
3'-pyrophosphatase) (ec:3.1.7.2) (db:pirl.dat) (mp:82 min) SHECGD B30374  
Escherichia coli 562 -11533037 236888 spot p ppgpp 3-pyrophosphohydrolase  
(sr:e. coli (strain k-12) dna, clone pgal) (db:genpept-bct1) (de:e. coli  
spot gene encoding (p)ppgpp 3'-pyrophosphohydrolase, omega(rpoz) protein  
genes, complete cds.) (nt:ttg start) (le:361) (re:2469) (di:direct) ECOSPOT  
M24503 g551840 Escherichia coli 562 -11533037 7500891988 spot::cg site no.  
156 p ppgpp 3-pyrophosphohydrolase (sr:escherichia coli k12 strain mg1655;  
lambda clones ecl4-52) (db:genpept-bct1) (de:e. coli; the region from 81.5  
to 84.5 minutes.) (le:11792) (re:13900) (di:direct) ECOUW82 L10328 g290500  
Escherichia coli 562 -11533037 236025 spot p ppgpp synthetase ii:also  
guanosine-3:5-bis (fn:enzyme; global regulatory functions) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 332 of 400 of the completegenome.)  
(nt:o702; 100 pct identical amino acid sequence and) (le:3791) (re:5899)  
(di:direct) AE000442 AE000442 g1790082 Escherichia coli 562 -11533037  
5000690292 (de:(ecoli\_3570) (pn:pppgpp synthetase ii; also  
guanosine-3"-5"-bis pyrophosphate, 3"-pyrophosphohydrolase::pppgpp  
synthetase ii; also guanosine-3",5"-bis pyrophosphate  
3"-pyrophosphohydrolase) (gn:spot) (gtcfc:4.1) (ec:2.7.6.5) (sp) ECOLI\_3570  
ECOLI\_3570 Escherichia coli 562 10041157

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826331	7827	29983	309	102

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826346	7828	29984	399	132
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826351	7829	29985	963	320
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826359	7830	29986	249	82
<u>Description</u>				

6500729180 yicp:b3665 probable adenine deaminase:adenase:adenine aminase (gtcfc:4.1) (ec:3.5.4.2) (keggfc:4.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3665 b3665 Escherichia coli 562 -11533038 58619 yicp (ec:3.5.4.2) (de:probable adenine deaminase, (adenase) (adenine aminase)) (db:swissprot) ADEC\_ECOLI P31441 ESCHERICHIA COLI 562 -11533038 7000684527 yicp probable adenine deaminase (cl:adenine deaminase adec) (ec:3.5.4.2) (db:pir2.dat) B65168 B65168 Escherichia coli 562 -11533038 7500876570 yicp probable adenine deaminase synthesis xanthine (fn:putative enzyme; purine ribonucleotide) (db:genpept-bct2) (ec:3.5.4.2) (de:escherichia coli k-12 mg1655 section 334 of 400 of the completegenome.) (nt:o588; 100 pct identical amino acid sequence and) (le:3778) (re:5544) (di:direct) AE000444 AE000444 g1790098 Escherichia coli 562 -11533038 5000690293 (de:(ecoli\_3584) (pn:probable adenine deaminase:adenase:adenine aminase) (gn:yicp) (gtcfc:4.1) (ec:3.5.4.2) (adec\_ecoli) (keggfc:4.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_3584 ECOLI\_3584 Escherichia coli 562 10124060

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826363	7831	29987	273	90
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826370	7832	29988	270	89
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826373	7833	29989	810	270

Description

6500729181 dnan:b3701 dna polymerase iii beta-subunit:dna polymerase  
 iii:beta chain (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2)  
 (rileyfc:3.1.7) (db:gtc-escherichia coli) b3701 b3701 Escherichia coli 562  
 -11533039 69056 dnan (ec:2.7.7.7) (de:dna polymerase iii, beta chain,)  
 (db:swissprot) DP3B\_ECOLI P00583 ESCHERICHIA COLI 562 -11533039 124037 dnan  
 dna-directed dna polymerase:iii beta chain (cl:dna-directed dna polymerase  
 iii beta chain) (ec:2.7.7.7) (db:pir1.dat) (mp:83 min) DJEC3B A91510  
 Escherichia coli 562 -11533039 236937 dnan (sr:escherichia coli (strain  
 k-12) (clone: ptc884 .) dna; escherichi) (db:genpept-bct1) (de:e.coli dnaa  
 operon: dnaa, dnan, and rpmh genes coding for dnaaprotein, dna polymerase  
 iii beta subunit, and ribosomal proteinl34.) (nt:dna polymerase iii  
 beta-s... ECODNAAOP J01602 g145761 Escherichia coli 562 -11533039  
 7500880548 dnan::cg site no. 842 dna polymerase iii beta-subunit  
 (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52)  
 (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.)  
 (le:70618) (re:71718) (di:complement) ECOUW82 L10328 g290549 Escherichia  
 coli 562 -11533039 234180 dnan dna polymerase iii:beta-subunit (fn:enzyme;  
 dna - replication, repair,) (db:genpept-bct2) (ec:2.7.7.7) (de:escherichia  
 coli k-12 mg1655 section 337 of 400 of the completegenome.) (nt:f366; 100  
 pct identical amino acid sequence and) (le:4234) (re:5334) (di:complement)  
 AE000447 AE000447 g1790136 Escherichia coli 562 -11533039 5000690294  
 (de:(ecoli\_3619) (pn:dna polymerase iii, beta-subunit) (gn:dnan)  
 (gtcfc:4.1:4.2) (ec:2.7.7.7) (dp3b\_ecoli) (keggfc:4.1:4.2) (rileyfc:3.1.7)  
 (db:gtc-escherichia coli)) ECOLI\_3619 ECOLI\_3619 Escherichia coli 562  
 10011639

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826390	7834	29990	375	125

Description

6500729182 gppa:b3779 guanosine  
pentaphosphatase:guanosine-5-triphosphate:3-diphosphate  
pyrophosphatase:guanosine pentaphosphate  
phosphohydrolase:pppgpp-5-phosphohydrolase (gtcfc:4.1:10.2) (ec:3.6.1.40)  
(keggfc:4.1) (rileyfc:2.0.0) (db:gtc-escherichia coli) b3779 b3779  
Escherichia coli 562 -11533040 74368 gppa (ec:3.6.1.40)  
(de:5'-phosphohydrolase)) (db:swissprot) GPPA\_ECOLI P25552 ESCHERICHIA COLI  
562 -11533040 163004 gppa  
exopolyphosphatase::guanosine-5-triphosphate:3-diphosphate pyrophosphatase  
guanosine pentaphosphatase (cl:exopolyphosphatase) (ec:3.6.1.11)  
(db:pir2.dat) A48285 A48285 Escherichia coli 562 -11533040 7500882667  
gppa::cgsc no. 664 guanosine pentaphosphatase (db:genpept-bct1) (de:e. coli  
genomic sequence of the region from 84.5 to 86.5 minutes.) (le:15873)  
(re:17357) (di:complement) ECOUW85 M87049 g148183 Escherichia coli 562  
-11533040 237008 gppa guanosine pentaphosphatase:exopolyphosphatase  
(fn:enzyme; global regulatory functions) (db:genpept-bct2) (de:escherichia  
coli k-12 mg1655 section 344 of 400 of the completegenome.) (nt:f494; 100  
pct identical to gppa\_ecoli sw: p25552) (le:4830) (re:6314) (di:complement)  
AE000454 AE000454 g1790213 Escherichia coli 562 -11533040 5000690295  
(de:(ecoli\_3689) (pn:guanosine pentaphosphatase ; exopolyphosphatase)  
(gn:gppa) (gtcfc:4.1) (ec:3.6.1.11) (gppa\_ecoli) (keggfc:4.1)  
(rileyfc:2.0.0) (db:gtc-escherichia coli)) ECOLI\_3689 ECOLI\_3689 Escherichia  
coli 562 10016885

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826391	7835	29991	1092	363

Description

6500729183 cyaa:cya:b3806 adenylate cyclase:atp pyrophosphate-lyase:adenylyl  
cyclase (gtcfc:4.1:10.2) (ec:4.6.1.1) (keggfc:4.1) (rileyfc:2.0.0)  
(db:gtc-escherichia coli) b3806 b3806 Escherichia coli 562 -11533041  
7000688900 cyaa adenylate cyclase (cl:adenylate cyclase) (ec:4.6.1.1)  
(db:pir1.dat) (mp:85 min) OYEC G65184 Escherichia coli 562 -11533041  
7500953348 cyaa::cgsc no. 902 adenylate cyclase (db:genpept-bct1) (de:e.  
coli genomic sequence of the region from 84.5 to 86.5 minutes.) (nt:unusual  
ttg start) (le:44265) (re:46811) (di:direct) ECOUW85 M87049 g148205  
Escherichia coli 562 -11533041 237030 cyaa adenylate cyclase (fn:enzyme;  
global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12  
mg1655 section 346 of 400 of the completegenome.) (nt:o848; ttg start; cgsc  
no. 902) (le:8295) (re:10841) (di:direct) AE000456 AE000456 g1790238  
Escherichia coli 562 -11533041 5000690296 (de:(ecoli\_3712) (pn:adenylate  
cyclase) (gn:cyaa) (gtcfc:4.1) (ec:4.6.1.1) (cyaa\_ecoli) (keggfc:4.1)  
(rileyfc:2.0.0) (db:gtc-escherichia coli)) ECOLI\_3712 ECOLI\_3712 Escherichia  
coli 562 10124101

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826405	7836	29992	312	103

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826407	7837	29993	201	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826424	7838	29994	567	188

Description

GTC ORF with score 327 to: (fn:probable transporter of sugars across plasma)  
(sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces  
cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208)  
(re:1818) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826429	7839	29995	795	264
<u>Description</u>				
6500729184 pola:resa:b3863 dna polymerase i:pol i (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b3863 b3863 Escherichia coli 562 -11533042 7500880573 pola:resa (ec:2.7.7.7) (de:dna polymerase i, (pol i)) (db:swissprot) DPO1_ECOLI P00582 ESCHERICHIA COLI 562 -11533042 124030 pola dna-directed dna polymerase:i (cl:dna-directed dna polymerase i) (ec:2.7.7.7) (db:pir1.dat) (mp:84 min) DJECI A92360 Escherichia coli 562 -11533042 237083 pola dna polymerase i (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli k12 pola gene coding for dna polymerase i, complete cds.) (le:301) (re:3087) (di:direct) ECOPOLA J01663 g147312 Escherichia coli 562 -11533042 237858 pola dna polymerase i (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 375) (le:8606) (re:11392) (di:direct) ECOUW87 L19201 g304969 Escherichia coli 562 -11533042 5000690297 (db:genpept-bct1) (de:e. coli gene pola coding for dna polymerase i.) (nt:dna polymerase i) (le:301) (re:3087) (di:direct) ECPOLA V00317 g42461 Escherichia coli 562 -11533042 235513 pola dna polymerase i:3 --5 polymerase:5 -- (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:2.7.7.7) (de:escherichia coli k-12 mg1655 section 351 of 400 of the completegenome.) (nt:o928; 100 pct identical to dpol_ecoli sw: p00582;) (le:9565) (re:12351) (di:direct) AE000461 AE000461 g1790294 Escherichia coli 562 -11533042 69100 pola:resa (ec:2.7.7.7) (de:dna polymerase i, (pol i)) (db:swissprot) DPO1_ECOLI P00582 ESCHERICHIA COLI 562 -11533042				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826431	7840	29996	249	82

Description

6500729185 rpob:gron:nitb:rif:ron:stl:stv:tabd:b3987 dna-directed rna polymerase:beta-subunit:dna-directed rna polymerase beta chain:transcriptase beta chain:rna polymerase beta subunit (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (rileyfc:3.1.9) (db:gtc-escherichia coli) b3987 b3987 Escherichia coli 562 -11533043 96192 rpob:gron:nitb:rif:ron:stl:stv:tabd (ec:2.7.7.6) (de:beta chain) (rna polymerase beta subunit)) (db:swissprot) RPOB\_ECOLI P00575 ESCHERICHIA COLI 562 -11533043 7000686461 rpob dna-directed rna polymerase:beta chain:transcriptase beta chain (cl:dna-directed rna polymerase beta chain) (ec:2.7.7.6) (db:pir1.dat) (mp:90 min) RNECB F65205 Escherichia coli 562 -11533043 7500890616 rpob rna polymerase beta subunit (db:genpept-bct1) (ec:2.7.7.6) (de:escherichia coli rna polymerase beta subunit (rpob) gene, completecds.) (le:57) (re:4085) (di:direct) ECU76222 U76222 g1666534 Escherichia coli 562 -11533043 240027 rpob rna polymerase:beta subunit (fn:enzyme; rna synthesis, modification, dna) (db:genpept-bct2) (ec:2.7.7.6) (de:escherichia coli k-12 mg1655 section 362 of 400 of the completegenome.) (nt:o1342; 99 pct identical amino acid sequence and) (le:6208) (re:10236) (di:direct) AE000472 AE000472 g1790419 Escherichia coli 562 -11533043 5000690298 (de:(ecoli\_3877) (pn:rna polymerase, beta subunit) (gn:rpob) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rpob\_ecoli) (keggfc:4.1:4.2) (rileyfc:3.1.9) (db:gtc-escherichia coli)) ECOLI\_3877 ECOLI\_3877 Escherichia coli 562 10124125

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826438	7841	29997	270	89

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826440	7842	29998	1905	634

Description

6500729186 rpoc:tabb:b3988 dna-directed rna  
polymerase:beta-subunit:dna-directed rna polymerase beta chain:transcriptase  
beta chain:rna polymerase beta subunit (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6)  
(keggfc:4.1:4.2) (rileyfc:3.1.9) (db:gtc-escherichia coli) b3988 b3988  
Escherichia coli 562 -11533044 96226 rpoc:tabb (ec:2.7.7.6) (de:beta'  
chain) (rna polymerase beta' subunit)) (db:swissprot) RPOC\_ECOLI P00577  
ESCHERICHIA COLI 562 -11533044 123939 rpoc dna-directed rna polymerase:beta  
chain:transcriptase beta chain (cl:escherichia coli dna-directed rna  
polymerase beta' chain) (ec:2.7.7.6) (db:pir1.dat) (mp:90 min) RNECC A00695  
Escherichia coli 562 -11533044 7500890627 (db:genpept-bct1) (ec:2.7.7.6)  
(de:e. coli operon rpobc coding for the beta- and beta'-subunits of  
rnapolymerase (genes rpoc and rpob), and genes rp11, rlpj, rpla, andrplk  
coding for 50s ribosomal subunit proteins 17/112, 110, 11, and111,  
respectively.... ECRPOBC V00339 g581221 Escherichia coli 562 -11533044  
238142 rpoc rna polymerase:beta prime subunit (fn:enzyme; rna synthesis,  
modification, dna) (db:genpept-bct2) (ec:2.7.7.6) (de:escherichia coli k-12  
mg1655 section 362 of 400 of the completegenome.) (nt:o1407; 99 pct  
identical amino acid sequence and) (le:10313) (re:14536) (di:direct)  
AE000472 AE000472 g2367335 Escherichia coli 562 -11533044

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826451	7843	29999	1923	640

Description

6500729187 purd:b4005 phosphoribosylglycineamide  
synthetase:phosphoribosylamine--glycine ligase:gars:glycinamide  
ribonucleotide synthetase:phosphoribosylglycinamide synthetase (gtcfc:4.1)  
(ec:6.3.4.13) (keggfc:4.1) (rileyfc:1.6.1) (db:gtc-escherichia coli) b4005  
b4005 Escherichia coli 562 -11533045 237967 purd (ec:6.3.4.13)  
(de:ribonucleotide synthetase) (phosphoribosylglycinamide synthetase))  
(db:swissprot) PUR2\_ECOLI P15640 ESCHERICHIA COLI 562 -11533045 126038 purd  
phosphoribosylamine--glycine ligase::glycinamide ribonucleotide synthetase  
(cl:phosphoribosylamine--glycine ligase:phosphoribosylamine--glycine ligase  
homology) (ec:6.3.4.13) (db:pir1.dat) (mp:90 min) AJECQG A33771 Escherichia  
coli 562 -11533045 5000690300 purd purd gene product (db:genpept-bct1)  
(de:e. coli purhd operon for aicar transformylase-imp cyclohydrolase(ec  
2.1.2.3) and gar synthetase (ec 6.3.4.13).) (le:1859) (re:3148) (di:direct)  
ECPURHD X51950 g42596 Escherichia coli 562 -11533045 237215 purd  
phosphoribosylglycinamide synthetase = gar (fn:enzyme; purine ribonucleotide  
biosynthesis) (db:genpept-bct2) (ec:6.3.4.13) (de:escherichia coli k-12  
mg1655 section 363 of 400 of the completegenome.) (nt:f429; 100 pct  
identical to pur2\_ecoli sw: p15640;) (le:15004) (re:16293) (di:complement)  
AE000473 AE000473 g1790438 Escherichia coli 562 -11533045 7500889035 purd  
phosphoribosylglycineamide synthetase (sr:escherichia coli (sub\_strain  
mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (ec:6.3.4.13)  
(de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no.  
342) (le:69883) (re:71172) (di:complement) ECOUW89 U00006 g396344  
Escherichia coli 562 -11533045 92391 purd (ec:6.3.4.13) (de:ribonucleotide  
synthetase) (phosphoribosylglycinamide synthetase)) (db:swissprot)  
PUR2\_ECOLI P15640 ESCHERICHIA COLI 562 -11533045

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826472	7844	30000	1359	452

Description

6500729188 purh:b4006 phosphoribosylaminoimidazolecarboxamide  
formyltransferase and imp cyclohydrolase:bifunctional  
enzyme:phosphoribosylaminoimidazolecarboxamide formyltransferase:aicar  
transformylase / imp cyclohydrolase:inosinase:imp synthetase:atic  
(gtcfc:4.1:9.6) (keggfc:4.1:9.8) (rileyfc:1.6.1) (db:gtc-escherichia coli)  
(gtcfc:nucleotide metabolism-purine metabolism:metabolism of cofactors and  
vitamins-biotin metabolism (b8) and folate biosynthesis) b4006 b4006  
Escherichia coli 562 -11533046 237966 purh (ec:2.1.2.3:3.5.4.10)  
(de:(inosinase) (imp synthetase) (atic)) (db:swissprot) PUR9\_ECOLI P15639  
ESCHERICHIA COLI 562 -11533046 123295 purh:purj purh bifunctional enzyme  
(cl:purh bifunctional enzyme) (db:pir1.dat) (mp:90 min) DTECPH B34193  
Escherichia coli 562 -11533046 237216 (sr:e.coli (k12, isolate w3110) dna,  
clone lambda-9b9) (db:genpept-bct1) (de:e.coli 5-phosphoribosylglycinamide  
synthetase (purh) and 5-phosphoribosyl 5-aminoimidazole-4-carboxamide  
transformylase (purh) genes, complete cds.) (nt:purh (ec 2.1.2.3)) (le:3...  
ECOPURHD J05126 g147420 Escherichia coli 562 -11533046 5000690301 purh purh  
gene product (db:genpept-bct1) (de:e. coli purhd operon for aicar  
transformylase-imp cyclohydrolase(ec 2.1.2.3) and gar synthetase (ec  
6.3.4.13).) (le:258) (re:1847) (di:direct) ECPURHD X51950 g42595 Escherichia  
coli 562 -11533046 235607 purh  
phosphoribosylaminoimidazolecarboxamideformyltra (fn:enzyme; purine  
ribonucleotide biosynthesis) (db:genpept-bct2) (ec:2.1.2.3:3.5.4.10)  
(de:escherichia coli k-12 mg1655 section 363 of 400 of the completegenome.)  
(nt:f529; 100 pct identical to pur9\_ecoli sw: p15639;) (le:16305) (re:17894)  
(di:complem... AE000473 AE000473 g1790439 Escherichia coli 562 -11533046  
7500889079 purh phosphoribosylaminoimidazolecarboxamide (sr:escherichia  
coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2)  
(ec:2.1.2.3:3.5.4.10) (de:e. coli chromosomal region from 89.2 to 92.8  
minutes.) (nt:cg site no. 338) (le:71184) (re:72773) (di:complement) ECOUW89  
U00006 g396345 Escherichia coli 562 -11533046 92447 purh  
(ec:2.1.2.3:3.5.4.10) (de:(inosinase) (imp synthetase) (atic))  
(db:swissprot) PUR9\_ECOLI P15639 ESCHERICHIA COLI 562 -11533046

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826475	7845	30001	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826505	7846	30002	306	101

Description

6500729189 pura:adek:b4177 adenylosuccinate synthetase:imp--aspartate ligase (gtcfc:4.1:5.2) (ec:6.3.4.4) (keggfc:4.1:5.2) (rileyfc:1.6.1) (db:gtc-escherichia coli) b4177 b4177 Escherichia coli 562 -11533047 142415 pura adenylosuccinate synthase::imp--aspartate ligase (cl:adenylosuccinate synthase) (ec:6.3.4.4) (db:pir1.dat) (mp:95 min) AJECDS S56402 Escherichia coli 562 -11533047 7500953386 pura adenylosuccinate synthetase (db:genpept-bct1) (ec:6.3.4.4) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 345; alternate gene names adek, ad4) (le:95515) (re:96813) (di:direct) ECOUW93 U14003 g537018 Escherichia coli 562 -11533047 237382 pura adenylosuccinate synthetase (fn:enzyme; purine ribonucleotide biosynthesis) (db:genpept-bct2) (ec:6.3.4.4) (de:escherichia coli k-12 mg1655 section 380 of 400 of the completegenome.) (nt:o432; 100 pct identical to pura\_ecoli sw: p12283;) (le:371) (re:1669) (di:direct) AE000490 AE000490 g1790620 Escherichia coli 562 -11533047 5000690302 (de:(ecoli\_4060) (pn:adenylosuccinate synthetase) (gn:pura) (gtcfc:4.1:5.2) (ec:6.3.4.4) (pura\_ecoli) (keggfc:4.1:5.2) (rileyfc:1.6.1) (db:gtc-escherichia coli)) ECOLI\_4060 ECOLI\_4060 Escherichia coli 562 10066519

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826506	7847	30003	297	98

Description

6500729190 nrdd:b4238 anaerobic ribonucleoside-triphosphate reductase  
 (gtcfc:4.1:4.2) (ec:1.17.4.2) (keggfc:4.1:4.2) (rileyfc:1.6.3)  
 (db:gtc-escherichia coli) (rileyfc:small-molecule metabolism,  
 2'-deoxyribonucleotide metabolism) b4238 b4238 Escherichia coli 562  
 -11533048 123179 nrdd ribonucleoside-triphosphate  
 reductase:oxygen-sensitive::anaerobic ribonucleotide reductase  
 (cl:escherichia coli oxygen-sensitive ribonucleoside-triphosphate  
 reductase:oxygen-sensitive ribonucleoside-triphosphate reductase  
 carboxyl-terminal homology:oxygen-sensitive ribonucleoside-triphosphate  
 reductase middle homology:rubredoxin homology) (e... A47331 A47331  
 Escherichia coli 562 -11533048 7500953221 nrdd ribonucleoside triphosphate  
 reductase (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region  
 from 92.8 to 00.1 minutes.) (le:151351) (re:153489) (di:complement) ECOUW93  
 U14003 g537080 Escherichia coli 562 -11533048 237444 nrdd anaerobic  
 ribonucleoside-triphosphate reductase (fn:enzyme; 2'-deoxyribonucleotide  
 metabolism) (db:genpept-bct2) (ec:1.17.4.2) (de:escherichia coli k-12 mg1655  
 section 385 of 400 of the completegenome.) (nt:f712; 99 pct identical amino  
 acid sequence and) (le:1164) (re:3302) (di:complement) AE000495 AE000495  
 g1790686 Escherichia coli 562 -11533048 5000690303 (de:(ecoli\_4121)  
 (pn:anaerobic ribonucleoside-triphosphate reductase) (gn:nrdd)  
 (gtcfc:4.1:4.2) (ec:1.17.4.2) (nrdd\_ecoli) (keggfc:4.1:4.2) (rileyfc:1.6.3)  
 (db:gtc-escherichia coli)) ECOLI\_4121 ECOLI\_4121 Escherichia coli 562  
 10065750

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826507	7848	30004	597	198

Description

6500729191 holc:b4259 dna polymerase iii chi subunit:dna polymerase iii:chi subunit (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b4259 b4259 Escherichia coli 562 -11533049 233988 holc (ec:2.7.7.7) (de:dna polymerase iii, chi subunit,) (db:swissprot) HOLC\_ECOLI P28905 ESCHERICHIA COLI 562 -11533049 162954 holc dna-directed dna polymerase:iii chi chain:dna polymerase iii chi chain (ec:2.7.7.7) (db:pir2.dat) (mp:96.5 min) A46739 A46739 Escherichia coli 562 -11533049 5000690304 holc dna polymerase iii holoenzyme chi subunit (db:genpept-bct1) (de:e.coli holc gene encoding chi subunit of dna polymerase iiiholoenzyme.) (le:211) (re:654) (di:direct) ECHOLCG Z14155 g41740 Escherichia coli 562 -11533049 237465 holc dna polymerase iii chi subunit (sr:escherichia coli (strain k-12) (tissue library: lamda-phage of y) (db:genpept-bct1) (de:escherichia coli (clone puc-chi) dna polymerase iii chi subunit(holc) gene, complete cds.) (le:176) (re:619) (di:direct) ECOCHI L04574 g145537 Escherichia coli 562 -11533049 304577 holc dna polymerase iii chi subunit (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:174672) (re:175115) (di:complement) ECOUW93 U14003 g537101 Escherichia coli 562 -11533049 233131 holc dna polymerase iii:chi subunit (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:2.7.7.7) (de:escherichia coli k-12 mg1655 section 386 of 400 of the completegenome.) (nt:f147; 100 pct identical amino acid sequence and) (le:9686) (re:10129) (di:complement) AE000496 AE000496 g1790709 Escherichia coli 562 -11533049 77466 holc (ec:2.7.7.7) (de:dna polymerase iii, chi subunit,) (db:swissprot) HOLC\_ECOLI P28905 ESCHERICHIA COLI 562 -11533049

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826517	7849	30005	300	99

Description

GTC ORF with score 97 to: (sr:human) (db:genpept-pri3) (de:homo sapiens chromosome 19, cosmid r32611, complete sequence.) (nt:hypothetical partial protein most similar to) (le:<3132:4854:5124:5940) (re:3229:4899:5224:6059) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826518	7850	30006	795	264

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826527	7851	30007	249	82

Description

6500729192 hold:b4372 dna polymerase iii psi subunit:dna polymerase iii:psi subunit (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b4372 b4372 Escherichia coli 562 -11533050 77468 hold (ec:2.7.7.7) (de:dna polymerase iii, psi subunit,) (db:swissprot) HOLD\_ECOLI P28632 ESCHERICHIA COLI 562 -11533050 162957 hold dna-directed dna polymerase:iii psi chain (cl:yeast peptidylprolyl isomerase fpr3:bkbp-type peptidylprolyl isomerase homology) (ec:2.7.7.7) (db:pir2.dat) A48647 A48647 Escherichia coli 562 -11533050 235585 hold dna polymerase iii psi subunit (sr:escherichia coli (strain maf102) dna) (db:genpept-bct1) (de:escherichia coli dna polymerase iii psi subunit (hold) andribosomal protein s18 acetylating enzyme (rimi) genes, completecds.) (nt:putative) (le:39) (re:452) (di:direct) ECOHOLDPSI L05387 g146390 Escherichia coli 562 -11533050 237577 hold dna polymerase iii psi subunit (sr:escherichia coli (strain k-12) (library: lambda-phage of y. kohara) (db:genpept-bct1) (de:escherichia coli (clone puc-psi) dna polymerase iii psi subunit(hold) gene, complete cds.) (le:78) (re:491) (di:direct) ECOPSI L04575 g147387 Escherichia coli 562 -11533050 7500883463 hold dna polymerase iii psi subunit (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:298635) (re:299048) (di:direct) ECOUW93 U14003 g537212 Escherichia coli 562 -11533050 234677 hold dna polymerase iii:psi subunit (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:2.7.7.7) (de:escherichia coli k-12 mg1655 section 397 of 400 of the completegenome.) (nt:o137; 100 pct identical to hold\_ecoli sw: p28632) (le:10752) (re:11165) (di:direct) AE000507 AE000507 g1790831 Escherichia coli 562 -11533050 5000690305 (de:(ecoli\_4254) (pn:dna polymerase iii, psi subunit) (gn:hold) (gtcfc:4.1:4.2) (ec:2.7.7.7) (hold\_ecoli) (keggfc:4.1:4.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_4254 ECOLI\_4254 Escherichia coli 562 10019828

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826528	7852	30008	204	67

Description

6500729193 deoa:tpp:ttg:b4382 thymidine phosphorylase:tdrpase  
(gtcf:4.1:4.2:4.4) (ec:2.4.2.4) (keggfc:4.1:4.2) (rileyfc:1.6.4)  
(db:gtc-escherichia coli) b4382 b4382 Escherichia coli 562 -11533051 102891  
deoa:tpp:ttg (ec:2.4.2.4) (de:thymidine phosphorylase, (tdrpase))  
(db:swissprot) TYPH\_ECOLI P07650 ESCHERICHIA COLI 562 -11533051 164687 deoa  
thymidine phosphorylase (cl:thymidine phosphorylase) (ec:2.4.2.4)  
(db:pir1.dat) (mp:100) S56606 S56606 Escherichia coli 562 -11533051  
7500893602 deoa thymidine phosphorylase (db:genpept-bct1) (ec:2.4.2.4)  
(de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.)  
(nt:cg site no. 868; alternate gene names tpp, tp; ttg) (le:309060)  
(re:310382) (di:direct) ECOUW93 U14003 g537222 Escherichia coli 562  
-11533051 237587 deoa thymidine phosphorylase (fn:enzyme; salvage of  
nucleosides and nucleotides) (db:genpept-bct2) (ec:2.4.2.4) (de:escherichia  
coli k-12 mg1655 section 398 of 400 of the completegenome.) (nt:o440; 100  
pct identical to typh\_ecoli sw: p07650;) (le:8877) (re:10199) (di:direct)  
AE000508 AE000508 g1790842 Escherichia coli 562 -11533051 5000690306  
(de:(ecoli\_4264) (pn:thymidine phosphorylase) (gn:deoa) (gtcf:4.1:4.2)  
(ec:2.4.2.4) (typh\_ecoli) (keggfc:4.1:4.2) (rileyfc:1.6.4)  
(db:gtc-escherichia coli)) ECOLI\_4264 ECOLI\_4264 Escherichia coli 562  
10044703

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826533	7853	30009	312	103

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826534	7854	30010	573	190

Description

GTC ORF with score 377 to: (or:Yarrowia lipolytica) (sr:yarrowia lipolytica  
(strain w29) dna) (db:genpept-pln1) (de:yarrowia lipolytica ras-like protein  
(ryl2) gene, complete cds.) (nt:ryl2 selected by hybridization with a)  
(le:253) (re:882) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826538	7855	30011	321	106

Description

GTC ORF with score 105 to: (or:Yarrowia lipolytica) (sr:yarrowia lipolytica (strain w29) dna) (db:genpept-pln1) (de:yarrowia lipolytica ras-like protein (ryl2) gene, complete cds.) (nt:ryl2 selected by hybridization with a) (le:253) (re:882) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826547	7856	30012	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826548	7857	30013	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826572	7858	30014	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826580	7859	30015	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826592	7860	30016	333	111

#### Description

6500729194 deod:pup:b4384 purine-nucleoside phosphorylase:purine nucleoside phosphorylase:inosine phosphorylase:pnf (gtcfc:4.1:4.2:4.4:9.4) (ec:2.4.2.1) (keggfc:4.1:4.2:9.4) (rileyfc:1.6.4) (db:gtc-escherichia coli) b4384 b4384 Escherichia coli 562 -11533052 164442 deod purine-nucleoside phosphorylase::inosine phosphorylase (cl:purine-nucleoside phosphorylase pnf) (ec:2.4.2.1) (db:pir2.dat) (mp:100) A27854 A41143 Escherichia coli 562 -11533052 237589 deod purine nucleoside phosphorylase (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (ec:2.4.2.1) (de:e.coli purine nucleoside phosphorylase (deod) gene, complete cds.) (nt:putative) (le:123) (re:842) (di:direct) ECOPNP M60917 g147309 Escherichia coli 562 -11533052 7500960441 deod purine-nucleoside phosphorylase (db:genpept-bct1) (ec:2.4.2.1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 865; alternate gene name pup) (le:311715) (re:312434) (di:direct) ECOUW93 U14003 g537224 Escherichia coli 562 -11533052 235510 deod purine-nucleoside phosphorylase (fn:enzyme; salvage of nucleosides and nucleotides) (db:genpept-bct2) (ec:2.4.2.1) (de:escherichia coli k-12 mg1655 section 398 of 400 of the complete genome.) (nt:o239; 100 pct identical to deod\_ecoli sw: p09743;) (le:11531) (re:12250) (di:direct) AE000508 AE000508 g1790844 Escherichia coli 562 -11533052 5000690307 (de:(ecoli\_4266) (pn:purine-nucleoside phosphorylase) (gn:deod) (gtcfc:4.1:4.2:9.4) (ec:2.4.2.1) (deod\_ecoli) (keggfc:4.1:4.2:9.4) (rileyfc:1.6.4) (db:gtc-escherichia coli)) ECOLI\_4266 ECOLI\_4266 Escherichia coli 562 10087319

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826600	7861	30017	192	63

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826609	7862	30018	501	166

#### Description

GTC ORF with score 112 to: (db:genpept-inv) (de:caenorhabditis elegans rna lariat debranching enzyme (ce-dbr1) gene, complete cds.) (nt:dbr1 homolog; similar to clone cm20f4, est) (le:135:432:943:1142:1360) (re:308:896:1092:1289:1622) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826619	7863	30019	636	211

#### Description

6500729195 purr:b1658 purine nucleotide synthesis repressor (gtcfc:4.1) (keggfc:14.2) (rileyfc:1.6.1) (db:gtc-escherichia coli) b1658 b1658 Escherichia coli 562 -11533053 130810 purr pur operon repressor purr (cl:lac repressor) (db:pir1.dat) (mp:36 min) RPECUDU A32027 Escherichia coli 562 -11533053 224102 purr pur repressor (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #318(37.2-37.6 min.)) (nt:orf\_id:o319#1; similar to (pir accession number) (le:9437) (re:10462) (di:direct) D90809 D90809 g1742731 Escherichia coli 562 -11533053 224111 purr pur repressor (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #319(37.4-37.8 min.)) (nt:orf\_id:o319#1; similar to (pir accession number) (le:1831) (re:2856) (di:direct) D90810 D90810 g1742741 Escherichia coli 562 -11533053 237968 (sr:e.coli (k12) cell line mc1040-2 dna, clone prrm127) (db:genpept-bct1) (de:e.coli purine nucleotide synthesis repressor protein (purr) gene,complete cds.) (nt:purine repressor (purr)) (le:361) (re:1386) (di:direct) ECOPURR J04212 g147428 Escherichia coli 562 -11533053 300780 (db:genpept-bct1) (de:escherichia coli purr gene for purr purine gene repressor.) (nt:purr gene product (aa 1-341)) (le:401) (re:1426) (di:direct) ECPURRRP X51368 g42598 Escherichia coli 562 -11533053 235613 purr transcriptional repressor for pur regulon:glya (fn:regulator; purine ribonucleotide biosynthesis) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 151 of 400 of the completegenome.) (nt:o341; 100 pct identical to purr\_ecoli sw: p15039;) (le:2560) (re:3585) (di:direct) AE000261 AE000261 g1787948 Escherichia coli 562 -11533053 5000690308 (de:(ecoli\_1617) (pn:repressor for pur regulon, glya, glnb, prsa, spea) (gn:purr) (gtcfc:4.1) (ec:) (purr\_ecoli) (keggfc:11.2) (rileyfc:1.6.1) (db:gtc-escherichia coli)) ECOLI\_1617 ECOLI\_1617 Escherichia coli 562 10034509

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826627	7864	30020	234	77

#### Description

GTC ORF with score 110 to: (fn:oxidation of p-hydroxybenzaldehyde to) (sr:pseudomonas putida (tissue library: n.c.i.m.b. 9866) dna) (db:genpept-bct1) (ec:1.2.1.3.) (de:pseudomonas putida aldehyde dehydrogenase gene, complete cds.) (nt:identified by ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826631	7865	30021	471	156

Description

6500729196 purt:b1849 phosphoribosylglycinamide formyltransferase 2:gart  
 2:gar transformylase 2:5-phosphoribosylglycinamide transformylase  
 2:formate-dependent gar transformylase (gtcfc:4.1) (ec:2.1.2.-)  
 (keggfc:14.1) (rileyfc:1.6.1) (db:gtc-escherichia coli) b1849 b1849  
 Escherichia coli 562 -11533054 141467 purt phosphoribosylglycinamide  
 formyltransferase:2:purt:gar transformylase:glycinamide ribonucleotide  
 transformylase (cl:phosphoribosylaminoimidazole carboxylase carbon  
 dioxide-fixation chain:phosphoribosylaminoimidazole carboxylase carbon  
 dioxide-fixation chain homology) (ec:2.1.2.-) (db:pir2.dat) A54227 A54227  
 Escherichia coli 562 -11533054 7500954387 purt glycinamide ribonucleotide  
 transformylase (fn:synthesis of fgat from gar) (sr:escherichia coli (strain  
 k-12) dna) (db:genpept-bct1) (de:escherichia coli glycinamide ribonucleotide  
 transformylase (purt)gene, 2-keto-3-deoxy-6-phosphogluconate aldolase (eda)  
 gene,6-phosphogluconate dehydratase (e... ECOGARA L20897 g304887 Escherichia  
 coli 562 -11533054 234462 purt phosphoribosylglycinamide formyltransferase  
 2 (fn:enzyme; purine ribonucleotide biosynthesis) (db:genpept-bct2)  
 (ec:2.1.2.-) (de:escherichia coli k-12 mg1655 section 169 of 400 of the  
 completegenome.) (nt:o392; 100 pct identical to purt\_ecoli sw: p33221;)  
 (le:97) (re:1275) (di:direct) AE000279 AE000279 g1788155 Escherichia coli  
 562 -11533054 5000690309 (de:(ecoli\_1806)  
 (pn:5"-phosphoribosyl-glycinamide:gar transferase 2) (gn:purt) (gtcfc:4.1)  
 (ec:2.1.2.-) (purt\_ecoli) (keggfc:11.1) (rileyfc:1.6.1) (db:gtc-escherichia  
 coli)) ECOLI\_1806 ECOLI\_1806 Escherichia coli 562 10072423

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826651	7866	30022	1176	391

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826665	7867	30023	330	109

Description

6500729197 dgt:b0160 deoxyguanosinetriphosphate triphosphohydrolase:dgtpase (gtcfc:4.1) (ec:3.1.5.1) (keggfc:14.1) (rileyfc:1.6.5) (db:gtc-escherichia coli) b0160 b0160 Escherichia coli 562 -11533055 162915 dgt dgtpase::deoxyguanosine triphosphate triphosphohydrolase (ec:3.1.5.1) (db:pir2.dat) (mp:3.8 min) A35993 A35993 Escherichia coli 562 -11533055 234142 dgt deoxyguanosine triphosphate (sr:escherichia coli (sub\_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (ec:3.1.5.1) (de:escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0 min).) (le:67833) (re:69350) (di:direct) ECO82K D26562 g473818 Escherichia coli 562 -11533055 239789 dgt dgtp triphosphohydrolase (sr:escherichia coli (individual\_isolate hr42, strain k-12) dna) (db:genpept-bct1) (ec:3.1.5.1) (de:e.coli dgtp triphosphohydrolase (dgt) gene, complete cds, andperiplasmic protease (htra) gene, 5'end.) (le:1066) (re:2583) (di:direct) ECODGTP M31772 g145735 Escherichia coli 562 -11533055 301629 dgt deoxyguanosine triphosphate (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:10312) (re:11829) (di:direct) ECU70214 U70214 g1552738 Escherichia coli 562 -11533055 233691 dgt deoxyguanosine triphosphate triphosphohydrolase (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:3.1.5.1) (de:escherichia coli k-12 mg1655 section 15 of 400 of the completegenome.) (nt:o505; 100 pct identical to dgtp\_ecoli sw: p15723;) (le:5744) (re:7261) (di:direct) AE000125 AE000125 g1786355 Escherichia coli 562 -11533055 5000690339 (de:(ecoli\_160) (pn:deoxyguanosine triphosphate triphosphohydrolase) (gn:dgt) (gtcfc:4.4) (ec:3.1.5.1) (dgtp\_ecoli) (keggfc:11.1) (rileyfc:1.6.5) (db:gtc-escherichia coli)) ECOLI\_160 ECOLI\_160 Escherichia coli 562 10086680

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826667	7868	30024	369	123

Description

6500729198 pyr\_h:smba:b0171 uridine 5-monophosphate kinase:uridylylate kinase:uk:uridine monophosphate kinase:ump kinase:smba protein (gtcfc:4.1) (ec:2.7.4.-) (keggfc:14.1) (rileyfc:1.6.5) (db:gtc-escherichia coli) b0171 b0171 Escherichia coli 562 -11533056 164108 pyr\_h:smb:mukb uridine 5-monophosphate kinase::mukb suppressor protein (cl:uridine 5'-monophosphate kinase) (ec:2.7.4.-) (db:pir2.dat) B45269 B45269 Escherichia coli 562 -11533056 236000 smba mukb suppressor protein smba (sr:escherichia coli (sub\_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0 min).) (le:80449) (re:81174) (di:direct) ECO82K D26562 g473826 Escherichia coli 562 -11533056 236162 smba smba (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli smba gene.) (le:465) (re:1190) (di:direct) ECOSMBA D13334 g216662 Escherichia coli 562 -11533056 303239 pyr\_h uridine monophosphate kinase (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (ec:2.7.4) (de:escherichia coli genome, 4.0 - 6.0 min region.) (le:1379) (re:2104) (di:direct) ECOTSF D83536 g1208944 Escherichia coli 562 -11533056 301637 smba uridine 5-monophosphate ump kinase (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:22930) (re:23655) (di:direct) ECU70214 U70214 g1552748 Escherichia coli 562 -11533056 233699 pyr\_h uridylylate kinase (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:2.7.4.-) (de:escherichia coli k-12 mg1655 section 16 of 400 of the completegenome.) (nt:o241; 100 pct identical to pyr\_h\_ecoli sw: p29464) (le:8221) (re:8946) (di:direct) AE000126 AE000126 g1786367 Escherichia coli 562 -11533056 239799 pyr\_h uridine monophosphate kinase (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (ec:2.7.4) (de:escherichia coli genome, 4.0 - 6.0 min region.) (le:1379) (re:2104) (di:direct) ECOTSF D83536 g1208944 Escherichia coli 562 -11533056 5000690340 (de:(ecoli\_171) (pn:uridylylate kinase) (gn:pyr\_h) (gtcfc:4.4) (ec:2.7.4.-) (pyr\_h\_ecoli) (keggfc:11.1) (rileyfc:1.6.5) (db:gtc-escherichia coli)) ECOLI\_171 ECOLI\_171 Escherichia coli 562 10087172

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826677	7869	30025	402	133

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826684	7870	30026	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826696	7871	30027	690	229
<u>Description</u>				
6500729199 udk:b2066 uridine kinase (gtcfc:4.1:4.2) (ec:2.7.1.48) (keggfc:4.2) (rileyfc:1.6.5) (db:gtc-escherichia coli) b2066 b2066 Escherichia coli 562 -11533057 7000691930 udk uridine kinase (cl:uridine kinase) (ec:2.7.1.48) (db:pir2.dat) A64973 A64973 Escherichia coli 562 -11533057 7500960479 udk uridine/cytidine kinase (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:2.7.1.48) (de:escherichia coli k-12 mg1655 section 186 of 400 of the completegenome.) (nt:f231; 100 pct identical to urk_ecoli sw: p31218 but) (le:8894) (re:9589) (di:complement) AE000296 AE000296 g1788380 Escherichia coli 562 -11533057 5000690319 (de:(ecoli_2014) (pn:uridine) (gn:udk) (gtcfc:4.2) (ec:2.7.1.48) (urk_ecoli) (keggfc:4.2) (rileyfc:1.6.5) (db:gtc-escherichia coli)) ECOLI_2014 ECOLI_2014 Escherichia coli 562 10123553				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826700	7872	30028	411	136
<u>Description</u>				
6500729200 mrp:b2113 mrp:protein (gtcfc:4.1) (keggfc:14.2) (rileyfc:1.6.5) (db:gtc-escherichia coli) b2113 b2113 Escherichia coli 562 -11533058 84230 mrp (de:mrp protein) (db:swissprot) MRP_ECOLI P21590 ESCHERICHIA COLI 562 -11533058 7000685871 mrp probable atpase mrp (cl:conserved probable membrane protein yil003w) (db:pir2.dat) H64978 H64978 Escherichia coli 562 -11533058 7500885882 mrp (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (nt:atpase of unknown function.) (le:5827) (re:6966) (di:complement) ECOHU47 U00007 g405896 Escherichia coli 562 -11533058 234722 mrp putative atpase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 190 of 400 of the completegenome.) (nt:f379; 100 pct identical to mrp_ecoli sw: p21590) (le:5750) (re:6889) (di:complement) AE000300 AE000300 g1788431 Escherichia coli 562 -11533058 5000690341 (de:(ecoli_2061) (pn:putative atpase) (gn:mrp) (gtcfc:4.4) (ec:) (mrp_ecoli) (keggfc:11.2) (rileyfc:1.6.5) (db:gtc-escherichia coli)) ECOLI_2061 ECOLI_2061 Escherichia coli 562 10026431				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826708	7873	30029	465	154
<u>Description</u>				
6500729201 xapr:pndr:b2405 xapr:xanthosine operon regulatory protein (gtcfc:4.1) (keggfc:14.2) (rileyfc:1.6.5) (db:gtc-escherichia coli) b2405 b2405 Escherichia coli 562 -11533059 237623 xapr:pndr (de:xanthosine operon regulatory protein) (db:swissprot) XAPR_ECOLI P23841 ESCHERICHIA COLI 562 -11533059 163483 xapr xapr protein (db:pir2.dat) S11407 S11407 Escherichia coli 562 -11533059 224960 pndr xanthosine operon regulatory protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #416(54.1-54.5 min.)) (nt:similar to (swissprot accession number p23841)) (le:14437) (re:15321) (di:complement) D90869 D90869 g1799815 Escherichia coli 562 -11533059 224963 pndr xanthosine operon regulatory protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #417(54.4-54.6 min.)) (nt:similar to (swissprot accession number p23841)) (le:919) (re:1803) (di:complement) D90870 D90870 g1799819 Escherichia coli 562 -11533059 7500894432 orf294 (db:genpept-bct1) (de:escherichia coli k12 valu, gltx and alaw region.) (le:73) (re:957) (di:direct) ECGLTXVA X63976 g41595 Escherichia coli 562 -11533059 7502851873 (sr:escherichia coli (sub_strain n99, strain k-12) dna) (db:genpept-bct1) (de:escherichia coli alaw (transfer rna-ala), valu (transfer rna-valand transfer rna-lys) operons and glutamyl-trna synthetase (gltx)gene, complete cds.) (nt:orf294) (le:73) (re:... ECOUXW M13687 g148255 Escherichia coli 562 -11533059 233018 xapr regulator for xapa (fn:regulator; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 218 of 400 of the completegenome.) (nt:f294; 100 pct identical to xapr_ecoli sw: p23841;) (le:3282) (re:4166) (di:complement) AE000328 AE000328 g2367136 Escherichia coli 562 -11533059 108072 xapr:pndr (de:xanthosine operon regulatory protein) (db:swissprot) XAPR_ECOLI P23841 ESCHERICHIA COLI 562 -11533059				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826710	7874	30030	975	324

Description

6500729202 xapa:pnda:b2407 xanthosine phosphorylase (gtcfc:4.1:5.11)  
(ec:2.4.2.-) (keggfc:5.11) (rileyfc:1.6.5) (db:gtc-escherichia coli) b2407  
b2407 Escherichia coli 562 -11533060 108070 xapa:pnda (ec:2.4.2.-)  
(de:xanthosine phosphorylase,) (db:swissprot) XAPA\_ECOLI P45563 ESCHERICHIA  
COLI 562 -11533060 7000687019 xapa xanthosine phosphorylase  
(cl:purine-nucleoside phosphorylase) (ec:2.4.2.-) (db:pir2.dat) F65014  
F65014 Escherichia coli 562 -11533060 224962 pnda xanthosine phosphorylase  
ec 2.4.2.-. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda  
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#416(54.1-54.5 min.)) (nt:similar to (swissprot accession number p45563))  
(le:16889) (re:17722) (di:complement) D90869 D90869 g1799817 Escherichia  
coli 562 -11533060 224965 pnda xanthosine phosphorylase ec 2.4.2.-.  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #417(54.4-54.6  
min.)) (nt:similar to (swissprot accession number p45563)) (le:3371)  
(re:4204) (di:complement) D90870 D90870 g1799821 Escherichia coli 562  
-11533060 7500894430 xapa xanthosine phosphorylase (fn:enzyme; central  
intermediary metabolism:) (db:genpept-bct2) (ec:2.4.2.-) (de:escherichia  
coli k-12 mgl655 section 218 of 400 of the completegenome.) (nt:f277;  
residues 1-258 are 86 pct identical to) (le:5734) (re:6567) (di:complement)  
AE000328 AE000328 g1788746 Escherichia coli 562 -11533060 5000690275  
(de:(ecoli\_2348) (pn:xanthosine phosphorylase) (gn:xapa) (gtcfc:4.1:4.2:9.4)  
(ec:2.4.2.1) (xapa\_ecoli) (keggfc:4.1:4.2:9.4) (rileyfc:1.6.5)  
(db:gtc-escherichia coli)) ECOLI\_2348 ECOLI\_2348 Escherichia coli 562  
10120180

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826711	7875	30031	264	87

Description

6500729203 lepa:b2569 gtp-binding protein lepa (gtcfc:4.1) (keggfc:14.2) (rileyfc:1.6.5) (db:gtc-escherichia coli) b2569 b2569 Escherichia coli 562 -11533061 81889 lepa (de:gtp-binding protein lepa) (db:swissprot) LEPA\_ECOLI P07682 ESCHERICHIA COLI 562 -11533061 7000685728 lepa gtp-binding membrane protein lepa (cl:gtp-binding membrane protein lepa:translation elongation factor tu homology) (db:pir1.dat) (mp:55 min) BVECLA H65034 Escherichia coli 562 -11533061 7500884919 lepa gtp-binding elongation factor:may be inner (fn:factor; proteins - translation and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 233 of 400 of the completegenome.) (nt:f599; 94 pct identical (1 gap) to lepa\_ecoli) (le:5085) (re:6884) (di:complement) AE000343 AE000343 g1788922 Escherichia coli 562 -11533061 5000690343 (de:(ecoli\_2509) (pn:gtp-binding elongation factor, may be inner membrane protein) (gn:lepa) (gtcfc:4.4) (ec:) (lepa\_ecoli) (keggfc:11.2) (rileyfc:1.6.5) (db:gtc-escherichia coli)) ECOLI\_2509 ECOLI\_2509 Escherichia coli 562 10123733

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826722	7876	30032	612	203

Description

6500729204 pyrg:b2780 ctp synthase:utp--ammonia ligase:ctp synthetase (gtcfc:4.1:4.2) (ec:6.3.4.2) (keggfc:4.2) (rileyfc:1.6.5) (db:gtc-escherichia coli) b2780 b2780 Escherichia coli 562 -11533062 7000688913 pyrg ctp synthase::ctp-synthetase:utp--ammonia ligase (cl:ctp synthase) (ec:6.3.4.2) (db:pir1.dat) (mp:60 min) SYECTP H65059 Escherichia coli 562 -11533062 7500953385 pyrg ctp synthetase (db:genpept-bct1) (ec:6.3.4.2) (de:escherichia coli k-12 genome; approximately 62 minute region.) (nt:cg site no. 325) (le:5894) (re:7531) (di:complement) ECU29580 U29580 g882674 Escherichia coli 562 -11533062 239354 pyrg ctp synthetase (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:6.3.4.2) (de:escherichia coli k-12 mg1655 section 251 of 400 of the completegenome.) (nt:f545; 99 pct identical to pyrg\_ecoli sw: p08398; cg) (le:8606) (re:10243) (di:complement) AE000361 AE000361 g1789142 Escherichia coli 562 -11533062 5000690322 (de:(ecoli\_2711) (pn:ctp synthetase) (gn:pyrg) (gtcfc:4.2) (ec:6.3.4.2) (pyrg\_ecoli) (keggfc:4.2) (rileyfc:1.6.5) (db:gtc-escherichia coli)) ECOLI\_2711 ECOLI\_2711 Escherichia coli 562 10123830

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826729	7877	30033	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826735	7878	30034	657	219

Description

GTC ORF with score 227 to: (fn:translation initiation factor) (sr:norway rat) (db:genpept-rod) (de:rattus norvegicus eif-2b beta subunit mrna, complete cds.) (nt:guanine nucleotide exchange factor for protein) (le:46) (re:1101) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826736	7879	30035	369	122

Description

6500729205 coda:b0337 cytosine deaminase (gtcfc:4.2:4.4) (ec:3.5.4.1) (keggfc:4.2) (rileyfc:1.6.4) (db:gtc-escherichia coli) b0337 b0337 Escherichia coli 562 -11533063 162898 coda cytosine deaminase::cytosine aminohydrolase (ec:3.5.4.1) (db:pir2.dat) S22662 S22662 Escherichia coli 562 -11533063 7500959718 coda cytosine deaminase (db:genpept-bct1) (de:e.coli codba operon encoding cytosine permease and cytosinedeaminase.) (le:1642) (re:2925) (di:direct) ECCODAB X63656 g581052 Escherichia coli 562 -11533063 232532 coda cytosine deaminase (fn:enzyme; salvage of nucleosides and nucleotides) (db:genpept-bct2) (ec:3.5.4.1) (de:escherichia coli k-12 mg1655 section 30 of 400 of the completegenome.) (nt:o427; 100 pct identical to coda\_ecoli sw: p25524) (le:11019) (re:12302) (di:direct) AE000140 AE000140 g1786531 Escherichia coli 562 -11533063 5000690310 (de:(ecoli\_321) (pn:cytosine deaminase) (gn:coda) (gtcfc:4.2) (ec:3.5.4.1) (coda\_ecoli) (keggfc:4.2) (rileyfc:1.6.4) (db:gtc-escherichia coli)) ECOLI\_321 ECOLI\_321 Escherichia coli 562 10086675

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826741	7880	30036	1584	527

Description

6500729206 trxb:b0888 thioredoxin reductase (gtcfc:9.13) (ec:1.6.4.5)  
(keggfc:4.2) (rileyfc:1.6.3) (db:gtc-escherichia coli)  
(rileyfc:small-molecule metabolism, 2'-deoxyribonucleotide metabolism) b0888  
b0888 Escherichia coli 562 -11533064 122797 trxb thioredoxin reductase  
nadph (cl:thioredoxin reductase:thioredoxin reductase homology) (ec:1.6.4.5)  
(db:pir1.dat) (mp:20 min) RDECT A28074 Escherichia coli 562 -11533064  
223249 trxb thioredoxin reductase nadph (sr:escherichia coli(strain:k12)  
dna, clone:kohara clone #214) (db:genpept-bct1) (de:escherichia coli genomic  
dna.(19.9 - 20.2 min).) (le:6965) (re:7930) (di:complement) D90726 D90726  
g1651410 Escherichia coli 562 -11533064 223254 trxb thioredoxin reductase  
nadph (sr:escherichia coli(strain:k12) dna, clone:kohara clone #215)  
(db:genpept-bct1) (de:escherichia coli genomic dna.(20.0 - 20.3 min).)  
(le:268) (re:1233) (di:complement) D90727 D90727 g1651416 Escherichia coli  
562 -11533064 7500953201 (sr:e.coli k12 dna, clones pmr(20,21))  
(db:genpept-bct1) (de:e.coli thioredoxin reductase gene, complete cds.)  
(nt:thioredoxin reductase) (le:86) (re:1051) (di:direct) ECOTRXB J03762  
g148073 Escherichia coli 562 -11533064 236157 trxb thioredoxin reductase  
(fn:enzyme; 2'-deoxyribonucleotide metabolism) (db:genpept-bct2)  
(ec:1.6.4.5) (de:escherichia coli k-12 mg1655 section 80 of 400 of the  
completegenome.) (nt:f321; 100 pct identical to trxb\_ecoli sw: p09625)  
(le:8786) (re:9751) (di:complement) AE000190 AE000190 g1787114 Escherichia  
coli 562 -11533064 5000690311 trxb thioredoxin reductase nadph ec 1.6.4.5  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #214) (db:genpept)  
(de:escherichia coli genomic dna. (19.9 - 20.3 min).) (nt:orf\_id:o215#1;  
similar to pir accession number) (le:6965) (re:7930) (di:complement) D90726  
D90726 g1651410 Escherichia coli 562 -11533064 7502851874 trxb thioredoxin  
reductase nadph ec 1.6.4.5 (sr:escherichia coli(strain:k12) dna,  
clone:kohara clone #215) (db:genpept) (de:escherichia coli genomic dna.  
(20.1 - 20.4 min).) (nt:orf\_id:o215#1; similar to pir accession number)  
(le:268) (re:1233) (di:complement) D90727 D90727 g1651416 Escherichia coli  
562 -11533064

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826767	7881	30037	465	154

# Description

6500729207 cmk:mssa:b0910 cytidylate kinase:ck:cytidine monophosphate kinase:cmp kinase:mssa protein:p25 (gtcfc:4.2) (ec:2.7.4.14) (keggfc:4.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0910 b0910 Escherichia coli 562 -11533065 80554 cmk:mssa (ec:2.7.4.14) (de:(cmp kinase) (mssa protein) (p25)) (db:swissprot) KCY\_ECOLI P23863 ESCHERICHIA COLI 562 -11533065 7000685667 cmk:mssa cytidylate kinase (cl:cytidylate kinase cmk) (ec:2.7.4.14) (db:pir2.dat) E64830 E64830 Escherichia coli 562 -11533065 223268 cmk cytidylate kinase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #216) (db:genpept-bct1) (de:escherichia coli genomic dna. (20.3 - 20.7 min).) (le:16894) (re:17577) (di:direct) D90728 D90728 g1651431 Escherichia coli 562 -11533065 223274 cmk cytidylate kinase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #217) (db:genpept-bct1) (de:escherichia coli genomic dna. (20.4 - 20.8 min).) (le:9361) (re:10044) (di:direct) D90729 D90729 g1651438 Escherichia coli 562 -11533065 7500884540 cmk cytidylate kinase (fn:enzyme; pyrimidine ribonucleotide biosynthesis) (db:genpept-bct2) (ec:2.7.4.14) (de:escherichia coli k-12 mg1655 section 83 of 400 of the completegenome.) (nt:o227; 99 pct identical to kcy\_ecoli sw: p23863) (le:4530) (re:5213) (di:direct) AE000193 AE000193 g1787139 Escherichia coli 562 -11533065 5000690312 cmk cytidylate kinase ec 2.7.4.14 ck cytidine (sr:escherichia coli(strain:k12) dna, clone:kohara clone #216) (db:genpept) (de:escherichia coli genomic dna. (20.4 - 20.8 min).) (nt:orf\_id:o217#7; similar to swissprot accession) (le:16894) (re:17577) (di:direct) D90728 D90728 g1651431 Escherichia coli 562 -11533065 7502851875 cmk cytidylate kinase ec 2.7.4.14 ck cytidine (sr:escherichia coli(strain:k12) dna, clone:kohara clone #217) (db:genpept) (de:escherichia coli genomic dna. (20.5 - 20.9 min).) (nt:orf\_id:o217#7; similar to swissprot accession) (le:9361) (re:10044) (di:direct) D90729 D90729 g1651438 Escherichia coli 562 -11533065

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826769	7882	30038	303	100

#### Description

6500729208 pyrd:b0945 dihydroorotate dehydrogenase:dihydroorotate oxidase:dhodehase (gtcfc:4.2) (ec:1.3.3.1) (keggfc:4.2) (rileyfc:1.6.2) (db:gtc-escherichia coli) b0945 b0945 Escherichia coli 562 -11533066 7500889162 pyrd (ec:1.3.3.1) (de:(dhodehase)) (db:swissprot) PYRD\_ECOLI P05021 ESCHERICHIA COLI 562 -11533066 122676 pyrd dihydroorotate oxidase::dihydroorotate dehydrogenase (cl:dihydroorotate oxidase) (ec:1.3.3.1) (db:pir1.dat) (mp:21 min) DEECDO A23109 Escherichia coli 562 -11533066 223293 pyrd dihydroorotate oxidase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #221) (db:genpept-bct1) (de:escherichia coli genomic dna. (21.3 - 21.7 min).) (le:12507) (re:13517) (di:direct) D90732 D90732 g1651460 Escherichia coli 562 -11533066 5000690313 (db:genpept-bct1) (de:e. coli pyrd gene for dihydroorotate dehydrogenase (ec 1.3.3.1).) (nt:dehydroorotate dehydrogenae (aa 1-336)) (le:331) (re:1341) (di:direct) ECPYRD X02826 g42609 Escherichia coli 562 -11533066 237976 pyrd dihydro-orotate dehydrogenase (fn:enzyme; pyrimidine ribonucleotide biosynthesis) (db:genpept-bct2) (ec:1.3.3.1) (de:escherichia coli k-12 mg1655 section 86 of 400 of the completegenome.) (nt:o336; 100 pct identical to pyrd\_ecoli sw: p05021) (le:7113) (re:8123) (di:direct) AE000196 AE000196 g1787177 Escherichia coli 562 -11533066 7502851876 pyrd dihydroorotate oxidase ec 1.3.3.1 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #221) (db:genpept) (de:escherichia coli genomic dna. (21.4 - 21.8 min).) (nt:orf\_id:o221#13; similar to pir accession number) (le:12507) (re:13517) (di:direct) D90732 D90732 g1651460 Escherichia coli 562 -11533066 92613 pyrd (ec:1.3.3.1) (de:(dhodehase)) (db:swissprot) PYRD\_ECOLI P05021 ESCHERICHIA COLI 562 -11533066

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826776	7883	30039	261	86

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826778	7884	30040	240	79

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826780	7885	30041	843	280

Description

6500729209 pyrc:b1062 dihydroorotase:dhoase (gtcfc:4.2) (ec:3.5.2.3) (keggfc:4.2) (rileyfc:1.6.2) (db:gtc-escherichia coli) b1062 b1062 Escherichia coli 562 -11533067 125036 pyrc dihydroorotase::carbamoylaspartic dehydrase (cl:dihydroorotase) (ec:3.5.2.3) (db:pir1.dat) (mp:23 min) DEECO A25008 Escherichia coli 562 -11533067 223346 pyrc dihydroorotase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #233) (db:genpept-bct1) (de:escherichia coli genomic dna. (24.0 - 24.4 min).) (le:7927) (re:8973) (di:complement) D90743 D90743 g1651523 Escherichia coli 562 -11533067 237975 pyrc (sr:e.coli (k-12 clt9, strain mc4100) dna, clone pbhml07) (db:genpept-bct1) (de:e.coli k-12 pyrc gene encoding dihydroorotase, complete cds.) (nt:dihydroorotase (ec 3.5.2.3)) (le:467) (re:1513) (di:direct) ECPYRCA M16752 g147473 Escherichia coli 562 -11533067 7500953314 pyrc dihydroorotase (db:genpept-bct1) (ec:3.5.2.3) (de:e. coli pyrc gene for dihydroorotase.) (le:881) (re:1927) (di:direct) ECPYRC X04469 g42607 Escherichia coli 562 -11533067 235644 pyrc dihydro-orotase (fn:enzyme; pyrimidine ribonucleotide biosynthesis) (db:genpept-bct2) (ec:3.5.2.3) (de:escherichia coli k-12 mg1655 section 97 of 400 of the completegenome.) (nt:f348; 100 pct identical to pyrc\_ecoli sw: p05020) (le:4897) (re:5943) (di:complement) AE000207 AE000207 g1787301 Escherichia coli 562 -11533067 5000690314 pyrc dihydroorotase ec 3.5.2.3 . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #233) (db:genpept) (de:escherichia coli genomic dna. (24.1 - 24.5 min).) (nt:orf\_id:o233#10; similar to pir accession number) (le:7927) (re:8973) (di:complement) D90743 D90743 g1651523 Escherichia coli 562 -11533067 7502851877 pyrc dihydroorotase (db:genpept) (ec:3.5.2.3) (de:e. coli pyrc gene for dihydroorotase.) (le:881) (re:1927) (di:direct) ECPYRC X04469 g42607 Escherichia coli 562 -11533067

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826783	7886	30042	441	146

Description

GTC ORF with score 146 to: (fn:actin patch assembly and localization) (sr:fission yeast) (db:genpept-pln1) (de:schizosaccharomyces pombe wiskott-aldrich syndrome protein homolog(wsp1+) gene, complete cds, and btf3/beta-nac gene, partialsequence.) ...



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826784	7887	30043	1083	360

Description

6500729210 tmk:b1098 hypothetical protein in pabc-holb intergenic region:thymidylate kinase:dtmp kinase (gtcfc:4.2) (ec:2.7.4.9) (keggfc:4.2) (rileyfc:1.6.3) (db:gtc-escherichia coli) (rileyfc:small-molecule metabolism, 2'-deoxyribonucleotide metabolism) b1098 b1098 Escherichia coli 562 -11533068 81196 tmk (ec:2.7.4.9) (de:thymidylate kinase, (dtmp kinase) (db:swissprot) KTHY\_ECOLI P37345 ESCHERICHIA COLI 562 -11533068 205593 tmk dtmp kinase::thymidylate kinase (cl:dtmp kinase) (ec:2.7.4.9) (db:pir2.dat) G64853 JC6006 Escherichia coli 562 -11533068 7500884759 tmk thymidylate kinase (fn:phosphorylation of dtmp to form dtdp in both de) (sr:escherichia coli strain=w3110) (db:genpept-bct1) (ec:2.7.4.9) (de:escherichia coli thymidylate kinase (tmk) gene, complete cds, holbgene, partial cds.) (nt:(deoxy)thymidylate kinase) (le:299) (re... ECU41456 U41456 g1244710 Escherichia coli 562 -11533068 239611 tmk thymidylate kinase (fn:enzyme; 2'-deoxyribonucleotide metabolism) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 100 of 400 of the completegenome.) (nt:o213; 100 pct identical to fragment ycfg\_ecoli) (le:6429) (re:7070) (di:direct) AE000210 AE000210 g1787340 Escherichia coli 562 -11533068 5000690315 tmk thymidylate kinase ec 2.7.4.9 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #236) (db:genpept) (de:escherichia coli genomic dna. (24.8 - 25.2 min).) (nt:orf\_id:o236#7; similar to pir accession number) (le:5766) (re:6407) (di:direct) D90745 D90745 g4062665 Escherichia coli 562 -11533068

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826793	7888	30044	483	160

Description

6500729211 tdk:b1238 thymidine kinase (gtcfc:4.2:4.4) (ec:2.7.1.21) (keggfc:4.2) (rileyfc:1.6.4) (db:gtc-escherichia coli) b1238 b1238 Escherichia coli 562 -11533069 301356 tdk (ec:2.7.1.21) (de:thymidine kinase,) (db:swissprot) KITH\_ECOLI P23331 ESCHERICHIA COLI 562 -11533069 138178 tdk thymidine kinase (cl:phage t4 thymidine kinase) (ec:2.7.1.21) (db:pir2.dat) JS0519 JS0519 Escherichia coli 562 -11533069 223447 tdk thymidine kinase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #250) (db:genpept-bct1) (de:escherichia coli genomic dna (27.6-28.0 min).) (le:10523) (re:11140) (di:direct) D90759 D90759 g1651638 Escherichia coli 562 -11533069 224716 tdk thymidine kinase ec 2.7.1.21 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #251(27.7-28.2 min).) (nt:orf\_id:o250#2; similar to (pir accession number) (le:10523) (re:11140) (di:direct) D90852 D90852 g1805515 Escherichia coli 562 -11533069 238335 tdk thymidine kinase aa 1-205 (db:genpept-bct1) (de:escherichia coli tdk gene for thymidine kinase (ec 2.7.1.21).) (le:109) (re:726) (di:direct) ECTDK X51523 g43047 Escherichia coli 562 -11533069 238358 tdk thymidine kinase (db:genpept-bct1) (ec:2.7.1.21) (de:e.coli tdk gene for thymidine kinase.) (le:316) (re:933) (di:direct) ECTDKG X53733 g43049 Escherichia coli 562 -11533069 238334 tdk thymidine kinase (fn:enzyme; salvage of nucleosides and nucleotides) (db:genpept-bct2) (ec:2.7.1.21) (de:escherichia coli k-12 mg1655 section 112 of 400 of the completegenome.) (nt:o205; 100 pct identical to kith\_ecoli sw: p23331) (le:3361) (re:3978) (di:direct) AE000222 AE000222 g1787490 Escherichia coli 562 -11533069 5000690316 tdk thymidine kinase (db:genpept-bct2) (de:e.coli genes for h-ns thymidine kinase alcohol dehydrogenase.) (le:1010) (re:1627) (di:direct) ECTKAD X67326 g43079 Escherichia coli 562 -11533069 7502851878 tdk thymidine kinase ec 2.7.1.21 . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #250) (db:genpept) (de:escherichia coli genomic dna. (27.7 - 28.1 min).) (nt:orf\_id:o251#4; similar to pir accession number) (le:10523) (re:11140) (di:direct) D90759 D90759 g1651638 Escherichia coli 562 -11533069 80752 tdk (ec:2.7.1.21) (de:thymidine kinase,) (db:swissprot) KITH\_ECOLI P23331 ESCHERICHIA COLI 562 -11533069

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826795	7889	30045	744	247

Description

GTC ORF with score 362 to: (fn:rna binding protein) (sr:drosophila melanogaster (strain oregon r) (library: lambda embl4) (db:genpept-inv) (de:drosophila melanogaster nucleolytic polyadenylate-binding proteinhomologue gene, complete cds.) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826821	7890	30046	378	125

Description

6500729212 pyrfb1281 orotidine-5-p decarboxylase:orotidine 5-phosphate decarboxylase:omp decarboxylase (gtcfc:4.2) (ec:4.1.1.23) (keggfc:4.2) (rileyfc:1.6.2) (db:gtc-escherichia coli) b1281 b1281 Escherichia coli 562 -11533070 68057 pyrfb (ec:4.1.1.23) (de:decarboxylase)) (db:swissprot) DCOP\_ECOLI P08244 ESCHERICHIA COLI 562 -11533070 125330 pyrfb:purf orotidine-5-phosphate decarboxylase::omp decarboxylase:orotidine-5-phosphate carboxy-lyase (cl:orotidine-5'-phosphate decarboxylase:orotidine-5'-phosphate decarboxylase homology) (ec:4.1.1.23) (db:pirl.dat) (mp:28 min) DCECOP A28440 Escherichia coli 562 -11533070 223509 pyrfb orotidine 5-phosphate decarboxylase ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #255(28.8-29.2 min.)) (nt:orf\_id:o255#6; similar to (swissprot accession) (le:4186) (re:4923) (di:direct) D90766 D90766 g1742095 Escherichia coli 562 -11533070 300312 pyrfb (sr:e.coli k12 (clt43) dna, clone pdk26) (db:genpept-bct1) (de:e.coli pyrfb operon encoding orotidine 5'-monophosphate (omp)decarboxylase.) (nt:orotidine 5' monophosphate (omp) decarboxylase) (le:320) (re:1057) (di:direct) ECOPYRF J02768 g147475 Escherichia coli 562 -11533070 235645 pyrfb orotidine-5-phosphate decarboxylase (fn:enzyme; pyrimidine ribonucleotide biosynthesis) (db:genpept-bct2) (ec:4.1.1.23) (de:escherichia coli k-12 mgl655 section 116 of 400 of the completegenome.) (nt:o245; 100 pct identical to dcop\_ecoli sw: p08244;) (le:3413) (re:4150) (di:direct) AE000226 AE000226 g1787537 Escherichia coli 562 -11533070 5000690317 (de:(ecoli\_1241) (pn:orotidine-5"-phosphate decarboxylase) (gn:pyrfb) (gtcfc:4.2) (ec:4.1.1.23) (dcop\_ecoli) (keggfc:4.2) (rileyfc:1.6.2) (db:gtc-escherichia coli)) ECOLI\_1241 ECOLI\_1241 Escherichia coli 562 10010650

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826829	7891	30047	765	254

# Description

6500729213 dcd:dus:paxa:b2065 deoxycytidine triphosphate deaminase:dctp  
deaminase (gtcfc:4.2) (ec:3.5.4.13) (keggfc:4.2) (rileyfc:1.6.3)  
(db:gtc-escherichia coli) (rileyfc:small-molecule metabolism,  
2'-deoxyribonucleotide metabolism) b2065 b2065 Escherichia coli 562  
-11533071 67981 dcd:dus:paxa (ec:3.5.4.13) (de:deaminase)) (db:swissprot)  
DCD\_ECOLI P28248 ESCHERICHIA COLI 562 -11533071 162911 dcd dctp  
deaminase::dut dutpase mutation suppressor (cl:dctp deaminase) (ec:3.5.4.13)  
(db:pir2.dat) A42940 A42940 Escherichia coli 562 -11533071 224601  
dcd:dus:paxa deoxycytidine triphosphate deaminase ec (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #355(45.9-46.2 min..))  
(nt:orf\_id:o355#4; similar to (swissprot accession) (le:8258) (re:8839)  
(di:complement) D90844 D90844 g1736769 Escherichia coli 562 -11533071  
301246 dcd:dus:paxa deoxycytidine triphosphate deaminase ec (sr:escherichia  
coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #356(46.1-46.5 min..))  
(nt:orf\_id:o355#4; similar to (swissprot accession) (le:355) (re:936)  
(di:complement) D90845 D90845 g1736775 Escherichia coli 562 -11533071  
301241 dcd deoxycytidine triphosphate deaminase (sr:escherichia coli  
(strain k-12) dna) (db:genpept-bct1) (ec:3.5.4.13) (de:e.coli deoxycytidine  
triphosphate deaminase (dcd) gene, completecds and orf, 5' end.) (le:94)  
(re:675) (di:direct) ECODCDA M90069 g145716 Escherichia coli 562 -11533071  
234129 dcd 2-deoxycytidine 5-triphosphate deaminase (fn:enzyme;  
2'-deoxyribonucleotide metabolism) (db:genpept-bct2) (ec:3.5.4.13)  
(de:escherichia coli k-12 mg1655 section 186 of 400 of the completegenome.)  
(nt:f193; 100 pct identical to dcd\_ecoli sw: p28248; cg) (le:8221) (re:8802)  
(di:complement) AE000296 AE000296 g1788379 Escherichia coli 562 -11533071  
224606 dcd:dus:paxa deoxycytidine triphosphate deaminase ec (sr:escherichia  
coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #356(46.1-46.5 min..))  
(nt:orf\_id:o355#4; similar to (swissprot accession) (le:355) (re:936)  
(di:complement) D90845 D90845 g1736775 Escherichia coli 562 -11533071  
5000690318 (de:(ecoli\_2013) (pn:2"-deoxycytidine 5"-triphosphate deaminase)  
(gn:dcd) (gtcfc:4.2) (ec:3.5.4.13) (dcd\_ecoli) (keggfc:4.2) (rileyfc:1.6.3)  
(db:gtc-escherichia coli)) ECOLI\_2013 ECOLI\_2013 Escherichia coli 562  
10010574

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826830	7892	30048	336	111
Description				
6500729214 cdd:b2143 cytidine deaminase:cytidine aminohydrolase:cda (gtcfc:4.2:4.4) (ec:3.5.4.5) (keggfc:4.2) (rileyfc:1.6.4) (db:gtc-escherichia coli) b2143 b2143 Escherichia coli 562 -11533072 63642 cdd (ec:3.5.4.5) (de:cytidine deaminase, (cytidine aminohydrolase) (cda)) (db:swissprot) CDD_ECOLI P13652 ESCHERICHIA COLI 562 -11533072 7000684781 cdd cytidine deaminase (cl:cdd protein) (ec:3.5.4.5) (db:pir2.dat) F64982 F64982 Escherichia coli 562 -11533072 234754 cdd cytidine deaminase (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (ec:3.5.4.5) (de:escherichia coli cytidine deaminase (cdd) gene, complete cds.) (nt:putative) (le:92) (re:976) (di:direct) ECOCDDA M60916 g145470 Escherichia coli 562 -11533072 7500878428 cytidine deaminase (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (nt:cytidine deaminase.) (le:44615) (re:45499) (di:direct) ECOHU47 U00007 g453291 Escherichia coli 562 -11533072 233943 cdd cytidine/deoxycytidine deaminase (fn:enzyme; salvage of nucleosides and nucleotides) (db:genpept-bct2) (ec:3.5.4.5) (de:escherichia coli k-12 mg1655 section 193 of 400 of the completegenome.) (nt:o294; 100 pct identical to cdd_ecoli sw: p13652; cg) (le:6913) (re:7797) (di:direct) AE000303 AE000303 g1788465 Escherichia coli 562 -11533072 5000690320 (de:(ecoli_2092) (pn:cytidine) (gn:cdd) (gtcfc:4.2) (ec:3.5.4.5) (cdd_ecoli) (keggfc:4.2) (rileyfc:1.6.4) (db:gtc-escherichia coli)) ECOLI_2092 ECOLI_2092 Escherichia coli 562 10006311				
ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826834	7893	30049	450	149
Description				
6500729215 upp:b2498 uracil phosphoribosyltransferase (gtcfc:4.2:4.4) (ec:2.4.2.9) (keggfc:4.2) (rileyfc:1.6.4) (db:gtc-escherichia coli) b2498 b2498 Escherichia coli 562 -11533073 7000691929 upp uracil phosphoribosyltransferase:upp (cl:uracil phosphoribosyltransferase upp) (ec:2.4.2.9) (db:pir2.dat) A65026 A65026 Escherichia coli 562 -11533073 7500960478 upp uracil phosphoribosyltransferase (fn:enzyme; salvage of nucleosides and nucleotides) (db:genpept-bct2) (ec:2.4.2.9) (de:escherichia coli k-12 mg1655 section 226 of 400 of the completegenome.) (nt:f208; 100 pct identical to upp_ecoli sw: p25532) (le:4289) (re:4942) (di:complement) AE000336 AE000336 g1788844 Escherichia coli 562 -11533073 5000690321 (de:(ecoli_2438) (pn:uracil phosphoribosyltransferase) (gn:upp) (gtcfc:4.2) (ec:2.4.2.9) (upp_ecoli) (keggfc:4.2) (rileyfc:1.6.4) (db:gtc-escherichia coli)) ECOLI_2438 ECOLI_2438 Escherichia coli 562 10123710				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826840	7894	30050	294	97

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826843	7895	30051	324	107

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826866	7896	30052	435	144

Description

6500729216 thya:b2827 thymidylate synthetase:thymidylate synthase:ts  
(gtcfc:4.2:9.6) (ec:2.1.1.45) (keggfc:4.2:9.7:9.8) (rileyfc:1.6.3)  
(db:gtc-escherichia coli) (gtcfc:nucleotide metabolism-pyrimidine  
metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and  
folate biosynthesis) (rileyfc:small-molecule... b2827 b2827 Escherichia coli  
562 -11533074 102942 thya (ec:2.1.1.45) (de:thymidylate synthase, (ts))  
(db:swissprot) TYSY\_ECOLI P00470 ESCHERICHIA COLI 562 -11533074 123227 thya  
thymidylate synthase (cl:thymidylate synthase:thymidylate synthase homology)  
(ec:2.1.1.45) (db:pir1.dat) (mp:61 min) SYECT A00549 Escherichia coli 562  
-11533074 7500893621 thya (sr:escherichia coli dna) (db:genpept-bct1)  
(de:e.coli thya gene coding for thymidylate synthase.) (nt:thymidylate  
synthase) (le:215) (re:1009) (di:direct) ECOTHYA J01710 g147987 Escherichia  
coli 562 -11533074 236101 thya thymidylate synthetase (fn:enzyme;  
2'-deoxyribonucleotide metabolism) (db:genpept-bct2) (ec:2.1.1.45)  
(de:escherichia coli k-12 mg1655 section 256 of 400 of the completegenome.)  
(nt:f264; 99 pct identical to tysy\_ecoli sw: p00470; cg) (le:5419) (re:6213)  
(di:complement) AE000366 AE000366 g1789191 Escherichia coli 562 -11533074  
5000690323 (de:(ecoli\_2755) (pn:thymidylate synthetase) (gn:thya)  
(gtcfc:4.2:9.6) (ec:2.1.1.45) (tysy\_ecoli) (keggfc:4.2:9.8) (rileyfc:1.6.3)  
(db:gtc-escherichia coli)) ECOLI\_2755 ECOLI\_2755 Escherichia coli 562  
10044754

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826870	7897	30053	951	317
<u>Description</u>				
6500729217 dut:dnas:sof:b3640 deoxyuridine 5-triphosphate nucleotidohydrolase:dutpase:dutp pyrophosphatase (gtcfc:4.2) (ec:3.6.1.23) (keggfc:4.2) (rileyfc:1.6.3) (db:gtc-escherichia coli) (rileyfc:small-molecule metabolism, 2'-deoxyribonucleotide metabolism) b3640 b3640 Escherichia coli 562 -11533075 236878 dut:dnas:sof (ec:3.6.1.23) (de:(dutpase) (dutp pyrophosphatase)) (db:swissprot) DUT_ECOLI P06968 ESCHERICHIA COLI 562 -11533075 125083 dut dutp pyrophosphatase (cl:dutp pyrophosphatase) (ec:3.6.1.23) (db:pir1.dat) (mp:82 min) WPECU A30388 Escherichia coli 562 -11533075 232716 (db:genpept-bct1) (de:e. coli dut gene for dutpase (ec 3.6.1.23) (deoxyuridine5'-triphosphate nucleotidohydrolase).) (nt:dutp-ase (aa 1-151)) (le:343) (re:798) (di:direct) ECDUT X01714 g41297 Escherichia coli 562 -11533075 5000690324 (db:genpept-bct1) (de:escherichia coli dut-pyre gene region.) (nt:dutpase (dut)) (le:343) (re:798) (di:direct) ECDUTPYR V01578 g41300 Escherichia coli 562 -11533075 7500880708 dut::cg site no. 832 deoxyuridinetriphosphatase (sr:escherichia coli k12 strain mgl655; lambda clones ecl4-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:3324) (re:3779) (di:direct) ECOUW82 L10328 g290490 Escherichia coli 562 -11533075 232714 dut deoxyuridinetriphosphatase (fn:enzyme; 2'-deoxyribonucleotide metabolism) (db:genpept-bct2) (ec:3.6.1.23) (de:escherichia coli k-12 mgl655 section 331 of 400 of the completegenome.) (nt:ol51; 100 pct identical amino acid sequence and) (le:5827) (re:6282) (di:direct) AE000441 AE000441 g1790071 Escherichia coli 562 -11533075 69365 dut:dnas:sof (ec:3.6.1.23) (de:(dutpase) (dutp pyrophosphatase)) (db:swissprot) DUT_ECOLI P06968 ESCHERICHIA COLI 562 -11533075				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826876	7898	30054	645	214

Description

6500729218 pyre:b3642 orotate phosphoribosyltransferase:oprt:oprtase (gtcfc:4.2) (ec:2.4.2.10) (keggfc:4.2) (rileyfc:1.6.2) (db:gtc-escherichia coli) b3642 b3642 Escherichia coli 562 -11533076 7000691876 pyre orotate phosphoribosyltransferase (cl:orotate phosphoribosyltransferase:orotate phosphoribosyltransferase homology) (ec:2.4.2.10) (db:pir1.dat) (mp:82 min) XJEC D65165 Escherichia coli 562 -11533076 237978 pyre::cg site no. 327 orotate phosphoribosyltransferase (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:4519) (re:5160) (di:complement) ECOUW82 L10328 g643610 Escherichia coli 562 -11533076 304618 orotate phosphoribosyltransferase (db:genpept-bct1) (ec:2.4.2.10) (de:e.coli pyre operon with orotate phosphoribosyltransferase gene andorfe gene.) (le:1153) (re:1794) (di:direct) ECPYRE X00781 g755728 Escherichia coli 562 -11533076 236880 pyre orotate phosphoribosyltransferase (fn:enzyme; pyrimidine ribonucleotide biosynthesis) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 331 of 400 of the completegenome.) (nt:f213; cg site no. 327) (le:7022) (re:7663) (di:complement) AE000441 AE000441 g1790073 Escherichia coli 562 -11533076 5000690325 (de:(ecoli\_3562) (pn:orotate phosphoribosyltransferase) (gn:pyre) (gtcfc:4.2) (ec:2.4.2.10) (pyre\_ecoli) (keggfc:4.2) (rileyfc:1.6.2) (db:gtc-escherichia coli)) ECOLI\_3562 ECOLI\_3562 Escherichia coli 562 10124049

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826894	7899	30055	630	209

Description

6500729219 udp:b3831 uridine phosphorylase:udrpase (gtcfc:4.2:4.4) (ec:2.4.2.3) (keggfc:4.2) (rileyfc:1.6.4) (db:gtc-escherichia coli) b3831 b3831 Escherichia coli 562 -11533077 164813 udp uridine phosphorylase (ec:2.4.2.3) (db:pir2.dat) (mp:86 min) S05491 S05491 Escherichia coli 562 -11533077 240328 udp::cgsc no. 41 uridine phosphorylase (db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (le:69504) (re:70265) (di:direct) ECOUW85 M87049 g148229 Escherichia coli 562 -11533077 7500960480 (db:genpept-bct1) (de:e. coli udp gene for uridine phosphorylase (ec 2.4.2.3).) (nt:uridine phosphorylase (aa 1 - 253)) (le:163) (re:924) (di:direct) ECUDP X15689 g43242 Escherichia coli 562 -11533077 237054 udp uridine phosphorylase (fn:enzyme; salvage of nucleosides and nucleotides) (db:genpept-bct2) (ec:2.4.2.3) (de:escherichia coli k-12 mg1655 section 349 of 400 of the completegenome.) (nt:o253; 100 pct identical to udp\_ecoli sw: p12758) (le:168) (re:929) (di:direct) AE000459 AE000459 g1790265 Escherichia coli 562 -11533077 5000690326 (de:(ecoli\_3736) (pn:uridine phosphorylase) (gn:udp) (gtcfc:4.2) (ec:2.4.2.3) (udp\_ecoli) (keggfc:4.2) (rileyfc:1.6.4) (db:gtc-escherichia coli)) ECOLI\_3736 ECOLI\_3736 Escherichia coli 562 10087476



ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826895	7900	30056	423	140

# Description

6500729220 pyri:b4244 aspartate carbamoyltransferase regulatory subunit:aspartate carbamoyltransferase regulatory chain (gtcfc:4.2:5.2) (ec:2.1.3.2) (keggfc:4.2:5.2) (rileyfc:1.6.2) (db:gtc-escherichia coli) b4244 b4244 Escherichia coli 562 -11533078 123298 pyri aspartate carbamoyltransferase:regulatory chain:aspartate transcarbamylase:carbamylaspartotranskinase (cl:aspartate carbamoyltransferase regulatory chain) (ec:2.1.3.2) (db:pir1.dat) (mp:97 min) DTECR A93985 Escherichia coli 562 -11533078 237450 (sr:escherichia coli dna, clones pdp8, ppyrb9(wt), pyrb554, pyrb730 an) (db:genpept-bct1) (de:e.coli pyrbi operon encoding aspartate transcarbamoylase (atcase).) (nt:aspartate transcarbamoylase regulatory chain) (le:949) (re:1410) (di:direct) ECOPYRBIA K01472 g147465 Escherichia coli 562 -11533078 7500953228 pyri aspartate carbamoyltransferase regulatory (db:genpept-bct1) (ec:2.1.3.2) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 323) (le:161815) (re:162276) (di:complement) ECOUW93 U14003 g537086 Escherichia coli 562 -11533078 235639 pyri aspartate carbamoyltransferase:regulatory (fn:enzyme; pyrimidine ribonucleotide biosynthesis) (db:genpept-bct2) (ec:2.1.3.2) (de:escherichia coli k-12 mg1655 section 385 of 400 of the completegenome.) (nt:f153; 100 pct identical to pyri\_ecoli sw: p00478;) (le:11628) (re:12089) (di:complement) AE000495 AE000495 g1790692 Escherichia coli 562 -11533078 5000690327 (de:(ecoli\_4127) (pn:aspartate carbamoyltransferase, regulatory subunit) (gn:pyri) (gtcfc:4.2:5.2) (ec:2.1.3.2) (pyri\_ecoli) (keggfc:4.2:5.2) (rileyfc:1.6.2) (db:gtc-escherichia coli)) ECOLI\_4127 ECOLI\_4127 Escherichia coli 562 10065777

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826896	7901	30057	489	162
<u>Description</u>				

6500729221 pyrb:b4245 aspartate carbamoyltransferase catalytic subunit:aspartate carbamoyltransferase catalytic chain:aspartate transcarbamylase:atcase (gtcfc:4.2:5.2) (ec:2.1.3.2) (keggfc:4.2:5.2) (rileyfc:1.6.2) (db:gtc-escherichia coli) b4245 b4245 Escherichia coli 562 -11533079 7000688855 pyrb aspartate carbamoyltransferase:catalytic chain:aspartate transcarbamylase catalytic chain:aspartyl carbamoyltransferase catalytic chain:carbamylaspartotranskinase catalytic chain (cl:ornithine carbamoyltransferase:aspartate/ornithine carbamoyltransferase homology) (ec:2.1.3.2) (db:pir1.dat) (mp:97 min) DTECC H65236 Escherichia coli 562 -11533079 7500953229 pyrb aspartate carbamoyltransferase:catalytic (fn:enzyme; pyrimidine ribonucleotide biosynthesis) (db:genpept-bct2) (ec:2.1.3.2) (de:escherichia coli k-12 mg1655 section 385 of 400 of the completegenome.) (nt:f311; 99 pct identical amino acid sequence and) (le:12102) (re:13037) (di:complement) AE000495 AE000495 g2367364 Escherichia coli 562 -11533079

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826898	7902	30058	702	233
<u>Description</u>				

GTC ORF with score 245 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana dna chromosome 4, essa i contig fragment no.2.) (nt:similarity to progesterone membrane binding protein) (le:110933:111226:111388) (re:111142:111304:111753) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826900	7903	30059	300	100
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826906	7904	30060	414	137
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826911	7905	30061	522	174

Description

6500729222 cara:pyra:b0032 carbamoyl-phosphate synthase small chain:carbamoyl-phosphate synthetase glutamine chain (gtcfc:4.2:5.1) (ec:6.3.5.5) (keggfc:5.1) (rileyfc:1.6.2) (db:gtc-escherichia coli) b0032 b0032 Escherichia coli 562 -11533080 62788 cara:pyra (ec:6.3.5.5) (de:phosphate synthetase glutamine chain)) (db:swissprot) CARA\_ECOLI P00907 ESCHERICHIA COLI 562 -11533080 125582 cara:pyra carbamoyl-phosphate synthase glutamine-hydrolyzing:small chain:carbamoyl-phosphate synthetase glutamine chain (cl:carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain:carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology:trpg homology) (ec:6.3.5.5) (db:pir1.dat) (mp:1 min) SYECCS A01128 Escherichia coli 562 -11533080 233936 cara carbamoyl-phosphate synthase small chain (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (ec:6.3.5.5) (de:e.coli k12 genome, 0-2.4min. region.) (le:29305) (re:30453) (di:direct) ECO110K D10483 g285764 Escherichia coli 562 -11533080 7500878174 cara (sr:escherichia coli k12 dna, clone pmc40 (2),(3)) (db:genpept-bct1) (de:e.coli carbamoyl-phosphate synthetase subunits a and b (carab)genes, complete cds.) (nt:carbamoyl-phosphate synthetase subunit a (ttg start) (le:474) (re:1622) (di:direct) ECOCARAB J01597 g551790 Escherichia coli 562 -11533080 233569 cara carbamoyl-phosphate synthetase:glutamine (fn:enzyme; pyrimidine ribonucleotide biosynthesis) (db:genpept-bct2) (ec:6.3.5.5) (de:escherichia coli k-12 mg1655 section 3 of 400 of the completegenome.) (nt:o382; 100 pct identical to cara\_ecoli sw:) (le:8992) (re:10140) (di:direct) AE000113 AE000113 g1786215 Escherichia coli 562 -11533080 5000690366 (de:(ecoli\_32) (pn:carbamoyl-phosphate synthetase, glutamine:small subunit) (gn:carab) (gtcfc:5.1) (ec:6.3.5.5) (cara\_ecoli) (keggfc:5.1) (rileyfc:1.6.2) (db:gtc-escherichia coli)) ECOLI\_32 ECOLI\_32 Escherichia coli 562 10005462

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826913	7906	30062	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826919	7907	30063	336	111

Description

6500729223 carb:pyra:b0033 carbamoyl-phosphate synthase large chain:carbamoyl-phosphate synthetase ammonia chain (gtcfc:4.2:5.1) (ec:6.3.5.5) (keggfc:5.1) (rileyfc:1.6.2) (db:gtc-escherichia coli) b0033 b0033 Escherichia coli 562 -11533081 126060 carb carbamoyl-phosphate synthase glutamine-hydrolyzing:large chain:carbamoyl-phosphate synthetase glutamine-hydrolyzing ammonia chain (cl:carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain:biotin carboxylase homology:carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology) (ec:6.3.5.5) (db:pir1.dat) (mp:1 min) SYECCP A01198 Escherichia coli 562 -11533081 233570 (db:genpept-bct1) (de:e. coli gene carb encoding carbamoyl-phosphate synthetase largesubunit (ec 6.3.5.5). map position is 1 minute.) (nt:carb reading frame) (le:87) (re:3308) (di:direct) ECCARB V01500 g41079 Escherichia coli 562 -11533081 233937 carb carbamoyl-phosphate synthase large chain (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (ec:6.3.5.5) (de:e.coli k12 genome, 0-2.4min. region.) (le:30471) (re:33692) (di:direct) ECO110K D10483 g216460 Escherichia coli 562 -11533081 7500953389 carb carbamoyl-phosphate synthetase subunit b (sr:escherichia coli k12 dna, clone pmc40 (2),(3)) (db:genpept-bct1) (de:e.coli carbamoyl-phosphate synthetase subunits a and b (carab)genes, complete cds.) (le:1640) (re:4861) (di:direct) ECOCARAB J01597 g145464 Escherichia coli 562 -11533081 232482 carb carbamoyl-phosphate synthase large subunit (fn:enzyme; pyrimidine ribonucleotide biosynthesis) (db:genpept-bct2) (ec:6.3.5.5) (de:escherichia coli k-12 mg1655 section 3 of 400 of the completegenome.) (nt:o1073; 100 pct identical to carb\_ecoli sw: p00968) (le:10158) (re:13379) (di:direct) AE000113 AE000113 g1786216 Escherichia coli 562 -11533081 5000690367 (de:(ecoli\_33) (pn:carbamoyl-phosphate synthase large subunit) (gn:carb) (gtcfc:5.1) (ec:6.3.5.5) (carb\_ecoli) (keggfc:5.1) (rileyfc:1.6.2) (db:gtc-escherichia coli)) ECOLI\_33 ECOLI\_33 Escherichia coli 562 10066530

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826921	7908	30064	906	301

Description

6500729224 pyrl:b4246 aspartate transcarbamoylase leader peptide:pyrbi operon leader peptide:attenuator (gtcfc:4.2) (keggfc:14.2) (rileyfc:1.6.2) (db:gtc-escherichia coli) b4246 b4246 Escherichia coli 562 -11533082 82418 pyrl (de:pyrbi operon leader peptide (attenuator)) (db:swissprot) LPPY\_ECOLI P09150 ESCHERICHIA COLI 562 -11533082 131598 pyrl:pyrbi pyrbi leader peptide:aspartate transcarbamoylase leader peptide (cl:pyrbi leader peptide) (db:pir1.dat) (mp:97 min) LPECBI A24926 Escherichia coli 562 -11533082 235642 pyrbi (sr:e.coli k-12 dna) (db:genpept-bct1) (de:e.coli pyrbi operon promoter-regulatory region including leaderpeptide and 5' end of pyrbi gene coding for the catalytic subunit of aspartate transcarbamoylase (atcase).) (nt:aspartate transcarbamoylase leader p... ECOPYRBIB M10743 g147467 Escherichia coli 562 -11533082 237452 pyrbi leader peptide (sr:e.coli (strain k12) dna) (db:genpept-bct1) (de:e.coli aspartate transcarbamoylase (pyrbi) operon promoter region, leader peptide, complete cds, and catalytic subunit, 5' end of cds.) (le:281) (re:415) (di:direct) ECOPYRBIC M60508 g147470 Escherichia coli 562 -11533082 7500885131 pyrl aspartate transcarbamoylase leader peptide (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:163228) (re:163362) (di:complement) ECOUW93 U14003 g537088 Escherichia coli 562 -11533082 235640 pyrl pyrbi operon leader peptide (fn:leader; pyrimidine ribonucleotide biosynthesis) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 385 of 400 of the complete genome.) (nt:f44; 100 pct identical amino acid sequence and) (le:13041) (re:13175) (di:complement) AE000495 AE000495 g1790694 Escherichia coli 562 -11533082 5000690329 (de:(ecoli\_4129) (pn:pyrbi operon leader peptide) (gn:pyrl) (gtcfc:4.2) (ec:) (lppy\_ecoli) (keggfc:11.2) (rileyfc:1.6.2) (db:gtc-escherichia coli)) ECOLI\_4129 ECOLI\_4129 Escherichia coli 562 10024642

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826927	7909	30065	225	74

Description

6500729225 mutt:b0099 mutator mutt  
protein:7:8-dihydro-8-oxoguanine-triphosphatase:8-oxo-dgtpase:dgtp  
pyrophosphohydrolase (gtcfc:4.2:9.6) (ec:3.6.1.-) (keggfc:9.7)  
(rileyfc:1.6.3) (db:gtc-escherichia coli) (gtcfc:nucleotide  
metabolism-pyrimidine metabolism:metabolism of cofactors and vitamins-biotin  
metabolism (b8) and folate biosynthesis) (rileyfc:small-molecule metaboli...  
b0099 b0099 Escherichia coli 562 -11533083 233623 mutt (ec:3.6.1.-)  
(de:(8-oxo-dgtpase), (dgtp pyrophosphohydrolase)) (db:swissprot) MUTT\_ECOLI  
P08337 ESCHERICHIA COLI 562 -11533083 131412 mutt  
7:8-dihydro-8-oxoguanine-triphosphatase::mutator mutt at-gc transversion  
(cl:mutator mutt:mutt domain homology) (ec:3.6.1.-) (db:pir1.dat) (mp:3 min)  
MVECMT A27890 Escherichia coli 562 -11533083 228006 mutt mutt protein  
(db:genpept-bct1) (de:e. coli 2 minute region.) (le:27574) (re:27963)  
(di:direct) EC2MIN X55034 g40867 Escherichia coli 562 -11533083 5000690650  
(db:genpept-bct1) (de:e. coli mutator gene mutt (a:t to c:g transversion).)  
(nt:mutt protein (aa 1-129)) (le:164) (re:553) (di:direct) ECMUTT X04831  
g42071 Escherichia coli 562 -11533083 304543 mutt mutator mutt at-gc  
transversion (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1)  
(de:e.coli k12 genome, 0-2.4min. region.) (le:110698) (re:111087)  
(di:direct) ECO110K D10483 g216513 Escherichia coli 562 -11533083 233442  
mutt 7:8-dihydro-8-oxoguanine-triphosphatase:prefers (fn:enzyme;  
2'-deoxyribonucleotide metabolism) (db:genpept-bct2) (ec:3.6.1.-)  
(de:escherichia coli k-12 mg1655 section 9 of 400 of the completegenome.)  
(nt:o129; 100 pct identical to mutt\_ecoli sw: p08337) (le:5800) (re:6189)  
(di:direct) AE000119 AE000119 g1786288 Escherichia coli 562 -11533083 84750  
mutt (ec:3.6.1.-) (de:(8-oxo-dgtpase), (dgtp pyrophosphohydrolase))  
(db:swissprot) MUTT\_ECOLI P08337 ESCHERICHIA COLI 562 -11533083

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826940	7910	30066	762	253

# Description

6500729226 grxa:grx:b0849 glutaredoxin 1:grx1 (gtcfc:4.2) (keggfc:14.2) (rileyfc:1.6.3) (db:gtc-escherichia coli) (rileyfc:small-molecule metabolism, 2'-deoxyribonucleotide metabolism) b0849 b0849 Escherichia coli 562 -11533084 74064 grxa:grx (de:glutaredoxin 1 (grx1)) (db:swissprot) GLR1\_ECOLI P00277 ESCHERICHIA COLI 562 -11533084 122376 grxa:grx glutaredoxin 1:thioltransferase (cl:glutaredoxin:glutaredoxin homology) (db:pir1.dat) (mp:19 min) GDEC A00283 Escherichia coli 562 -11533084 223226 grxa glutaredoxin 1 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #210) (db:genpept-bct1) (de:escherichia coli genomic dna.(19.0 - 19.3 min).) (le:7180) (re:7437) (di:complement) D90723 D90723 g1655499 Escherichia coli 562 -11533084 238751 (sr:e.coli k12 (strain c10-17) dna, clone pembl9ecg) (db:genpept-bct1) (de:e. coli grx gene encoding glutaredoxin.) (nt:glutaredoxin (grx)) (le:285) (re:542) (di:direct) ECOGRX M13449 g146273 Escherichia coli 562 -11533084 234581 grxa glutaredoxin1 redox coenzyme for (fn:carrier; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 77 of 400 of the completegenome.) (nt:f85; 100 pct identical to glr1\_ecoli sw: p00277;) (le:2480) (re:2737) (di:complement) AE000187 AE000187 g1787073 Escherichia coli 562 -11533084 7500882525 glutaredoxin (db:genpept-bct2) (de:escherichia coli modulator of drug activity (mda18) andglutaredoxin genes, complete cds.) (le:3) (re:260) (di:complement) ECU18655 U18655 g609325 Escherichia coli 562 -11533084 5000690891 grx glutaredoxin 1 grx1 . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #210) (db:genpept) (de:escherichia coli genomic dna. (19.1 - 19.4 min).) (nt:orf\_id:o210#7; similar to swissprot accession) (le:7180) (re:7437) (di:complement) D90723 D90723 g1655499 Escherichia coli 562 -11533084

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826945	7911	30067	720	239

#### Description

6500729227 grxb:b1064 glutaredoxin 2:grx2 (gtcfc:4.2) (keggfc:14.2) (rileyfc:1.6.3) (db:gtc-escherichia coli) (rileyfc:small-molecule metabolism, 2'-deoxyribonucleotide metabolism) b1064 b1064 Escherichia coli 562 -11533085 7500882530 grxb (de:glutaredoxin 2 (grx2)) (db:swissprot) GLR2\_ECOLI P39811 ESCHERICHIA COLI 562 -11533085 7000685421 grxb glutaredoxin 2 (db:pir2.dat) E64849 E64849 Escherichia coli 562 -11533085 5000690892 grxb glutaredoxin 2 (db:genpept-bct1) (de:e.coli grxb gene.) (le:1296) (re:1943) (di:direct) ECGRXB X92076 g1743238 Escherichia coli 562 -11533085 233038 grxb glutaredoxin 2 (fn:carrier; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 97 of 400 of the completegenome.) (nt:f215; 94 pct identical to fragment grl2\_ecoli) (le:6743) (re:7390) (di:complement) AE000207 AE000207 g1787303 Escherichia coli 562 -11533085 7502851879 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #233) (db:genpept) (de:escherichia coli genomic dna. (24.1 - 24.5 min).) (nt:orf\_id:o233#12) (le:9773) (re:10420) (di:complement) D90743 D90743 g4062644 Escherichia coli 562 -11533085 74068 grxb (de:glutaredoxin 2 (grx2)) (db:swissprot) GLR2\_ECOLI P39811 ESCHERICHIA COLI 562 -11533085

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501826949	7912	30068	186	61

#### Description

6500729228 grxc:b3610 glutaredoxin 3:grx3 (gtcfc:4.2) (keggfc:14.2) (rileyfc:1.6.3) (db:gtc-escherichia coli) (rileyfc:small-molecule metabolism, 2'-deoxyribonucleotide metabolism) b3610 b3610 Escherichia coli 562 -11533086 163692 grxc glutaredoxin 3 grx3:hypothetical protein f83 (cl:glutaredoxin:glutaredoxin homology) (db:pir2.dat) S47831 S47831 Escherichia coli 562 -11533086 7500959751 (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:198441) (re:198692) (di:complement) ECOUW76 U00039 g466748 Escherichia coli 562 -11533086 236847 grxc glutaredoxin 3 (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 329 of 400 of the completegenome.) (nt:f83; 100 pct identical amino acid sequence and) (le:1619) (re:1870) (di:complement) AE000439 AE000439 g1790039 Escherichia coli 562 -11533086 5000690893 (de:(ecoli\_3530) (pn:glutaredoxin 3) (gn:grxc) (gtcfc:10.8) (ec:) (glr3\_ecoli) (keggfc:11.2) (rileyfc:1.6.3) (db:gtc-escherichia coli)) ECOLI\_3530 ECOLI\_3530 Escherichia coli 562 10087020



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826955	7913	30069	378	125
<u>Description</u>				
6500729229 yagh:b0271 hypothetical protein:putative beta-xylosidase:1:4-beta-d-xylan xylohydrolase:xylan 1:4-beta-xylosidase (gtcfc:4.3:7.2) (ec:3.2.1.37) (keggfc:4.3:7.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0271 b0271 Escherichia coli 562 -11533087 4000708008 yagh (ec:3.2.1.37) (de:xylohydrolase) (xylan 1,4-beta-xylosidase)) (db:swissprot) YAGH_ECOLI P77713 ESCHERICHIA COLI 562 -11533087 7000687208 xynb xylan 1:4-beta-xylosidase (ec:3.2.1.37) (db:pir2.dat) G64752 G64752 Escherichia coli 562 -11533087 7500896153 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:similar to xylan 1,4-beta-xylosidase of bacillus) (le:117087) (re:118697) (di:direct) ECU70214 U70214 g1552840 Escherichia coli 562 -11533087 239891 yagh putative beta-xylosidase ec 3.2.1.37 (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 25 of 400 of the completegenome.) (nt:o536; 52 pct identical (3 gaps) to 534 residues of) (le:1538) (re:3148) (di:direct) AE000135 AE000135 g1786467 Escherichia coli 562 -11533087 5000691474 (de:(ecoli_262) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_262 ECOLI_262 Escherichia coli 562 10122739				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826972	7914	30070	1641	546

#### Description

6500729230 rfba:b2039 tdp-glucose pyrophosphorylase:glucose-1-phosphate thymidyltransferase:dt dp-glucose synthase:dt dp-glucose pyrophosphorylase (gtcfc:4.3) (ec:2.7.7.24) (keggfc:4.3) (rileyfc:1.3.3) (db:gtc-escherichia coli) b2039 b2039 Escherichia coli 562 -11533088 93154 rfba (ec:2.7.7.24) (de:synthase) (dt dp-glucose pyrophosphorylase)) (db:swissprot) RBA1\_ECOLI P37744 ESCHERICHIA COLI 562 -11533088 7000686272 rfba glucose-1-phosphate thymidyltransferase (cl:glucose-1-phosphate thymidyltransferase) (sr:strain k-12, , strain k-12) (sr:strain k-12, ) (ec:2.7.7.24) (db:pir2.dat) F64969 F64969 Escherichia coli 562 -11533088 224564 rfba glucose-1-phosphate thymidyltransferase ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #351(45.1-45.5 min.)) (nt:orf\_id:o351#15; similar to (swissprot accession) (le:16438) (re:17319) (di:complement) D90841 D90841 g1736729 Escherichia coli 562 -11533088 224576 rfba glucose-1-phosphate thymidyltransferase ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #352(45.3-45.7 min.)) (nt:orf\_id:o351#15; similar to (swissprot accession) (le:7227) (re:8108) (di:complement) D90842 D90842 g1736742 Escherichia coli 562 -11533088 7000686273 rmla glucose-1-phosphate thymidyltransferase (db:genpept-bct1) (de:escherichia coli k-12 dt dp-d-glucose 4,6-dehydratase (rmlb), dt dp-6-deoxy-1-mannose-dehydrogenase (rml d), glucose-1-phosphatethymidyltransferase (rmla), dt dp-6-deoxy-d-glucose-3,5 epimerase(rmlc), putative o-antigen transporter (... ECU09876 U09876 g2665491 Escherichia coli 562 -11533088 301204 rfba glucose-1-phosphate thymidyltransferase (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:2.7.7.24) (de:escherichia coli k-12 mg1655 section 184 of 400 of the completegenome.) (nt:f293; 99 pct identical to rfba\_ecoli sw: p37744; cg) (le:12895) (re:13776) (di:complement) AE000294 AE000294 g1788351 Escherichia coli 562 -11533088 301216 rmla glucose-1-phosphate thymidyltransferase (db:genpept-bct1) (de:escherichia coli k-12 dt dp-d-glucose 4,6-dehydratase (rmlb), dt dp-6-deoxy-1-mannose-dehydrogenase (rml d), glucose-1-phosphatethymidyltransferase (rmla), dt dp-6-deoxy-d-glucose-3,5 epimerase(rmlc), putative o-antigen transporter (... ECU09876 U09876 g2665491 Escherichia coli 562 -11533088 5000690330 (de:(ecoli\_1987) (pn:tdp-glucose pyrophosphorylase) (gn:rfba) (gtcfc:4.3) (ec:2.7.7.24) (rba1\_ecoli) (keggfc:4.3) (rileyfc:1.3.3) (db:gtc-escherichia coli)) ECOLI\_1987 ECOLI\_1987 Escherichia coli 562 10119969

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826974	7915	30071	231	76

#### Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501826975	7916	30072	564	187

# Description

6500729231 mltb:b2701 membrane-bound lytic transglycosylase b precursor:membrane-bound lytic murein transglycosylase b precursor:murein hydrolase b:35 kd soluble lytic transglycosylase:slt35 (gtcfc:4.3:7.1:11.4) (ec:3.2.1.-) (keggfc:4.3:4.4) (rileyfc:3.3.4) (db:gtc-escherichia coli) b2701 b2701 Escherichia coli 562 -11533089 83904 mltb (ec:3.2.1.-) (de:(murein hydrolase b) (35 kd soluble lytic transglycosylase) (slt35)) (db:swissprot) MLTB\_ECOLI P41052 ESCHERICHIA COLI 562 -11533089 7000685853 mltb membrane-bound lytic transglycosylase:b precursor:mltb protein (ec:3.2.1.-) (db:pir2.dat) A65050 A65050 Escherichia coli 562 -11533089 225253 mltb membrane-bound lytic murein transglycosylase b (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #446(60.5-60.9 min.)) (nt:similar to (swissprot accession number p41052)) (le:13397) (re:14482) (di:complement) D90892 D90892 g1800087 Escherichia coli 562 -11533089 7500885686 mltb membrane-bound lytic transglycosylase precursor (db:genpept-bct1) (de:escherichia coli membrane-bound lytic transglycosylase (mltb) gene, and ygad (ygad) gene, complete cds.) (le:151) (re:1236) (di:direct) ECU18785 U18785 g642538 Escherichia coli 562 -11533089 238755 mltb membrane-bound lytic murein transglycosylase b (fn:enzyme; murein sacculus, peptidoglycan) (db:genpept-bct2) (ec:3.2.1.-) (de:escherichia coli k-12 mgl655 section 244 of 400 of the completegenome.) (nt:f361; 100 pct identical to mltb\_ecoli sw: p41052;) (le:2447) (re:3532) (di:complement) AE000354 AE000354 g1789053 Escherichia coli 562 -11533089 5000690331 (de:(ecoli\_2629) (pn:membrane-bound lytic murein transglycosylase b) (gn:mltb) (gtcfc:4.3:7.2) (ec:3.2.1.-) (mltb\_ecoli) (keggfc:4.3:7.1) (rileyfc:3.3.4) (db:gtc-escherichia coli)) ECOLI\_2629 ECOLI\_2629 Escherichia coli 562 10026111

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826997	7917	30073	330	109

Description

6500729232 mlta:mlt:b2813 membrane-bound lytic murein transglycosylase a precursor:murein hydrolase a:mlt38 (gtcfc:4.3:7.1:11.4) (ec:3.2.1.-) (keggfc:4.3:4.4) (rileyfc:3.3.4) (db:gtc-escherichia coli) b2813 b2813 Escherichia coli 562 -11533090 83903 mlta:mlt (ec:3.2.1.-) (de:(murein hydrolase a) (mlt38)) (db:swissprot) MLTA\_ECOLI P46885 ESCHERICHIA COLI 562 -11533090 7000685852 mlta membrane-bound lytic murein transglycosylase a precursor (ec:3.2.1.-) (db:pir2.dat) A65064 A65064 Escherichia coli 562 -11533090 7500885685 mlta membrane-bound lytic murein transglycosylase a (fn:enzyme; murein sacculus, peptidoglycan) (db:genpept-bct2) (ec:3.2.1.-) (de:escherichia coli k-12 mg1655 section 255 of 400 of the completegenome.) (nt:f365; 99 pct identical to mlta\_ecoli sw:) (le:150) (re:1247) (di:complement) AE000365 AE000365 g1789179 Escherichia coli 562 -11533090 5000690332 (de:(ecoli\_2744) (pn:membrane-bound lytic murein transglycosylase a; mlt38) (gn:mlta) (gtcfc:4.3:7.2) (ec:3.2.1.-) (mlta\_ecoli) (keggfc:4.3:7.1) (rileyfc:3.3.4) (db:gtc-escherichia coli)) ECOLI\_2744 ECOLI\_2744 Escherichia coli 562 10123845

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501826998	7918	30074	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827002	7919	30075	465	154

Description

6500729233 mltc:b2963 yggz:membrane-bound lytic murein transglycosylase c precursor:murein hydrolase c (gtcfc:4.3:7.1:11.4) (ec:3.2.1.-) (keggfc:4.3:4.4) (rileyfc:5.9.0:5.9.0) (db:gtc-escherichia coli) b2963 b2963 Escherichia coli 562 -11533091 7000691955 yggz yggz protein (db:pir2.dat) B65082 B65082 Escherichia coli 562 -11533091 7500960514 mltc membrane-bound lytic murein transglycosylase c (fn:putative enzyme; murein sacculus,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 269 of 400 of the completegenome.) (nt:o360; formerly designated yggz) (le:61) (re:1143) (di:direct) AE000379 AE000379 g2367180 Escherichia coli 562 -11533091

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827010	7920	30076	444	147
<u>Description</u>				
6500729234 glgx:glyx:b3431 glycogen operon protein glgx (gtcfc:1.1) (ec:3.2.1.-) (keggfc:4.3:4.4) (rileyfc:3.1.10) (db:gtc-escherichia coli) b3431 b3431 Escherichia coli 562 -11533092 73815 glgx:glyx (ec:3.2.1.-) (de:glycogen operon protein glgx,) (db:swissprot) GLGX_ECOLI P15067 ESCHERICHIA COLI 562 -11533092 7000685405 glgx glycogen operon protein glgx (cl:glyx protein) (ec:3.2.1.-) (db:pir1.dat) (mp:75 min) BVECGX B65139 Escherichia coli 562 -11533092 7500882408 glgx part of glycogen operon:a glycosyl hydrolase (fn:enzyme; macromolecule synthesis, modification:) (db:genpept-bct2) (ec:3.2.1.-) (de:escherichia coli k-12 mg1655 section 309 of 400 of the completegenome.) (nt:f657; longer orf due to differences from ecoglg;) (le:5755) (re:7728) (di:complement) AE000419 AE000419 g2367229 Escherichia coli 562 -11533092				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827011	7921	30077	1683	561
<u>Description</u>				
6500729235 rffh:b3789 hypothetical 32.7 kd protein in rffe-rfft intergenic region:glucose-1-phosphate thymidyltransferase:ddp-glucose synthase:ddp-glucose pyrophosphorylase (gtcfc:4.3) (ec:2.7.7.24) (keggfc:4.3) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3789 b3789 Escherichia coli 562 -11533093 94207 rffh (ec:2.7.7.24) (de:synthase) (ddp-glucose pyrophosphorylase)) (db:swissprot) RFFH_ECOLI P27831 ESCHERICHIA COLI 562 -11533093 7000686315 rffh glucose-1-phosphate thymidyltransferase::protein o292 (cl:glucose-1-phosphate thymidyltransferase) (ec:2.7.7.24) (db:pir2.dat) H65182 Escherichia coli 562 -11533093 7500889704 rffh glucose-1-phosphate thymidyltransferase (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 345 of 400 of the completegenome.) (nt:o293; formerly designated yifg) (le:3525) (re:4406) (di:direct) AE000455 AE000455 g1790224 Escherichia coli 562 -11533093 5000690334 (de:(ecoli_3699) (pn:glucose-1-phosphate thymidyltransferase:ddp-glucose synthase:ddp-glucose pyrophosphorylase) (gn:rffh) (gtcfc:4.3) (ec:2.7.7.24) (rffh_ecoli) (keggfc:4.3) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3699 ECOLI_3699 Escherichia coli 562 10124098				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501827016	7922	30078	528	175

Description

6500729236 slt:b4392 soluble lytic transglycosylase (gtcfc:4.3:7.1:11.4) (ec:3.2.1.-) (keggfc:4.3:4.4) (rileyfc:3.3.4) (db:gtc-escherichia coli) b4392 b4392 Escherichia coli 562 -11533094 140113 slt soluble lytic transglycosylase:precursor (cl:soluble lytic transglycosylase) (ec:3.2.1.-) (db:pir1.dat) (mp:100 min) QQECW1 S56616 Escherichia coli 562 -11533094 7500953300 slt soluble lytic transglycosylase (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:321539) (re:323503) (di:direct) ECOUW93 U14003 g537232 Escherichia coli 562 -11533094 237597 slt soluble lytic murein transglycosylase (fn:enzyme; murein sacculus, peptidoglycan) (db:genpept-bct2) (ec:3.2.1.-) (de:escherichia coli k-12 mg1655 section 399 of 400 of the completegenome.) (nt:o654; 99 pct identical to 645 amino acids) (le:5894) (re:7858) (di:direct) AE000509 AE000509 g1790853 Escherichia coli 562 -11533094 5000690335 (de:(ecoli\_4274) (pn:soluble lytic murein transglycosylase) (gn:slt) (gtcfc:4.3:7.2) (ec:3.2.1.-) (slt\_ecoli) (keggfc:4.3:7.1) (rileyfc:3.3.4) (db:gtc-escherichia coli)) ECOLI\_4274 ECOLI\_4274 Escherichia coli 562 10071637

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501827036	7923	30079	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501827056	7924	30080	330	109

Description

6500729237 glmu:b3730 udp-n-acetylglucosamine pyrophosphorylase:n-acetylglucosamine-1-phosphate uridyltransferase (gtcfc:4.3:7.1) (ec:2.7.7.23) (keggfc:4.4) (rileyfc:1.3.3) (db:gtc-escherichia coli) b3730 b3730 Escherichia coli 562 -11533095 73871 glmu (ec:2.7.7.23) (de:acetylglucosamine-1-phosphate uridyltransferase) (db:swissprot) GLMU\_ECOLI P17114 ESCHERICHIA COLI 562 -11533095 7000685406 glmu glmu protein (cl:n-acetylglucosamine-1-phosphate uridyltransferase) (db:pir2.dat) C65176 C65176 Escherichia coli 562 -11533095 7500882448 glmu n-acetyl glucosamine-1-phosphate (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 340 of 400 of the completegenome.) (nt:f456; ??? pct identical to glmu\_ecoli sw:) (le:2283) (re:3653) (di:complement) AE000450 AE000450 g1790168 Escherichia coli 562 -11533095 5000690536 (de:(ecoli\_3648) (pn:n-acetyl glucosamine-1-phosphate uridyltransferase) (gn:glmu) (gtcfc:7.1) (ec:2.7.7.23) (glmu\_ecoli) (keggfc:4.4) (rileyfc:1.3.3) (db:gtc-escherichia coli)) ECOLI\_3648 ECOLI\_3648 Escherichia coli 562 10124085

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827082	7925	30081	219	72
<u>Description</u>				
Hypothetical protein				

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827091	7926	30082	645	214

Description

6500729238 gpt:gpp:gxu:b0238 xanthine-guanine  
phosphoribosyltransferase: xgprt (gtcfc:4.4) (ec:2.4.2.22) (keggfc:14.1)  
(rileyfc:1.6.4) (db:gtc-escherichia coli) b0238 b0238 Escherichia coli 562  
-11533096 234572 gpt:gpp:gxu (ec:2.4.2.22) (de:xanthine-guanine  
phosphoribosyltransferase, (xgprt)) (db:swissprot) XGPT\_ECOLI P00501  
ESCHERICHIA COLI 562 -11533096 123448 gpt xanthine  
phosphoribosyltransferase::xanthine--guanine phosphoribosyltransferase  
(cl:xanthine phosphoribosyltransferase) (ec:2.4.2.22) (db:pir1.dat) (mp:6  
min) RTECGX A00587 Escherichia coli 562 -11533096 233030 gpt  
xanthine-guanine phospho-ribosyl transferase (db:genpept-bct1) (ec:2.4.2.22)  
(de:e.coli xanthine-guanine phosphoribosyl transferase gene (gpt)  
(ec2.4.2.22).) (le:199) (re:657) (di:direct) ECGPT1 X00221 g41607  
Escherichia coli 562 -11533096 236202 (db:genpept-bct1) (de:e. coli  
xanthine guanine phosphorybosyl transferase gene (genecode: gpt).)  
(nt:xanthine guanine phosphorybosyl-transferase) (le:200) (re:658)  
(di:direct) ECGPT2 X00222 g41609 Escherichia coli 562 -11533096 234573  
(sr:escherichia coli dna, clone gpt2eco (derivative of sv2-gpt) (1))  
(db:genpept-bct1) (de:e.coli gpt gene, coding for xanthine guanine  
phosphoribosyltransferase (xgprt), complete cds.) (nt:xanthine guanine  
phosphorybosyl-transferase (gpt)) (le:194) (r... ECOGPT K01784 g146254  
Escherichia coli 562 -11533096 234577 gpt (sr:e.coli k12 dna, clone pjp14)  
(db:genpept-bct1) (de:e.coli gpt gene encoding xanthine-guanine  
phosphoribosyltransferase (xgprt), complete cds.) (nt:xanthine-guanine  
phosphoribosyl transferase (ec) (le:303) (re:761) (di:direct) ECOGPTA M13422  
g146256 Escherichia coli 562 -11533096 408613 (sr:e.coli dna from psv-2-gpt  
plasmid) (db:genpept-bct1) (de:e.coli gpt gene encoding xanthine guanine  
phosphoribosyltransferase, complete cds.) (nt:xanthine-guanine  
phosphoribosyl transferase) (le:200) (re:658) (di:direct) ECOGPTC M12907  
g146262 Escherichia coli 562 -11533096 239857 gpt xanthine-guanine  
phosphoribosyltransferase (sr:escherichia coli (strain:k12) dna)  
(db:genpept-bct1) (ec:2.4.2.22) (de:escherichia coli genome, 4.0 - 6.0 min  
region.) (le:65518) (re:65976) (di:direct) ECOTSF D83536 g1208984  
Escherichia coli 562 -11533096 303279 gpt xanthine-guanine  
phosphoribosyltransferase (db:genpept-bct1) (de:escherichia coli chromosome  
minutes 4-6.) (le:87052) (re:87510) (di:direct) ECU70214 U70214 g1552806  
Escherichia coli 562 -11533096 233029 gpt guanine-hypoxanthine  
phosphoribosyltransferase (fn:enzyme; salvage of nucleosides and  
nucleotides) (db:genpept-bct2) (ec:2.4.2.22) (de:escherichia coli k-12  
mg1655 section 22 of 400 of the completegenome.) (nt:o152; 100 pct to  
xgpt\_ecoli sw: p00501; alternate) (le:2693) (re:3151) (di:direct) AE000132  
AE000132 g1786433 Escherichia coli 562 -11533096 407922 (sr:sv40 dna and  
e.coli dna) (db:genpept-syn) (de:synthetic plasmid pdsp1: a cloning vector  
for eukaryotic genes andgene regulatory elements, segment 2.) (nt:xpgprt)  
(le:434) (re:892) (di:direct) SYNDSP2 K03394 g208231 unidentified cloning  
vector 45196 -11533096 408610 gpt xanthine-guanine phosphoribosyl  
transferase (db:genpept-syn) (ec:2.4.2.22) (de:pmsg cloning vector, complete



transferase (db:genpept-syn) (ec:2.4.2.22) (de:pmsg cloning vector, complete sequence) (le:1416) (re:1874) (di:direct) YXII3860 III3860 g595749

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827104	7927	30083	1068	356

Description

GTC ORF with score 625 to: (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (ec:1.6.4.2) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 665) (le:60558) (re:61910) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827106	7928	30084	918	305

Description

6500729239 deor:nucr:b0840 deoxyribose operon repressor (gtcfc:4.4) (keggfc:14.2) (rileyfc:1.6.4) (db:gtc-escherichia coli) b0840 b0840 Escherichia coli 562 -11533097 7500880181 deor:nucr (de:deoxyribose operon repressor) (db:swissprot) DEOR\_ECOLI P06217 ESCHERICHIA COLI 562 -11533097 131527 deor:nucr deoxyribose operon repressor:deo operon repressor (cl:deo operon repressor) (db:pir1.dat) (mp:19 min) RPECDO A24076 Escherichia coli 562 -11533097 223224 deor deoxyribose operon repressor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #209) (db:genpept-bct1) (de:escherichia coli genomic dna. (18.7 - 19.1 min).) (le:11076) (re:11834) (di:complement) D90722 D90722 g1651382 Escherichia coli 562 -11533097 5000690337 (db:genpept-bct1) (de:e. coli gene for deor repressor.) (nt:deor repressor (aa 1-252)) (le:181) (re:939) (di:direct) ECDEOR X02837 g41260 Escherichia coli 562 -11533097 232664 deor transcriptional repressor for deo operon:tsx (fn:regulator; salvage of nucleosides and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 76 of 400 of the completegenome.) (nt:f252; 100 pct identical to deor\_ecoli sw: p06217) (le:3865) (re:4623) (di:complement) AE000186 AE000186 g1787063 Escherichia coli 562 -11533097 7502851881 deor deoxyribose operon repressor. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #209) (db:genpept) (de:escherichia coli genomic dna. (18.8 - 19.2 min).) (nt:orf\_id:o209#10; similar to swissprot accession) (le:11076) (re:11834) (di:complement) D90722 D90722 g1651382 Escherichia coli 562 -11533097 68269 deor:nucr (de:deoxyribose operon repressor) (db:swissprot) DEOR\_ECOLI P06217 ESCHERICHIA COLI 562 -11533097

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827109	7929	30085	2226	741

Description

GTC ORF with score 467 to: (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 260 of 400 of the completegenome.) (nt:o398; this 398 aa orf is 27 pct identical (19 gaps)) (le:7409) (re:8605) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501827125	7930	30086	357	118
Description				
6500729240 cpdb:b4213 2:3-cyclic-nucleotide 2-phosphodiesterase:2:3-cyclic-nucleotide 2-phosphodiesterase precursor (gtcfc:4.4) (ec:3.1.4.16) (keggfc:14.1) (rileyfc:1.6.4) (db:gtc-escherichia coli) b4213 b4213 Escherichia coli 562 -11533098 64892 cpdb (ec:3.1.4.16) (de:2',3'-cyclic-nucleotide 2'-phosphodiesterase precursor,) (db:swissprot) CN16_ECOLI P08331 ESCHERICHIA COLI 562 -11533098 7000684854 cpdb 2:3-cyclic-nucleotide 2-phosphodiesterase:precursor (cl:2',3'-cyclic-nucleotide 2'-phosphodiesterase:2',3'-cyclic-nucleotide 2'-phosphodiesterase homology:phosphoesterase core homology) (ec:3.1.4.16) (db:pir1.dat) (mp:96 min) ESECPC H65232 Escherichia coli 562 -11533098 7500878922 cpdb 2:3-cyclic-nucleotide 2-phosphodiesterase (db:genpept-bct1) (ec:3.1.4.16) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 909) (le:125454) (re:127397) (di:complement) ECOUW93 U14003 g537054 Escherichia coli 562 -11533098 237418 cpdb 2:3-cyclic-nucleotide 2-phosphodiesterase (fn:enzyme; salvage of nucleosides and nucleotides) (db:genpept-bct2) (ec:3.1.4.16) (de:escherichia coli k-12 mg1655 section 382 of 400 of the completegenome.) (nt:f647; 100 pct identical to cn16_ecoli sw: p08331;) (le:7194) (re:9137) (di:complement) AE000492 AE000492 g1790658 Escherichia coli 562 -11533098 5000690338 (de:(ecoli_4096) (pn:; 2"-3" cyclic-nucleotide, :2"phosphodiesterase:2":3"-cyclic-nucleotide 2"-phosphodiesterase) (gn:cpdb) (gtcfc:4.4) (ec:3.1.4.16) (cn16_ecoli) (keggfc:11.1) (rileyfc:1.6.4) (db:gtc-escherichia coli)) ECOLI_4096 ECOLI_4096 Escherichia coli 562 10007553				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827132	7931	30087	288	96
<u>Description</u>				
6500729241 glns:b0680 glutaminyl-trna synthetase:glutamine--trna ligase:glhrs (gtcfc:10.6:5.1) (ec:6.1.1.18) (keggfc:5.1:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli) b0680 b0680 Escherichia coli 562 -11533099 7000688910 glns glutamine--trna ligase::glutaminyl-trna synthetase (cl:glutamine--trna ligase:glutamine--trna ligase homology) (ec:6.1.1.18) (db:pir1.dat) (mp:15 min) SYECQT G64802 Escherichia coli 562 -11533099 7500953371 glns glutaminyl-trna synthetase precursor (db:genpept-bct1) (ec:6.1.1.18) (de:e. coli gene glns for glutaminyl-trna synthetase.) (le:310) (re:1974) (di:direct) ECGLNS V01575 g463198 Escherichia coli 562 -11533099 233005 glns glutamine trna synthetase (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:6.1.1.18) (de:escherichia coli k-12 mg1655 section 61 of 400 of the completegenome.) (nt:o554; 100 pct identical to syq_ecoli sw: p00962) (le:8800) (re:10464) (di:direct) AE000171 AE000171 g1786895 Escherichia coli 562 -11533099 5000690368 glns glutaminyl-trna synthetase ec 6.1.1.18 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #172) (db:genpept) (de:escherichia coli genomic dna. (15.1 - 15.5 min).) (nt:orf_id:ol72#5; similar to swissprot accession) (le:5921) (re:7585) (di:direct) D90707 D90707 g4062281 Escherichia coli 562 -11533099				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827133	7932	30088	540	179
<u>Description</u>				
6500729242 puta:poaa:b1014 proline oxidase:proline dehydrogenase:proline oxidase / delta-1-pyrroline-5-carboxylate dehydrogenase:p5c dehydrogenase (gtcfc:5.1:5.10:6.6) (keggfc:5.1:5.10) (rileyfc:1.1.2) (db:gtc-escherichia coli) b1014 b1014 Escherichia coli 562 -11533100 92492 puta:poaa (ec:1.5.99.8:1.5.1.12) (de:dehydrogenase)) (db:swissprot) PUTA_ECOLI P09546 ESCHERICHIA COLI 562 -11533100 7000686247 puta:poaa proline dehydrogenase:1-pyrroline-5-carboxylate dehydrogenase::proline oxidase (cl:bifunctional protein puta) (ec:1.5.99.8:1.5.1.12) (db:pir2.dat) (mp:23 min) D64843 D64843 Escherichia coli 562 -11533100 223331 puta proline dehydrogenase proline oxidase / (sr:escherichia coli(strain:k12) dna, clone:kohara clone #228) (db:genpept-bct1) (de:escherichia coli genomic dna. (22.9 - 23.3 min).) (le:8881) (re:12843) (di:complement) D90738 D90738 g1651503 Escherichia coli 562 -11533100 7500889106 puta proline dehydrogenase:p5c dehydrogenase (fn:enzyme; degradation of small molecules: amino) (db:genpept-bct2) (ec:1.5.99.8) (de:escherichia coli k-12 mg1655 section 93 of 400 of the completegenome.) (nt:f1320; 99 pct identical to puta_ecoli sw: p09546) (le:824) (re:4786) (di:complement) AE000203 AE000203 g1787250 Escherichia coli 562 -11533100 5000690352 poaa proline dehydrogenase ec 1.5.99.8 proline (sr:escherichia coli(strain:k12) dna, clone:kohara clone #228) (db:genpept) (de:escherichia coli genomic dna. (23.0 - 23.4 min).) (nt:orf_id:o228#12; similar to swissprot accession) (le:8881) (re:12843) (di:complement) D90738 D90738 g1651503 Escherichia coli 562 -11533100				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827135	7933	30089	207	68
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827142	7934	30090	240	79
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827145	7935	30091	186	61
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827150	7936	30092	558	185

Description

6500729243 nade:efg:ntrl:b1740 nh3-dependent nad synthetase:nh:3-dependent nad+ synthetase:nitrogen-regulatory protein (gtcfc:5.1:9.4) (ec:6.3.5.1) (keggfc:5.1:9.4) (rileyfc:1.7.7) (db:gtc-escherichia coli) b1740 b1740 Escherichia coli 562 -11533101 85146 nade:efg:ntrl (ec:6.3.5.1) (de:protein)) (db:swissprot) NADE\_ECOLI P18843 ESCHERICHIA COLI 562 -11533101 7000685905 nade nad+ synthase glutamine-hydrolyzing::nitrogen-regulatory protein (cl:spore outgrowth factor b) (ec:6.3.5.1) (db:pir2.dat) (mp:34-39 min) D64933 D64933 Escherichia coli 562 -11533101 224209 nade:efg:ntrl\_\_ nh 3 -dependent nad + synthetase ec 6.3.5.1 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #326(39.1-39.4 min.)) (nt:orf\_id:o326#9; similar to (swissprot accession) (le:7818) (re:8645) (di:direct) D90817 D90817 g1742846 Escherichia coli 562 -11533101 300857 nade:efg:ntrl\_\_ nh 3 -dependent nad + synthetase ec 6.3.5.1 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #327(39.2-39.5 min.)) (nt:orf\_id:o326#9; similar to (swissprot accession) (le:2186) (re:3013) (di:direct) D90818 D90818 g1742853 Escherichia coli 562 -11533101 300851 nade nad synthetase:prefers nh3 over glutamine (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:6.3.5.1) (de:escherichia coli k-12 mg1655 section 159 of 400 of the completegenome.) (nt:o275; residues 32-274 are 100 pct identical to) (le:1232) (re:2059) (di:direct) AE000269 AE000269 g1788036 Escherichia coli 562 -11533101 224215 nade:efg:ntrl\_\_ nh 3 -dependent nad + synthetase ec 6.3.5.1 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #327(39.2-39.5 min.)) (nt:orf\_id:o326#9; similar to (swissprot accession) (le:2186) (re:3013) (di:direct) D90818 D90818 g1742853 Escherichia coli 562 -11533101 5000690369 (de:(ecoli\_1697) (pn:nad synthetase, prefers nh3 over glutamine) (gn:nade) (gtcfc:5.1:9.4) (ec:6.3.5.1) (nade\_ecoli) (keggfc:5.1:9.4) (rileyfc:1.7.7) (db:gtc-escherichia coli)) ECOLI\_1697 ECOLI\_1697 Escherichia coli 562 10119805

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827159	7937	30093	480	159

Description

6500729244 gltx:b2400 glutamyl-trna synthetase:glutamate--trna ligase:glurs (gtcfc:10.6:5.1) (ec:6.1.1.17) (keggfc:5.1:9.10:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli) b2400 b2400 Escherichia coli 562 -11533102 237624 gltx (ec:6.1.1.17) (de:(glurs)) (db:swissprot) SYE\_ECOLI P04805 ESCHERICHIA COLI 562 -11533102 125920 gltx glutamate--trna ligase::glutamyl-trna synthetase (cl:glutamate--trna ligase:glutamine--trna ligase homology) (ec:6.1.1.17) (db:pir1.dat) (mp:52 min) SYECET A25956 Escherichia coli 562 -11533102 224959 gltx glutamate--trna ligase ec 6.1.1.17 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #416(54.1-54.5 min.)) (nt:similar to (pir accession number a25956)) (le:12101) (re:13516) (di:complement) D90869 D90869 g1799814 Escherichia coli 562 -11533102 7500892373 gltx glutamyl-trna synthetase (db:genpept-bct1) (de:escherichia coli k12 valu, gltx and alaw region.) (le:1877) (re:3292) (di:direct) ECGLTXVA X63976 g41596 Escherichia coli 562 -11533102 5000690370 gltx glutamyl-trna synthetase (sr:escherichia coli (sub\_strain n99, strain k-12) dna) (db:genpept-bct1) (de:escherichia coli alaw (transfer rna-ala), valu (transfer rna-valand transfer rna-lys) operons and glutamyl-trna synthetase (gltx)gene, complete cds.) (le:1877) (re:3292) (di:... ECOUXW M13687 g148256 Escherichia coli 562 -11533102 233019 gltx glutamate trna synthetase:catalytic subunit (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 218 of 400 of the completegenome.) (nt:f471; 100 pct identical to sye\_ecoli sw: p04805) (le:946) (re:2361) (di:complement) AE000328 AE000328 g1788743 Escherichia coli 562 -11533102 100020 gltx (ec:6.1.1.17) (de:(glurs)) (db:swissprot) SYE\_ECOLI P04805 ESCHERICHIA COLI 562 -11533102

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827160	7938	30094	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827161	7939	30095	534	177

Description

6500729245 gsha:gsh-i:b2688 glutamate--cysteine  
 ligase:gamma-glutamylcysteine synthetase:gamma-ecs:gcs (gtcfc:5.1:6.16:9.2)  
 (ec:6.3.2.2) (keggfc:5.1:6.9) (rileyfc:1.7.9) (db:gtc-escherichia coli)  
 (gtcfc:l-amino acid metabolism-glutamate metabolism:metabolism of other  
 amino acids-glutathione metabolism:metabolism of cofactors and  
 vitamins-riboflavin meta... b2688 b2688 Escherichia coli 562 -11533103  
 7000688911 gsha::gshi glutamate--cysteine ligase::gamma-glutamylcysteine  
 synthetase (cl:glutamate--cysteine ligase) (ec:6.3.2.2) (db:pir1.dat) (mp:58  
 min) SYECEC A65049 Escherichia coli 562 -11533103 225245 gsha  
 glutamate--cysteine ligase ec 6.3.2.2 (sr:escherichia coli (strain:k12) dna,  
 clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
 kohara clone #446(60.5-60.9 min.)) (nt:similar to (pir accession number  
 a24136)) (le:3790) (re:5346) (di:complement) D90892 D90892 g1800079  
 Escherichia coli 562 -11533103 7500953381 gsha gamma-glutamate-cysteine  
 ligase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2)  
 (ec:6.3.2.2) (de:escherichia coli k-12 mg1655 section 243 of 400 of the  
 completegenome.) (nt:f518; 99 pct identical to gsh1\_ecoli sw: p06980 cg)  
 (le:5359) (re:6915) (di:complement) AE000353 AE000353 g1789044 Escherichia  
 coli 562 -11533103 5000690371 (de:(ecoli\_2621) (pn:gamma-glutamate-cysteine  
 ligase) (gn:gsha) (gtcfc:5.1:6.16) (ec:6.3.2.2) (gsh1\_ecoli)  
 (keggfc:5.1:6.9) (rileyfc:1.7.9) (db:gtc-escherichia coli)) ECOLI\_2621  
 ECOLI\_2621 Escherichia coli 562 10120326

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827162	7940	30096	513	170

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827163	7941	30097	495	165

Description

6500729246 spea:b2938 biosynthetic arginine decarboxylase:adc  
 (gtcfc:5.1:5.10:5.16) (ec:4.1.1.19) (keggfc:5.1:5.10) (rileyfc:1.5.0)  
 (db:gtc-escherichia coli) b2938 b2938 Escherichia coli 562 -11533104  
 7000689183 spea arginine decarboxylase (cl:arginine decarboxylase)  
 (ec:4.1.1.19) (db:pir2.dat) (mp:64 min) A65079 A65079 Escherichia coli 562  
 -11533104 7500954386 spea (fn:arginine decarboxylase) (db:genpept-bct1)  
 (ec:4.1.1.19) (de:escherichia coli k-12 genome; approximately 65 to 68  
 minutes.) (nt:cg site no. 161) (le:38330) (re:40306) (di:complement)  
 ECU28377 U28377 g882467 Escherichia coli 562 -11533104 239151 spea  
 biosynthetic arginine decarboxylase (fn:enzyme; central intermediary  
 metabolism:) (db:genpept-bct2) (ec:4.1.1.19) (de:escherichia coli k-12  
 mg1655 section 267 of 400 of the completegenome.) (nt:f658; 99 pct identical  
 to spea\_ecoli sw: p21170; cg) (le:2253) (re:4229) (di:complement) AE000377  
 AE000377 g1789307 Escherichia coli 562 -11533104 5000690357  
 (de:(ecoli\_2860) (pn:biosynthetic arginine decarboxylase) (gn:spea)  
 (gtcfc:5.10:5.1) (ec:4.1.1.19) (spea\_ecoli) (keggfc:5.1:5.10)  
 (rileyfc:1.5.0) (db:gtc-escherichia coli)) ECOLI\_2860 ECOLI\_2860 Escherichia  
 coli 562 10123911

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827196	7942	30098	210	69

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827204	7943	30099	1371	456

Description

6500729247 gshb:gsh-ii:b2947 glutathione synthetase:glutathione synthase:gsh synthetase:gsh-s:gshase (gtcfc:5.1:6.16:9.2) (ec:6.3.2.3) (keggfc:5.1:6.9) (rileyfc:1.7.9) (db:gtc-escherichia coli) (gtcfc:l-amino acid metabolism-glutamate metabolism:metabolism of other amino acids-glutathione metabolism:metabolism of cofactors and vitamins-riboflavin meta... b2947 b2947 Escherichia coli 562 -11533105 239160 gshb:gsh-ii (ec:6.3.2.3) (de:synthetase) (gsh-s) (gshase)) (db:swissprot) GSHB\_ECOLI P04425 ESCHERICHIA COLI 562 -11533105 125999 gshb:gsh-ii glutathione synthase::glutathione synthetase (cl:glutathione synthase) (ec:6.3.2.3) (db:pir1.dat) SYECGS A01194 Escherichia coli 562 -11533105 5000690372 (db:genpept-bct1) (de:e. coli gene for glutathione synthetase (gsh-ii e.c. 6.3.2.3).) (nt:gsh-ii) (le:366) (re:1316) (di:direct) ECGSHII X01666 g41625 Escherichia coli 562 -11533105 7500882790 gshb glutathione synthetase (db:genpept-bct1) (ec:6.3.2.3) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:gshii) (le:46272) (re:47222) (di:direct) ECU28377 U28377 g882476 Escherichia coli 562 -11533105 233041 gshb glutathione synthetase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:6.3.2.3) (de:escherichia coli k-12 mg1655 section 267 of 400 of the completegenome.) (nt:o316; 100 pct identical to gsh2\_ecoli sw: p04425) (le:10196) (re:11146) (di:direct) AE000377 AE000377 g1789316 Escherichia coli 562 -11533105 74631 gshb:gsh-ii (ec:6.3.2.3) (de:synthetase) (gsh-s) (gshase)) (db:swissprot) GSHB\_ECOLI P04425 ESCHERICHIA COLI 562 -11533105

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827211	7944	30100	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827216	7945	30101	600	199

Description

6500729248 gor:b3500 glutathione oxidoreductase:glutathione reductase:gr:grase (gtcfc:5.1:6.16:9.2) (ec:1.6.4.2) (keggfc:5.1:6.9) (rileyfc:1.7.9) (db:gtc-escherichia coli) (gtcfc:l-amino acid metabolism-glutamate metabolism:metabolism of other amino acids-glutathione metabolism:metabolism of cofactors and vitamins-riboflavin meta... b3500 b3500 Escherichia coli 562 -11533106 74665 gor (ec:1.6.4.2) (de:glutathione reductase, (gr) (grase)) (db:swissprot) GSHR\_ECOLI P06715 ESCHERICHIA COLI 562 -11533106 122781 gor glutathione reductase nadph (cl:dihydrolipoamide dehydrogenase:dihydrolipoamide dehydrogenase homology) (ec:1.6.4.2) (db:pirl.dat) (mp:78 min) RDECU A24409 Escherichia coli 562 -11533106 236736 (sr:e.coli (clarke and carbon gene bank) dna, clone pgr) (db:genpept-bct1) (de:e.coli gor gene encoding glutathione reductase, complete cds.) (nt:glutathione reductase (ec 1.6.4.2)) (le:79) (re:1431) (di:direct) ECOGOR M13141 g146248 Escherichia coli 562 -11533106 7500882796 gor glutathione oxidoreductase (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (ec:1.6.4.2) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 665) (le:60558) (re:61910) (di:direct) ECOUW76 U00039 g466637 Escherichia coli 562 -11533106 234569 gor glutathione oxidoreductase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:1.6.4.2) (de:escherichia coli k-12 mg1655 section 316 of 400 of the completegenome.) (nt:o450; 100 pct identical to gshr\_ecoli sw: p06715;) (le:5598) (re:6950) (di:direct) AE000426 AE000426 g1789915 Escherichia coli 562 -11533106 5000690373 (de:(ecoli\_3419) (pn:glutathione oxidoreductase) (gn:gor) (gtcfc:5.1:6.16) (ec:1.6.4.2) (gshr\_ecoli) (keggfc:5.1:6.9) (rileyfc:1.7.9) (db:gtc-escherichia coli)) ECOLI\_3419 ECOLI\_3419 Escherichia coli 562 10017179

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827231	7946	30102	456	152

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827235	7947	30103	459	152

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827239	7948	30104	1251	416

#### Description

6500729249 glms:b3729 glutamine  
amidotransferase:glucosamine--fructose-6-phosphate  
aminotransferase:glucosamine--fructose-6-phosphate  
aminotransferase:isomerizing:hexosephosphate  
aminotransferase:d-fructose-6-phosphate  
amidotransferase:gfat:l-glutamine-d-fructose-6-phosphate  
amidotransferase:glucosamine-6-phosphate synthase (gtcfc:5.1:7.1)  
(ec:2.6.1.16) (keggfc:5.1) (rileyfc:1.3.4) (db:gtc-escherichia coli) b3729  
b3729 Escherichia coli 562 -11533107 7000688861 glms  
glutamine--fructose-6-phosphate transaminase  
isomerizing::glucosamine-6-phosphate synthase:glucosaminephosphate isomerase  
glutamine-forming:glutamine--fructose-6-phosphate aminotransferase  
isomerizing:hexosephosphate aminotransferase  
(cl:glutamine--fructose-6-phosphate aminotransferase (isomerizing))  
(ec:2.6.1.16) (db:pir1.dat) (mp:4 min) XNECGM B65176 Escherichia coli 562  
-11533107 7500953243 glms l-glutamine:d-fructose-6-phosphate (fn:enzyme;  
central intermediary metabolism: amino) (db:genpept-bct2) (de:escherichia  
coli k-12 mg1655 section 340 of 400 of the completegenome.) (nt:f609; 99 pct  
identical amino acid sequence and) (le:292) (re:2121) (di:complement)  
AE000450 AE000450 g1790167 Escherichia coli 562 -11533107 5000690374  
(de:(ecoli\_3647) (pn:l-glutamine:d-fructose-6-phosphate  
aminotransferase:l-glutamine, d-fructose-6-phosphate aminotransferase)  
(gn:glms) (gtcfc:5.1) (ec:2.6.1.16) (glms\_ecoli) (keggfc:5.1)  
(rileyfc:1.3.4) (db:gtc-escherichia col) ECOLI\_3647 ECOLI\_3647 Escherichia  
coli 562 10124084

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827259	7949	30105	216	71

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827266	7950	30106	186	61

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827275	7951	30107	351	116

Description

6500729250 muri:dga:glr:b3967 glutamate racemase (gtcfc:11.4:5.1:6.7) (ec:5.1.1.3) (keggfc:5.1:6.6) (rileyfc:3.3.4) (db:gtc-escherichia coli) b3967 b3967 Escherichia coli 562 -11533108 163122 muri:dga glutamate racemase (ec:5.1.1.3) (db:pir2.dat) (mp:89.8 min) I41187 I41187 Escherichia coli 562 -11533108 237185 dga glutamate synthase (fn:synthesis of d-glutamic acid in e. coli) (sr:escherichia coli (strain rdd020) dna) (db:genpept-bct1) (de:escherichia coli d-glutamate synthesis required peptidoglycan (dga)gene, complete cds, and btub protein, 3' end.) (le:415) (re:1284) (di:direct) ECODGABTU L14556 g290428 Escherichia coli 562 -11533108 238181 (db:genpept-bct1) (de:e. coli 3' noncoding region preceding the gene rrnb which codes for16s ribosomal rna.) (nt:unidentified reading frame) (le:579) (re:1448) (di:direct) ECCRNB V00347 g42876 Escherichia coli 562 -11533108 238182 (db:genpept-bct1) (de:e. coli ribosomal operon rrnb encoding the 16s ribosomal rna. alsotransfer rna specific for glu, 23s ribosomal rna and twounidentified open reading frames. this sequence was obtained fromthe transducing phage lambda-rif-d 18 (bamh... ECCRNBZ V00348 g42878 Escherichia coli 562 -11533108 234140 muri glutamate racemase:required for biosynthesis of (fn:enzyme; murein sacculus, peptidoglycan) (db:genpept-bct2) (ec:5.1.1.3) (de:escherichia coli k-12 mg1655 section 361 of 400 of the completegenome.) (nt:o289; 100 pct identical to 285 amino acids) (le:2001) (re:2870) (di:direct) AE000471 AE000471 g1790406 Escherichia coli 562 -11533108 7500959749 muri glutamate synthase (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:alternate gene name dga) (le:30658) (re:31527) (di:direct) ECOUW89 U00006 g396314 Escherichia coli 562 -11533108 5000690375 (de:(ecoli\_3865) (pn:glutamate racemase, required for biosynthesis of d-glutamate and peptidoglycan) (gn:muri) (gtcfc:5.1:6.7) (ec:5.1.1.3) (muri\_ecoli) (keggfc:5.1:6.6) (rileyfc:3.3.4) (db:gtc-escherichia coli)) ECOLI\_3865 ECOLI\_3865 Escherichia coli 562 10086778

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827276	7952	30108	525	174

Description

6500729251 adi:b4117 biodegradative arginine decarboxylase:adc  
 (gtcfc:5.1:5.10:6.6) (ec:4.1.1.19) (keggfc:5.1:5.10) (rileyfc:1.1.2)  
 (db:gtc-escherichia coli) b4117 b4117 Escherichia coli 562 -11533109 162753  
 adi arginine decarboxylase:biodegradative adc (ec:4.1.1.19) (db:pir2.dat)  
 S56346 S56346 Escherichia coli 562 -11533109 7500959676 adi  
 (fn:biodegradative arginine decarboxylase) (db:genpept-bct1) (de:escherichia  
 coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:29082)  
 (re:31352) (di:complement) ECOUW93 U14003 g536962 Escherichia coli 562  
 -11533109 237326 adia biodegradative arginine decarboxylase (fn:enzyme;  
 degradation of small molecules: amino) (db:genpept-bct2) (ec:4.1.1.19)  
 (de:escherichia coli k-12 mg1655 section 374 of 400 of the completegenome.)  
 (nt:f756; 100 pct identical amino acid sequence and) (le:2627) (re:4897)  
 (di:complement) AE000484 AE000484 g1790558 Escherichia coli 562 -11533109  
 5000690364 (de:(ecoli\_4004) (pn:biodegradative arginine decarboxylase)  
 (gn:adi) (gtcfc:5.10:5.1) (ec:4.1.1.19) (adi\_ecoli) (keggfc:5.1:5.10)  
 (rileyfc:1.1.2) (db:gtc-escherichia coli)) ECOLI\_4004 ECOLI\_4004 Escherichia  
 coli 562 10086609

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827280	7953	30109	384	128

Description

6500729252 glnd:b0167 uridylyltransferase (gtcfc:5.1:12.13) (ec:2.7.7.59)  
 (keggfc:12.1) (rileyfc:1.4.1) (db:gtc-escherichia coli) b0167 b0167  
 Escherichia coli 562 -11533110 73980 glnd (ec:2.7.7.59) (de:transferase)  
 (uridylyl removing enzyme) (utase)) (db:swissprot) GLND\_ECOLI P27249  
 ESCHERICHIA COLI 562 -11533110 7000685408 glnd uridylyltransferase  
 (cl:uridylyltransferase) (ec:2.7.7.59) (db:pir2.dat) G64740 G64740  
 Escherichia coli 562 -11533110 7500882469 glnd pii uridylyl-transferase  
 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:17053)  
 (re:19725) (di:complement) ECU70214 U70214 g1552744 Escherichia coli 562  
 -11533110 239795 glnd protein pii:uridylyltransferase acts on (fn:enzyme;  
 amino acid biosynthesis: glutamine) (db:genpept-bct2) (ec:2.7.7.59)  
 (de:escherichia coli k-12 mg1655 section 16 of 400 of the completegenome.)  
 (nt:f890; 100 pct identical to glnd\_ecoli sw: p27249) (le:2344) (re:5016)  
 (di:complement) AE000126 AE000126 g1786363 Escherichia coli 562 -11533110

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827292	7954	30110	546	181

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827297	7955	30111	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827314	7956	30112	399	132

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827336	7957	30113	333	111

Description

6500729253 prob:b0242 glutamate 5-kinase:gamma-glutamyl kinase:gk  
(gtcfc:5.1:5.16) (ec:2.7.2.11) (keggfc:5.16) (rileyfc:1.4.1)  
(db:gtc-escherichia coli) b0242 b0242 Escherichia coli 562 -11533111 91175  
prob (ec:2.7.2.11) (de:glutamate 5-kinase, (gamma-glutamyl kinase) (gk))  
(db:swissprot) PROB\_ECOLI P07005 ESCHERICHIA COLI 562 -11533111 7000686182  
prob glutamate 5-kinase::gamma-glutamyl kinase (cl:glutamate 5-kinase)  
(ec:2.7.2.11) (db:pirl.dat) (mp:6 min) KIECEG C64749 Escherichia coli 562  
-11533111 7500888526 prob glutamate 5-kinase (db:genpept-bct1)  
(de:escherichia coli chromosome minutes 4-6.) (le:90687) (re:91790)  
(di:direct) ECU70214 U70214 g1552810 Escherichia coli 562 -11533111 239861  
prob gamma-glutamate kinase (fn:enzyme; amino acid biosynthesis: proline)  
(db:genpept-bct2) (ec:2.7.2.11) (de:escherichia coli k-12 mg1655 section 22  
of 400 of the completengenome.) (nt:o367; 99 pct to prob\_ecoli sw: p07005)  
(le:6328) (re:7431) (di:direct) AE000132 AE000132 g1786437 Escherichia coli  
562 -11533111 5000690413 (de:(ecoli\_235) (pn:gamma-glutamate kinase)  
(gn:prob) (gtcfc:5.16) (ec:2.7.2.11) (prob\_ecoli) (keggfc:5.16)  
(rileyfc:1.4.1) (db:gtc-escherichia coli)) ECOLI\_235 ECOLI\_235 Escherichia  
coli 562 10122718

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827344	7958	30114	246	82

Description

6500729254 proa:b0243 gamma-glutamyl phosphate  
reductase:gpr:glutamate-5-semialdehyde  
dehydrogenase:glutamyl-gamma-semialdehyde dehydrogenase  
(gtcfc:5.1:5.16:9.10) (ec:1.2.1.41) (keggfc:5.16:9.10) (rileyfc:1.4.1)  
(db:gtc-escherichia coli) b0243 b0243 Escherichia coli 562 -11533112 91162  
proa (ec:1.2.1.41) (de:dehydrogenase)) (db:swissprot) PROA\_ECOLI P07004  
ESCHERICHIA COLI 562 -11533112 7000686181 proa glutamate-5-semialdehyde  
dehydrogenase::gamma-glutamylphosphate reductase  
(cl:glutamate-5-semialdehyde dehydrogenase) (ec:1.2.1.41) (db:pir1.dat)  
(mp:6 min) RDECER D64749 Escherichia coli 562 -11533112 7500888518 proa  
gamma-glutamyl phosphate reductase (db:genpept-bct1) (de:escherichia coli  
chromosome minutes 4-6.) (le:91802) (re:93055) (di:direct) ECU70214 U70214  
g1552811 Escherichia coli 562 -11533112 239862 proa gamma-glutamylphosphate  
reductase (fn:enzyme; amino acid biosynthesis: proline) (db:genpept-bct2)  
(de:escherichia coli k-12 mgl655 section 22 of 400 of the completegenome.)  
(nt:o417; 100 pct identical to proa\_ecoli sw: p07004) (le:7443) (re:8696)  
(di:direct) AE000132 AE000132 g1786438 Escherichia coli 562 -11533112  
5000690414 (de:(ecoli\_236) (pn:gamma-glutamylphosphate reductase) (gn:proa)  
(gtcfc:5.16:9.10) (ec:1.2.1.41) (proa\_ecoli) (keggfc:5.16:9.10)  
(rileyfc:1.4.1) (db:gtc-escherichia coli)) ECOLI\_236 ECOLI\_236 Escherichia  
coli 562 10122719

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827346	7959	30115	336	111

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827350	7960	30116	396	131
<u>Description</u>				
6500729255 argf:b0273 ornithine carbamoyltransferase chain f:otcase-2 (gtcf:5.1:5.10:5.16) (ec:2.1.3.3) (keggfc:5.10:5.16) (rileyfc:1.4.1) (db:gtc-escherichia coli) b0273 b0273 Escherichia coli 562 -11533113 7000688856 argf ornithine carbamoyltransferase:chain f:citrulline phosphorylase f:ornithine carbamoyltransferase argf:ornithine transcarbamylase f:otcase chain f (cl:ornithine carbamoyltransferase:aspartate/ornithine carbamoyltransferase homology) (ec:2.1.3.3) (db:pir1.dat) (mp:7 min) OWECF A64753 Escherichia coli 562 -11533113 7500953232 argf otcase (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:119599) (re:120603) (di:complement) ECU70214 U70214 g1552842 Escherichia coli 562 -11533113 239893 argf ornithine carbamoyltransferase 2:chain f (fn:enzyme; amino acid biosynthesis: arginine) (db:genpept-bct2) (ec:2.1.3.3) (de:escherichia coli k-12 mg1655 section 25 of 400 of the completegenome.) (nt:f334; 99 pct identical to otc2_ecoli sw: p06960) (le:4050) (re:5054) (di:complement) AE000135 AE000135 g1786469 Escherichia coli 562 -11533113 5000690349 (de:(ecoli_264) (pn:ornithine carbamoyltransferase 2) (gn:argf) (gtcf:5.10:5.16) (ec:2.1.3.3) (otc2_ecoli) (keggfc:5.10:5.16) (rileyfc:1.4.1) (db:gtc-escherichia coli)) ECOLI_264 ECOLI_264 Escherichia coli 562 10122741				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827367	7961	30117	849	282

Description

6500729256 proc:b0386 pyrroline-5-carboxylate reductase:p5cr:p5c reductase (gtcfc:5.1:5.10:5.16) (ec:1.5.1.2) (keggfc:5.10:5.16) (rileyfc:1.4.1) (db:gtc-escherichia coli) b0386 b0386 Escherichia coli 562 -11533114 91182 proc (ec:1.5.1.2) (de:pyrroline-5-carboxylate reductase, (p5cr) (p5c reductase)) (db:swissprot) PROC\_ECOLI P00373 ESCHERICHIA COLI 562 -11533114 122741 proc pyrroline-5-carboxylate reductase (cl:pyrroline-5-carboxylate reductase) (ec:1.5.1.2) (db:pir1.dat) (mp:9 min) RDECC A00385 Escherichia coli 562 -11533114 240003 proc (sr:escherichia coli k12 dna) (db:genpept-bct1) (de:e.coli proc gene coding for pyrroline carboxylate reductase.) (nt:pyrroline carboxylate reductase) (le:88) (re:897) (di:direct) ECOPROC J01665 g147359 Escherichia coli 562 -11533114 7500888537 proc pyrroline-5-carboxylate reductase (db:genpept-bct1) (ec:1.5.1.2) (de:escherichia coli chromosome minutes 6-8.) (le:112425) (re:113234) (di:complement) ECU73857 U73857 g1657582 Escherichia coli 562 -11533114 235558 proc pyrroline-5-carboxylate reductase (fn:enzyme; amino acid biosynthesis: proline) (db:genpept-bct2) (ec:1.5.1.2) (de:escherichia coli k-12 mg1655 section 35 of 400 of the completegenome.) (nt:f269; 100 pct identical to proc\_ecoli sw: p00373) (le:3711) (re:4520) (di:complement) AE000145 AE000145 g1786585 Escherichia coli 562 -11533114 5000690350 (de:(ecoli\_370) (pn:pyrroline-5-carboxylate reductase) (gn:proc) (gtcfc:5.10:5.16) (ec:1.5.1.2) (proc\_ecoli) (keggfc:5.10:5.16) (rileyfc:1.4.1) (db:gtc-escherichia coli)) ECOLI\_370 ECOLI\_370 Escherichia coli 562 10033281

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827370	7962	30118	921	306

Description

6500729257 glnb:b2553 nitrogen regulatory protein p-ii:nitrogen regulatory protein p-ii 1 (gtcfc:5.1:12.13) (keggfc:12.1) (rileyfc:1.4.1) (db:gtc-escherichia coli) b2553 b2553 Escherichia coli 562 -11533115 258596 glnb (de:nitrogen regulatory protein p-ii 1) (db:swissprot) GLNB\_ECOLI P05826 ESCHERICHIA COLI 562 -11533115 131518 glnb nitrogen regulatory protein p-ii.1 (cl:regulatory protein p-ii) (db:pir1.dat) RGECP2 C49940 Escherichia coli 562 -11533115 225150 glnb regulatory protein p-ii (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #432(57.5-57.9 min.)) (nt:similar to (pir accession number c49940)) (le:15099) (re:15437) (di:complement) D90885 D90885 g1799977 Escherichia coli 562 -11533115 304576 glnb p-ii protein (db:genpept-bct1) (de:e.coli hmp and glnb genes for hmp haemoprotein and p-ii protein.) (le:1528) (re:1866) (di:complement) ECHMPGLNB X58872 g41732 Escherichia coli 562 -11533115 7502851882 glnb small protein pii (db:genpept-bct1) (de:glnb region: nitrogen regulator i homolog, glnb=small protein pii(escherichia coli, genomic, 3 genes, 2641 nt.)) (nt:transcriptional regulator; glutamine synthetase) (le:2226) (re:2564) (di:direct) S67014 S67014 g455663 Escherichia coli 562 -11533115 233126 glnb regulatory protein p-ii for glutamine (fn:regulator; amino acid biosynthesis: glutamine) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 231 of 400 of the completgenome.) (nt:f112; 100 pct identical to glnb\_ecoli sw: p05826) (le:7685) (re:8023) (di:complement) AE000341 AE000341 g1788904 Escherichia coli 562 -11533115 73970 glnb (de:nitrogen regulatory protein p-ii 1) (db:swissprot) GLNB\_ECOLI P05826 ESCHERICHIA COLI 562 -11533115

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827384	7963	30119	2061	687

Description

6500729258 arga:b2818 amino-acid acetyltransferase:n-acetylglutamate synthase:ags (gtcfc:5.1:5.16) (ec:2.3.1.1) (keggfc:5.16) (rileyfc:1.4.1) (db:gtc-escherichia coli) b2818 b2818 Escherichia coli 562 -11533116 239389 arga (ec:2.3.1.1) (de:synthase) (ags)) (db:swissprot) ARGA\_ECOLI P08205 ESCHERICHIA COLI 562 -11533116 123330 arga amino-acid n-acetyltransferase (cl:amino-acid acetyltransferase) (ec:2.3.1.1) (db:pir1.dat) (mp:61 min) XYECAA A30372 Escherichia coli 562 -11533116 5000690415 (db:genpept-bct1) (de:e. coli arga gene for n-acetylglutamate synthase (ec 2.3.1.1).) (nt:n-acetylglutamate synthase (aa 1 - 443)) (le:244) (re:1575) (di:direct) ECARGA Y00492 g581038 Escherichia coli 562 -11533116 7500877110 arga n-acetylglutamate synthase (db:genpept-bct1) (ec:2.3.1.1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:cg site no. 1021; alternate names argb, arg1, arg2) (le:30797) (re:32128) (di:direct) ECU29581 U29581 g882710 Escherichia coli 562 -11533116 232380 arga n-acetylglutamate synthase:amino acid (fn:enzyme; amino acid biosynthesis: arginine) (db:genpept-bct2) (ec:2.3.1.1) (de:escherichia coli k-12 mg1655 section 255 of 400 of the completegenome.) (nt:o443; 100 pct identical to arga\_ecoli sw: p08205;) (le:3311) (re:4642) (di:direct) AE000365 AE000365 g1789181 Escherichia coli 562 -11533116 60059 arga (ec:2.3.1.1) (de:synthase) (ags)) (db:swissprot) ARGA\_ECOLI P08205 ESCHERICHIA COLI 562 -11533116

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827399	7964	30120	363	120

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501827403	7965	30121	1032	343

Description

6500729259 argg:b3172 argininosuccinate synthetase:argininosuccinate synthase:citrulline--aspartate ligase (gtcfc:5.1:5.10:5.16:5.2) (ec:6.3.4.5) (keggfc:5.2:5.10:5.16) (rileyfc:1.4.1) (db:gtc-escherichia coli) b3172 b3172 Escherichia coli 562 -11533117 7000688914 argg argininosuccinate synthase::citrulline--aspartate ligase (cl:argininosuccinate synthase) (ec:6.3.4.5) (db:pir1.dat) AJECRS G65107 Escherichia coli 562 -11533117 7500953387 argg argininosuccinate synthetase (db:genpept-bct1) (ec:6.3.4.5) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 1015) (le:99389) (re:100732) (di:direct) ECOUW67 U18997 g606111 Escherichia coli 562 -11533117 236410 argg argininosuccinate synthetase (fn:enzyme; amino acid biosynthesis: arginine) (db:genpept-bct2) (ec:6.3.4.5) (de:escherichia coli k-12 mg1655 section 288 of 400 of the completegenome.) (nt:o447; cg site no. 1015; 100 pct identical) (le:498) (re:1841) (di:direct) AE000398 AE000398 g1789563 Escherichia coli 562 -11533117 5000690362 (de:(ecoli\_3095) (pn:argininosuccinate synthetase) (gn:argg) (gtcfc:5.10:5.16:5.2) (ec:6.3.4.5) (assy\_ecoli) (keggfc:5.2:5.10:5.16) (rileyfc:1.4.1) (db:gtc-escherichia coli)) ECOLI\_3095 ECOLI\_3095 Escherichia coli 562 10123987

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501827405	7966	30122	354	117

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501827423	7967	30123	357	118

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501827436	7968	30124	360	119

Description

GTC ORF with score 167 to: (fn:required for the 3' processing of 5.8s rrna) (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome i cosmid c3g9.) (nt:spac3g9.10c; len:242aa; similarity: to ygr195w,) (le:19450:20247:20335) (re:20135:20286:20337) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827441	7969	30125	840	280

Description

GTC ORF with score 172 to: (sr:thale cress) (db:genpept) (de:arabidopsis thaliana chromosome i bac f21ml1 genomic sequence,complete sequence.)  
(nt:hypothetical protein; similar to dna helicases and) (le:115812:116202)  
(re:116107:116427) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827468	7970	30126	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827471	7971	30127	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827472	7972	30128	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827476	7973	30129	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827478	7974	30130	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827508	7975	30131	738	245

Description

GTC ORF with score 496 to: (sr:bacillus subtilis (strain:jh642 (trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which islocated between spoivcb and spoiiic.) (nt:similarity to arsenic efflux pump protein...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827511	7976	30132	183	60

Description

6500729260 argr:xera:b3237 arginine repressor (gtcfc:5.1) (keggfc:14.2) (rileyfc:1.4.1) (db:gtc-escherichia coli) b3237 b3237 Escherichia coli 562 -11533118 7500877143 argr:xera (de:arginine repressor) (db:swissprot) ARGR\_ECOLI P15282 ESCHERICHIA COLI 562 -11533118 162754 argr:xera arginine repressor protein:argr protein (db:pir2.dat) (mp:70.5 min) A33888 A33888 Escherichia coli 562 -11533118 236475 (sr:e.coli (strain k12) dna, clones per3 and pdb100) (db:genpept-bct1) (de:e.coli argr gene encoding arginine repressor protein (argr),complete cds.) (nt:arginine regulatory protein) (le:154) (re:624) (di:direct) ECOARGR M17532 g145356 Escherichia coli 562 -11533118 240383 argr (fn:arginine regulatory protein) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 1011; alternate name rarg) (le:165448) (re:165918) (di:direct) ECOUW67 U18997 g606176 Escherichia coli 562 -11533118 7502851883 (db:genpept-bct1) (de:e. coli xera (argr) gene for cer-mediated site-specificrecombination.) (nt:xera gene product (aa 1 - 156)) (le:156) (re:626) (di:direct) ECXERA X13968 g43307 Escherichia coli 562 -11533118 233848 argr repressor of arg regulon:cer-mediated site (fn:regulator; amino acid biosynthesis: arginine) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 293 of 400 of the completegenome.) (nt:o156; cg site no. 1011; alternate name rarg; 100) (le:1435) (re:1905) (di:direct) AE000403 AE000403 g1789633 Escherichia coli 562 -11533118 60099 argr:xera (de:arginine repressor) (db:swissprot) ARGR\_ECOLI P15282 ESCHERICHIA COLI 562 -11533118

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827514	7977	30133	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827520	7978	30134	234	77
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827526	7979	30135	315	104
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827527	7980	30136	813	270
<u>Description</u>				

6500729261 argd:dtu:b3359 acetylornitine  
delta-aminotransferase:acetylornithine aminotransferase:acoat  
(gtcfc:5.1:5.16) (ec:2.6.1.11) (keggfc:5.16) (rileyfc:1.4.1)  
(db:gtc-escherichia coli) b3359 b3359 Escherichia coli 562 -11533119  
7000684611 argd acetylornithine transaminase::acetylornithine  
aminotransferase (ec:2.6.1.11) (db:pir2.dat) (mp:74 min) B65130 B65130  
Escherichia coli 562 -11533119 7500877131 argd acetylornitine  
delta-aminotransferase (db:genpept-bct1) (ec:2.6.1.11) (de:escherichia coli  
k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 1018;  
alternate names argg, arg1) (le:269707) (re:270927) (di:complement) ECOUW67  
U18997 g606293 Escherichia coli 562 -11533119 236592 argd acetylornithine  
delta-aminotransferase (fn:enzyme; amino acid biosynthesis: arginine)  
(db:genpept-bct2) (ec:2.6.1.11) (de:escherichia coli k-12 mg1655 section 302  
of 400 of the completegenome.) (nt:f406; cg site no. 1018; alternate names  
argg,) (le:64) (re:1284) (di:complement) AE000412 AE000412 g1789759  
Escherichia coli 562 -11533119 60077 argd:dtu (ec:2.6.1.11)  
(de:acetylornithine aminotransferase, (acoat)) (db:swissprot) ARGD\_ECOLI  
P18335 ESCHERICHIA COLI 562 -11533119 5000690416 (de:(ecoli\_3277)  
(pn:acetylornithine delta-aminotransferase) (gn:argd) (gtcfc:5.16)  
(ec:2.6.1.11) (argd\_ecoli) (keggfc:5.16) (rileyfc:1.4.1) (db:gtc-escherichia  
coli)) ECOLI\_3277 ECOLI\_3277 Escherichia coli 562 10002803

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827531	7981	30137	357	118

Description

6500729262 glng:ntrc:glnt:b3868 glng:nitrogen regulation protein nr:i  
(gtcfc:5.1:12.13) (keggfc:12.1) (rileyfc:1.4.1) (db:gtc-escherichia coli)  
b3868 b3868 Escherichia coli 562 -11533120 86643 glng:ntrc:glnt  
(de:nitrogen regulation protein nr(i)) (db:swissprot) NTRC\_ECOLI P06713  
ESCHERICHIA COLI 562 -11533120 237087 glng (fn:negative regulation of glna)  
(sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda)  
(db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.)  
(nt:cg site no. 702) (le:15509) (re:16918) (di:complement) ECOUW87 L19201  
g304973 Escherichia coli 562 -11533120 7500886633 glng response regulator  
for gln sensor glnl (fn:regulator; amino acid biosynthesis: glutamine)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 352 of 400 of the  
completegenome.) (nt:f469; 100 pct identical to ntrc\_ecoli sw: p06713;)  
(le:3802) (re:5211) (di:complement) AE000462 AE000462 g1790299 Escherichia  
coli 562 -11533120 154770 (de:gln protein - escherichia coli) S40813  
S40813 Escherichia coli 562 10028807

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827543	7982	30138	561	186

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827544	7983	30139	438	145

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827545	7984	30140	324	107

Description

6500729263 glnl:ntrb:glmr:b3869 glnl:nitrogen regulation protein nr:ii  
(gtcf:5.1:12.13) (ec:2.7.3.-) (keggfc:12.1) (rileyfc:1.4.1)  
(db:gtc-escherichia coli) b3869 b3869 Escherichia coli 562 -11533121 237088  
glnl:ntrb:glmr (ec:2.7.3.-) (de:nitrogen regulation protein nr(ii),)  
(db:swissprot) NTRB\_ECOLI P06712 ESCHERICHIA COLI 562 -11533121 130852  
glnl:ntrb nitrogen regulation protein ii:ntrb:regulatory protein glnl  
(cl:glnl regulatory protein ii:sensor histidine kinase homology)  
(ec:2.7.3.-) (db:pir1.dat) (mp:87 min) RGEGL A30377 Escherichia coli 562  
-11533121 7500886632 (db:genpept-bct1) (de:e.coli glna/g operon with glna  
gene for glutamine synthetase and glnl and glng (ntrb and ntrc) genes for  
nr(ii) and nr(i).) (nt:nr(ii) (glnl gene product) (aa 1-349)) (le:1725)  
(re:2774) (di:direct) ECGLN X05173 g41564 Escherichia coli 562 -11533121  
7502851884 glnl (fn:negative regulation of glna) (sr:escherichia coli  
(sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e.  
coli chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 701)  
(le:16930) (re:17979) (di:complement) ECOUW87 L19201 g304974 Escherichia  
coli 562 -11533121 232997 glnl histidine protein kinase sensor for glng  
(fn:enzyme; amino acid biosynthesis: glutamine) (db:genpept-bct2)  
(ec:2.7.3.-) (de:escherichia coli k-12 mg1655 section 352 of 400 of the  
completegenome.) (nt:f349; 100 pct identical to ntrb\_ecoli sw: p06712;)  
(le:5223) (re:6272) (di:complement) AE000462 AE000462 g1790300 Escherichia  
coli 562 -11533121 86633 glnl:ntrb:glmr (ec:2.7.3.-) (de:nitrogen  
regulation protein nr(ii),) (db:swissprot) NTRB\_ECOLI P06712 ESCHERICHIA  
COLI 562 -11533121

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827549	7985	30141	978	325

Description

6500729264 arge:b3957 acetylornithine  
 deacetylase:acetylornithinase:ao:n-acetylornithinase:nao (gtcfc:5.1:5.16)  
 (ec:3.5.1.16) (keggfc:5.16) (rileyfc:1.4.1) (db:gtc-escherichia coli) b3957  
 b3957 Escherichia coli 562 -11533122 237175 arge (ec:3.5.1.16)  
 (de:(n-acetylornithinase) (nao)) (db:swissprot) ARGE\_ECOLI P23908  
 ESCHERICHIA COLI 562 -11533122 162658 arge:arg4 acetylornithine  
 deacetylase::n-acetylornithinase (ec:3.5.1.16) (db:pir2.dat) (mp:90 min)  
 B42377 B42377 Escherichia coli 562 -11533122 232382 arge acetylornithine  
 deacetylase subunit a2 (db:genpept-bct1) (ec:3.5.1.16) (de:e.coli arge gene  
 for acetylornithine deacetylase.) (le:1) (re:1152) (di:direct) ECARGE X62807  
 g40955 Escherichia coli 562 -11533122 5000690417 arge n-acetylornithinase  
 (db:genpept-bct1) (de:e.coli arge gene.) (le:211) (re:1362) (di:direct)  
 ECARGE1 X55417 g40957 Escherichia coli 562 -11533122 232381 arge  
 acetylornithine deacetylase (fn:enzyme; amino acid biosynthesis: arginine)  
 (db:genpept-bct2) (ec:3.5.1.16) (de:escherichia coli k-12 mg1655 section 360  
 of 400 of the completegenome.) (nt:f383; 100 pct identical to arge\_ecoli sw:  
 p23908 cg) (le:582) (re:1733) (di:complement) AE000470 AE000470 g1790395  
 Escherichia coli 562 -11533122 7500877136 arge acetylornithine deacetylase  
 (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda)  
 (db:genpept-bct2) (ec:3.5.1.16) (de:e. coli chromosomal region from 89.2 to  
 92.8 minutes.) (nt:cg site no. 1017) (le:18937) (re:20088) (di:complement)  
 ECOUW89 U00006 g396304 Escherichia coli 562 -11533122 60082 arge  
 (ec:3.5.1.16) (de:(n-acetylornithinase) (nao)) (db:swissprot) ARGE\_ECOLI  
 P23908 ESCHERICHIA COLI 562 -11533122

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827567	7986	30142	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827570	7987	30143	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827571	7988	30144	309	102

#### Description

6500729265 argc:b3958 n-acetyl-gamma-glutamyl-phosphate reductase:agpr:n-acetyl-glutamate semialdehyde dehydrogenase:nagsa dehydrogenase (gtcfc:5.1:5.16) (ec:1.2.1.38) (keggfc:5.16) (rileyfc:1.4.1) (db:gtc-escherichia coli) b3958 b3958 Escherichia coli 562 -11533123 60070 argc (ec:1.2.1.38) (de:acetyl-glutamate semialdehyde dehydrogenase) (nagsa dehydrogenase)) (db:swissprot) ARGC\_ECOLI P11446 ESCHERICHIA COLI 562 -11533123 122647 argc n-acetyl-gamma-glutamyl-phosphate reductase (cl:n-acetyl-gamma-glutamyl-phosphate reductase) (ec:1.2.1.38) (db:pir1.dat) (mp:90 min) RDECEP JT0332 Escherichia coli 562 -11533123 237176 (sr:e.coli (strain k) cell line p4x dna, clones pmc(7,31)) (db:genpept-bct1) (de:e.coli n-acetylglutamate-gamma-semialdehyde dehydrogenase(argc) andn-acetylglutamate kinase (argb) genes complete cds andargininosuccinate lyase (argh) gene, 5' end.) (nt:... ECOARGBCH M21446 g145333 Escherichia coli 562 -11533123 233836 argc n-acetyl-gamma-glutamylphosphate reductase (fn:enzyme; amino acid biosynthesis: arginine) (db:genpept-bct2) (ec:1.2.1.38) (de:escherichia coli k-12 mg1655 section 360 of 400 of the completegenome.) (nt:o334; 100 pct identical to argc\_ecoli sw: p11446;) (le:1887) (re:2891) (di:direct) AE000470 AE000470 g1790396 Escherichia coli 562 -11533123 7500877118 argc n-acetyl-gamma-glutamyl-phosphate reductase (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (ec:1.2.1.38) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 1019) (le:20242) (re:21246) (di:direct) ECOUW89 U00006 g396305 Escherichia coli 562 -11533123 5000690418 (de:(ecoli\_3856) (pn:n-acetyl-gamma-glutamylphosphate reductase) (gn:argc) (gtcfc:5.16) (ec:1.2.1.38) (argc\_ecoli) (keggfc:5.16) (rileyfc:1.4.1) (db:gtc-escherichia coli)) ECOLI\_3856 ECOLI\_3856 Escherichia coli 562 10002796

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827579	7989	30145	501	166

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827586	7990	30146	327	108

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827602	7991	30147	2376	791

Description

6500729266 argb:b3959 acetylglutamate kinase:nag  
kinase:agk:n-acetylglutamate 5-phosphotransferase (gtcfc:5.1:5.16)  
(ec:2.7.2.8) (keggfc:5.16) (rileyfc:1.4.1) (db:gtc-escherichia coli) b3959  
b3959 Escherichia coli 562 -11533124 60064 argb (ec:2.7.2.8)  
(de:(n-acetylglutamate 5-phosphotransferase)) (db:swissprot) ARGB\_ECOLI  
P11445 ESCHERICHIA COLI 562 -11533124 123868 argb acetylglutamate kinase  
(cl:acetylglutamate kinase) (ec:2.7.2.8) (db:pir1.dat) (mp:90 min) KIECAE  
JT0331 Escherichia coli 562 -11533124 237177 (sr:e.coli (strain k) cell  
line p4x dna, clones pmc(7,31)) (db:genpept-bct1) (de:e.coli  
n-acetylglutamate-gamma-semialdehyde dehydrogenase(argc)  
andn-acetylglutamate kinase (argb) genes complete cds andargininosuccinate  
lyase (argh) gene, 5' end.) (nt:... ECOARGBCH M21446 g145334 Escherichia  
coli 562 -11533124 233837 argb acetylglutamate kinase (fn:enzyme; amino  
acid biosynthesis: arginine) (db:genpept-bct2) (ec:2.7.2.8) (de:escherichia  
coli k-12 mg1655 section 360 of 400 of the completegenome.) (nt:o258; cg  
site no. 1020) (le:2899) (re:3675) (di:direct) AE000470 AE000470 g1790397  
Escherichia coli 562 -11533124 7500877113 argb acetylglutamate kinase  
(sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda)  
(db:genpept-bct2) (ec:2.7.2.8) (de:e. coli chromosomal region from 89.2 to  
92.8 minutes.) (nt:cg site no. 1020) (le:21254) (re:22030) (di:direct)  
ECOUW89 U00006 g396306 Escherichia coli 562 -11533124 5000690419  
(de:(ecoli\_3857) (pn:acetylglutamate kinase) (gn:argb) (gtcfc:5.16)  
(ec:2.7.2.8) (argb\_ecoli) (keggfc:5.16) (rileyfc:1.4.1) (db:gtc-escherichia  
coli)) ECOLI\_3857 ECOLI\_3857 Escherichia coli 562 10002791

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827611	7992	30148	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827623	7993	30149	441	146

Description

GTC ORF with score 326 to: (sr:caenorhabditis elegans strain=bristol n2)  
(db:genpept-inv) (de:caenorhabditis elegans cosmid f18a12.) (nt:similar to  
the m13 or zinc metalloprotease family) (le:24587:24868:25253)  
(re:24763:25032:25503) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827648	7994	30150	963	320
<u>Description</u>				
6500729267 argh:b3960 argininosuccinate lyase:arginosuccinase:asal (gtcfc:5.1:5.10:5.16:5.2) (ec:4.3.2.1) (keggfc:5.2:5.10:5.16) (rileyfc:1.4.1) (db:gtc-escherichia coli) b3960 b3960 Escherichia coli 562 -11533125 60130 argh (ec:4.3.2.1) (de:argininosuccinate lyase, (arginosuccinase) (asal)) (db:swissprot) ARLY_ECOLI P11447 ESCHERICHIA COLI 562 -11533125 7000684616 argh argininosuccinate lyase::argininosuccinase (cl:argininosuccinate lyase) (ec:4.3.2.1) (db:pir2.dat) C65203 C65203 Escherichia coli 562 -11533125 237178 argh argininosuccinate lyase (fn:enzyme; amino acid biosynthesis: arginine) (db:genpept-bct2) (ec:4.3.2.1) (de:escherichia coli k-12 mg1655 section 360 of 400 of the completegenome.) (nt:o457; 100 pct identical to arly_ecoli sw: p11447;) (le:3736) (re:5109) (di:direct) AE000470 AE000470 g1790398 Escherichia coli 562 -11533125 7500877154 argh argininosuccinate lyase (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (ec:4.3.2.1) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 1014) (le:22091) (re:23464) (di:direct) ECOUW89 U00006 g396307 Escherichia coli 562 -11533125 5000690363 (de:(ecoli_3858) (pn:argininosuccinate lyase) (gn:argh) (gtcfc:5.10:5.16:5.2) (ec:4.3.2.1) (arly_ecoli) (keggfc:5.2:5.10:5.16) (rileyfc:1.4.1) (db:gtc-escherichia coli)) ECOLI_3858 ECOLI_3858 Escherichia coli 562 10002856				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827657	7995	30151	672	223

Description

6500729268 argi:b4254 ornithine carbamoyltransferase:ornithine carbamoyltransferase chain i:otcase-1 (gtcfc:5.1:5.10:5.16) (ec:2.1.3.3) (keggfc:5.10:5.16) (rileyfc:1.4.1) (db:gtc-escherichia coli) b4254 b4254 Escherichia coli 562 -11533126 123313 argi ornithine carbamoyltransferase:chain i:citrulline phosphorylase chain i:ornithine transcarbamylase chain i (cl:ornithine carbamoyltransferase:aspartate/ornithine carbamoyltransferase homology) (ec:2.1.3.3) (db:pir1.dat) (mp:97 min) OWECI A31314 Escherichia coli 562 -11533126 7500953231 argi ornithine carbamoyltransferase (db:genpept-bct1) (ec:2.1.3.3) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 1013; duplicate gene) (le:168131) (re:169135) (di:complement) ECOUW93 U14003 g537095 Escherichia coli 562 -11533126 237459 argi ornithine carbamoyltransferase 1 (fn:enzyme; amino acid biosynthesis: arginine) (db:genpept-bct2) (ec:2.1.3.3) (de:escherichia coli k-12 mg1655 section 386 of 400 of the completegenome.) (nt:f334; 100 pct identical to otcl\_ecoli sw: p04391;) (le:3151) (re:4155) (di:complement) AE000496 AE000496 g1790703 Escherichia coli 562 -11533126 5000690365 (de:(ecoli\_4137) (pn:ornithine carbamoyltransferase 1) (gn:argi) (gtcfc:5.10:5.16) (ec:2.1.3.3) (otcl\_ecoli) (keggfc:5.10:5.16) (rileyfc:1.4.1) (db:gtc-escherichia coli)) ECOLI\_4137 ECOLI\_4137 Escherichia coli 562 10065784

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827659	7996	30152	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827670	7997	30153	354	117

Description

6500729269 lpxc:enva:asmb:b0096 udp-3-o-3-hydroxymyristoyl  
n-acetylglucosamine deacetylase:enva protein  
(gtcfc:11.3:11.4:5.10:5.11:7.1:9.4:9.5) (ec:3.5.1.-)  
(keggfc:4.4:5.10:5.11:9.4:9.5) (rileyfc:5.8.0) (db:gtc-escherichia coli)  
b0096 b0096 Escherichia coli 562 -11533127 228003 lpxc:enva:asmb  
(ec:3.5.1.-) (de:(ec 3.5.1.-) (enva protein)) (db:swissprot) LPXC\_ECOLI  
P07652 ESCHERICHIA COLI 562 -11533127 131350 lpxc:enva  
udp-3-o-3-hydroxymyristoyl n-acetylglucosamine deacetylase,) (cl:enva  
protein) (ec:3.5.1.-) (db:pir1.dat) (mp:2 min) BVECEA A28381 Escherichia  
coli 562 -11533127 5000690344 enva enva protein (db:genpept-bct1) (de:e.  
coli 2 minute region.) (le:23087) (re:24004) (di:direct) EC2MIN X55034  
g40864 Escherichia coli 562 -11533127 234248 enva enva protein  
(sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12  
genome, 0-2.4min. region.) (le:106211) (re:107128) (di:direct) ECO110K  
D10483 g216510 Escherichia coli 562 -11533127 304540 enva ell  
permeability-cell separation protein (sr:escherichia coli (strain k-12)  
(clone: pacyc184.) dna) (db:genpept-bct1) (de:e.coli cell permeability-cell  
separation protein (enva) gene,complete cds., ftsz gene, 3' end, and seca  
gene, 5' end.) (le:125) (re:1042) (di:direct) ECOENVAA M19211 g145848  
Escherichia coli 562 -11533127 233620 lpxc udp-3-o-acyl n-acetylglucosamine  
deacetylase (fn:enzyme; surface polysaccharides and antigens)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 9 of 400 of the  
completegenome.) (nt:o305; 100 pct identical to lpxc\_ecoli sw: p07652;)  
(le:1313) (re:2230) (di:direct) AE000119 AE000119 g1786285 Escherichia coli  
562 -11533127 82459 lpxc:enva:asmb (ec:3.5.1.-) (de:(ec 3.5.1.-) (enva  
protein)) (db:swissprot) LPXC\_ECOLI P07652 ESCHERICHIA COLI 562 -11533127

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827707	7998	30154	618	205
<u>Description</u>				
6500729270 sped:b0120 s-adenosylmethionine decarboxylase proenzyme:adometdc (gtcfc:5.10:5.16) (ec:4.1.1.50) (keggfc:5.10) (rileyfc:1.5.0) (db:gtc-escherichia coli) b0120 b0120 Escherichia coli 562 -11533128 67955 sped (ec:4.1.1.50) (de:s-adenosylmethionine decarboxylase proenzyme, (adometdc)) (db:swissprot) DCAM_ECOLI P09159 ESCHERICHIA COLI 562 -11533128 125489 sped adenosylmethionine decarboxylase:precursor (cl:bacterial adenosylmethionine decarboxylase) (ec:4.1.1.50) (db:pir1.dat) (mp:3 min) DCECDM B29778 Escherichia coli 562 -11533128 301598 sped adenosylmethionine decarboxylase proenzyme (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (ec:4.1.1.50) (de:escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0 min).) (le:23398) (re:24192) (di:complement) ECO82K D26562 g1841386 Escherichia coli 562 -11533128 7500880043 sped s-adenosylmethionine decarboxylase (sr:e.coli k12 dna, clones pt7-5-1 and lc37-29) (db:genpept-bct1) (de:e.coli speed operon spee and sped genes encoding s-adenosyl-methionine decarboxylase and spermidine synthase, complete cds.) (le:1649) (re:2443) (di:direct) ECOSPDE J02804 g551838 Escherichia coli 562 -11533128 236015 sped s-adenosylmethionine decarboxylase (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:4.1.1.50) (de:escherichia coli k-12 mg1655 section 11 of 400 of the completegenome.) (nt:f264; 100 pct identical to dcam_ecoli sw: p09159) (le:7069) (re:7863) (di:complement) AE000121 AE000121 g1786311 Escherichia coli 562 -11533128 5000690345 (de:(ecoli_120) (pn:s-adenosylmethionine decarboxylase) (gn:sped) (gtcfc:5.10) (ec:4.1.1.50) (dcam_ecoli) (keggfc:5.10) (rileyfc:1.5.0) (db:gtc-escherichia coli)) ECOLI_120 ECOLI_120 Escherichia coli 562 10010548				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827708	7999	30155	270	89

Description

6500729271 spee:b0121 spermidine synthase:putrescine  
aminopropyltransferase:spdsy (gtcfc:5.10:5.16:6.1) (ec:2.5.1.16)  
(keggfc:5.10:5.16:6.1) (rileyfc:1.5.0) (db:gtc-escherichia coli) b0121 b0121  
Escherichia coli 562 -11533129 123463 spee spermidine synthase  
(cl:spermidine synthase) (ec:2.5.1.16) (db:pir1.dat) (mp:3 min) SYECSD  
A29778 Escherichia coli 562 -11533129 236014 spee spermidine synthase  
(sr:escherichia coli (sub\_strain w3110, strain k-12) (library: kohara')  
(db:genpept-bct1) (ec:2.5.1.16) (de:escherichia coli genome, 2.4-4.1 min  
region (110,917-193,643 bpfrom 0 min).) (le:24208) (re:25074)  
(di:complement) ECO82K D26562 g473788 Escherichia coli 562 -11533129 301599  
spee spermidine synthase (sr:e.coli k12 dna, clones pt7-5-1 and lc37-29)  
(db:genpept-bct1) (de:e.coli speed operon spee and sped genes encoding  
s-adenosyl-methionine decarboxylase and spermidine synthase, complete cds.)  
(le:767) (re:1633) (di:direct) ECOSPDE J02804 g147852 Escherichia coli 562  
-11533129 233661 spee spermidine synthase = putrescine (fn:enzyme; central  
intermediary metabolism:) (db:genpept-bct2) (ec:2.5.1.16) (de:escherichia  
coli k-12 mg1655 section 11 of 400 of the completengenome.) (nt:f288; 100 pct  
identical to spee\_ecoli sw: p09158) (le:7879) (re:8745) (di:complement)  
AE000121 AE000121 g1786312 Escherichia coli 562 -11533129 5000690346  
(de:(ecoli\_121) (pn:spermidine synthase , putrescine  
aminopropyltransferase:spermidine synthase ) (gn:spee) (gtcfc:5.10:5.16:6.1)  
(ec:2.5.1.16) (spee\_ecoli) (keggfc:5.10:5.16:6.1) (rileyfc:1.5.0)  
(db:gtc-escherichia coli)) ECOLI\_121 ECOLI\_121 Escherichia coli 562 10065831

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827710	8000	30156	456	151

Description

6500729272 pros:drpa:b0194 prolyl-trna synthetase:proline--trna  
ligase:prors:global rna synthesis factor (gtcfc:10.6:5.10) (ec:6.1.1.15)  
(keggfc:5.10:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli) b0194  
b0194 Escherichia coli 562 -11533130 7000688909 pros:drpa proline--trna  
ligase::global rna synthesis factor:prolyl-trna synthetase (cl:proline--trna  
ligase) (ec:6.1.1.15) (db:pir1.dat) (mp:5 min) YPEC B64744 Escherichia coli  
562 -11533130 7500953368 pros proline-trna ligase (db:genpept-bct1)  
(de:escherichia coli chromosome minutes 4-6.) (le:48132) (re:49850)  
(di:complement) ECU70214 U70214 g1552770 Escherichia coli 562 -11533130  
239821 pros proline trna synthetase (fn:enzyme; aminoacyl trna synthetases,  
trna) (db:genpept-bct2) (ec:6.1.1.15) (de:escherichia coli k-12 mg1655  
section 18 of 400 of the completegenome.) (nt:f572; 100 pct identical to  
syp\_ecoli sw: p16659;) (le:7458) (re:9176) (di:complement) AE000128 AE000128  
g1786392 Escherichia coli 562 -11533130 5000690347 (de:(ecoli\_194)  
(pn:proline trna synthetase) (gn:pros) (gtcfc:5.10:10.6) (ec:6.1.1.15)  
(syp\_ecoli) (keggfc:5.10:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia  
coli)) ECOLI\_194 ECOLI\_194 Escherichia coli 562 10122701

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827711	8001	30157	423	140

Description

6500729273 pepd:peph:b0237 aminoacyl-histidine dipeptidase  
precursor:aminoacyl-histidine dipeptidase:xaa-his dipeptidase:x-his  
dipeptidase:beta-alanyl-histidine dipeptidase:carnosinase:peptidase d  
(gtcfc:5.10:5.11:5.2:6.1:10.11) (ec:3.4.13.3) (keggfc:5.2:5.10:5.11:6.1)  
(rileyfc:3.2.3) (db:gtc-escherichia coli) b0237 b0237 Escherichia coli 562  
-11533131 164832 pepd x-his dipeptidase::aminoacylhistidine  
dipeptidase:aminopeptidase d:beta-alanyl-histidine dipeptidase:carnosinase  
(ec:3.4.13.3) (db:pir2.dat) (mp:6 min) JU0300 JU0300 Escherichia coli 562  
-11533131 236201 (sr:e.coli (strain k12; substrain cm17) dna)  
(db:genpept-bct1) (de:e. coli, peptidase d (pepd) gene, complete cds.)  
(nt:peptidase d) (le:187) (re:1644) (di:direct) ECOPEPD M34034 g147140  
Escherichia coli 562 -11533131 239856 pepd aminoacylhistidine dipeptidase  
precursor (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1)  
(ec:3.4.13.3) (de:escherichia coli genome, 4.0 - 6.0 min region.) (le:63798)  
(re:65255) (di:complement) ECOTSF D83536 g1208983 Escherichia coli 562  
-11533131 303278 pepd aminoacylhistidine dipeptidase precursor  
(db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:85334)  
(re:86791) (di:complement) ECU70214 U70214 g1552805 Escherichia coli 562  
-11533131 235385 pepd aminoacyl-histidine dipeptidase peptidase d  
(fn:enzyme; degradation of proteins, peptides,) (db:genpept-bct2)  
(ec:3.4.13.3) (de:escherichia coli k-12 mg1655 section 22 of 400 of the  
completegenome.) (nt:f485; 100 pct to pepd\_ecoli sw: p15288 excluding)  
(le:975) (re:2432) (di:complement) AE000132 AE000132 g1786432 Escherichia  
coli 562 -11533131 5000690348 (de:(ecoli\_230) (pn:peptidase d, a  
dipeptidase where amino-terminal residue is histidine) (gn:pepd)  
(gtcfc:5.10:5.11:5.2:6.1) (ec:3.4.13.3) (pepd\_ecoli)  
(keggfc:5.2:5.10:5.11:6.1) (rileyfc:3.2.3) (db:gtc-escherichia coli))  
ECOLI\_230 ECOLI\_230 Escherichia coli 562 10087483

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827719	8002	30158	2145	715

# Description

6500729274 spef:b0693 ornithine decarboxylase:inducible (gtcfc:5.10:5.16) (ec:4.1.1.17) (keggfc:5.10:5.16) (rileyfc:1.5.0) (db:gtc-escherichia coli) b0693 b0693 Escherichia coli 562 -11533132 68097 spef (ec:4.1.1.17) (de:ornithine decarboxylase, inducible,) (db:swissprot) DCOS\_ECOLI P24169 ESCHERICHIA COLI 562 -11533132 164209 spef ornithine decarboxylase::inducible (ec:4.1.1.17) (db:pir2.dat) A40839 A40839 Escherichia coli 562 -11533132 223155 spef ornithine decarboxylase:inducible (sr:escherichia coli(strain:k12) dna, clone:kohara clone #173) (db:genpept-bct1) (de:escherichia coli genomic dna. (15.3 - 15.6 min).) (le:7884) (re:10082) (di:complement) D90708 D90708 g1651300 Escherichia coli 562 -11533132 7500880070 spef ornithine decarboxylase (sr:e.coli (strain dr112) dna, clone ppt71) (db:genpept-bct1) (de:e.coli ornithine decarboxylase (spef) and putrescine transportprotein (pote) genes, complete cds.) (le:660) (re:2858) (di:direct) ECOPTESPE M64495 g147331 Escherichia coli 562 -11533132 235526 spef ornithine decarboxylase isozyme:inducible (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:4.1.1.17) (de:escherichia coli k-12 mg1655 section 62 of 400 of the completegenome.) (nt:f732; 100 pct identical to dcos\_ecoli sw: p24169) (le:10247) (re:12445) (di:complement) AE000172 AE000172 g1786909 Escherichia coli 562 -11533132 5000690351 spef ornithine decarboxylase ec 4.1.1.17 . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #173) (db:genpept) (de:escherichia coli genomic dna. (15.3 - 15.7 min).) (nt:orf\_id:o173#10; similar to pir accession number) (le:7884) (re:10082) (di:complement) D90708 D90708 g1651300 Escherichia coli 562 -11533132

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827757	8003	30159	477	158

# Description

GTC ORF with score 154 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k06a9.) (nt:partial cds; coded for by c. elegans cdna yk50c7.5) (le:27212:27374:27536:27666) (re:27323:27486:27619:27751) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827764	8004	30160	999	332

# Description

6500729275 tyna:maoa:bl386 copper amine oxidase precursor:tyramine oxidase (gtcfc:5.10:5.11:5.12:5.13:5.14:5.3:6.1:14.3) (ec:1.4.3.6) (keggfc:5.3:5.10:5.11:5.12:5.13:5.14:6.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) bl386 bl386 Escherichia coli 562 -11533133 59330 tyna:maoa (ec:1.4.3.6) (de:(2-phenylenthyllamine oxidase)) (db:swissprot) AMO\_ECOLI P46883 ESCHERICHIA COLI 562 -11533133 7000684573 tyna:maoa amine oxidase copper-containing:tyna precursor:monoamine oxidase:tyraminase:tyramine oxidase (ec:1.4.3.6) (db:pir2.dat) E64889 E64889 Escherichia coli 562 -11533133 223669 tyna:maoa copper amine oxidase precursor ec 1.4.3.6 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #266(31.1-31.5 min.)) (nt:orf\_id:o266#1; similar to (swissprot accession) (le:5294) (re:7567) (di:complement) D90777 D90777 g1742266 Escherichia coli 562 -11533133 235057 tyna copper amine oxidase tyramine oxidase (fn:enzyme; degradation of small molecules: amines) (db:genpept-bct2) (ec:1.4.3.6) (de:escherichia coli k-12 mg1655 section 125 of 400 of the completegenome.) (nt:f757; 100 pct identical to amo\_ecoli sw: p46883; cg) (le:8054) (re:10327) (di:complement) AE000235 AE000235 g1787651 Escherichia coli 562 -11533133 300442 maola copper amine oxidase (sr:escherichia coli (strain k10) (clone: pec1) dna) (db:genpept-bct2) (de:escherichia coli copper amine oxidase (maola) gene, complete cds.) (nt:precursor; aa 496 tpq cofacor, aa 554, 556, 719) (le:16) (re:2289) (di:direct) ECOMAOA L47571 g1000851 Escherichia coli 562 -11533133 5000690353 (de:(ecoli\_1346) (pn:periplasmic copper amine oxidase:tyramine oxidase) (gn:tyna) (gtcfc:5.10:5.11:5.13:5.3:6.1) (ec:1.4.3.6) (amo\_ecoli) (keggfc:5.3:5.10:5.11:5.13:6.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_1346 ECOLI\_1346 Escherichia coli 562 10002068

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827767	8005	30161	378	125

Description

6500729276 speg:b1584 spermidine n1-acetyltransferase:diamine  
acetyltransferase:sat (gtcfc:5.10:14.3) (ec:2.3.1.57) (keggfc:5.10)  
(rileyfc:5.8.0) (db:gtc-escherichia coli) b1584 b1584 Escherichia coli 562  
-11533134 162916 speg diamine n-acetyltransferase::spermidine  
acetyltransferase (ec:2.3.1.57) (db:pir2.dat) A55345 A55345 Escherichia coli  
562 -11533134 7500959720 spermidine acetyltransferase (sr:escherichia coli  
(strain:k-12, sub\_strain:w3110) dna) (db:genpept-bct1) (de:escherichia coli  
gene for spermidine acetyltransferase, completecds.) (le:21) (re:581)  
(di:direct) ECOSN1A D25276 g517105 Escherichia coli 562 -11533134 236006  
speg spermidine n1-acetyltransferase (fn:enzyme; central intermediary  
metabolism:) (db:genpept-bct2) (ec:2.3.1.57) (de:escherichia coli k-12  
mg1655 section 144 of 400 of the completegenome.) (nt:o186; 100 pct  
identical to atda\_ecoli sw: p37354) (le:3412) (re:3972) (di:direct) AE000254  
AE000254 g1787867 Escherichia coli 562 -11533134 5000690354  
(de:(ecoli\_1543) (pn:spermidine n1-acetyltransferase:diamine  
acetyltransferase:sat) (gn:speg) (gtcfc:5.10) (ec:2.3.1.57) (atda\_ecoli)  
(keggfc:5.10) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_1543  
ECOLI\_1543 Escherichia coli 562 10086681

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501827786	8006	30162	459	152

#### Description

6500729277 args:b1876 arginyl-trna synthetase:arginine--trna ligase:argrs (gtcfc:10.6:5.10) (ec:6.1.1.19) (keggfc:5.10:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli) b1876 b1876 Escherichia coli 562 -11533135 301009 args (ec:6.1.1.19) (de:arginyl-trna synthetase, (arginine--trna ligase) (argrs)) (db:swissprot) SYR\_ECOLI P11875 ESCHERICHIA COLI 562 -11533135 125927 args arginine--trna ligase::arginyl-trna synthetase (cl:arginine--trna ligase) (ec:6.1.1.19) (db:pir1.dat) (mp:40 min) SYECRT JS0267 Escherichia coli 562 -11533135 224369 args arginine--trna ligase ec 6.1.1.19 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #337(41.9-42.3 min.)) (nt:orf\_id:o337#17; similar to (pir accession number) (le:16864) (re:18597) (di:direct) D90829 D90829 g1736522 Escherichia coli 562 -11533135 301016 args arginine--trna ligase ec 6.1.1.19 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #338(42.1-42.5 min.)) (nt:orf\_id:o337#17; similar to (pir accession number) (le:4429) (re:6162) (di:direct) D90830 D90830 g1736530 Escherichia coli 562 -11533135 5000690355 (db:genpept-bct1) (de:escherichia coli args gene for arginyl-trna-synthetase (ec6.1.1.19).) (nt:arginyl-trna-synthetase (aa 1-577)) (le:249) (re:1982) (di:direct) ECARGS X15320 g581040 Escherichia coli 562 -11533135 232386 args arginine trna synthetase (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:6.1.1.19) (de:escherichia coli k-12 mg1655 section 171 of 400 of the completegenome.) (nt:o577; 100 pct identical to syr\_ecoli sw: p11875; cg) (le:5597) (re:7330) (di:direct) AE000281 AE000281 g1788184 Escherichia coli 562 -11533135 100164 args (ec:6.1.1.19) (de:arginyl-trna synthetase, (arginine--trna ligase) (argrs)) (db:swissprot) SYR\_ECOLI P11875 ESCHERICHIA COLI 562 -11533135 224376 args arginine--trna ligase ec 6.1.1.19 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #338(42.1-42.5 min.)) (nt:orf\_id:o337#17; similar to (pir accession number) (le:4429) (re:6162) (di:direct) D90830 D90830 g1736530 Escherichia coli 562 -11533135

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501827790	8007	30163	186	61

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827797	8008	30164	402	133

Description

6500729278 speb:b2937 agmatinase:agmatine ureohydrolase:auh  
 (gtcfc:5.10:5.16) (ec:3.5.3.11) (keggfc:5.10) (rileyfc:1.5.0)  
 (db:gtc-escherichia coli) b2937 b2937 Escherichia coli 562 -11533136 99235  
 speb (ec:3.5.3.11) (de:agmatinase, (agmatine ureohydrolase) (auh))  
 (db:swissprot) SPEB\_ECOLI P16936 ESCHERICHIA COLI 562 -11533136 162689 speb  
 agmatinase::agmatine ureohydrolase (ec:3.5.3.11) (db:pir2.dat) (mp:64 min)  
 C42604 C42604 Escherichia coli 562 -11533136 239150 speb agmatine  
 ureohydrolase (sr:escherichia coli (strain k-12) (clone: plc(2-5,5-8,5-14).)  
 dna) (db:genpept-bct1) (ec:3.5.3.11) (de:e.coli agmatine ureohydrolase  
 (speb) gene, complete cds.) (le:214) (re:1134) (di:direct) ECOSPEAA M32363  
 g147859 Escherichia coli 562 -11533136 7500891973 speb agmatine  
 ureohydrolase (db:genpept-bct1) (ec:3.5.3.11) (de:escherichia coli k-12  
 genome; approximately 65 to 68 minutes.) (nt:cg site no. 160) (le:37272)  
 (re:38192) (di:complement) ECU28377 U28377 g882466 Escherichia coli 562  
 -11533136 236019 speb agmatinase (fn:enzyme; central intermediary  
 metabolism:) (db:genpept-bct2) (ec:3.5.3.11) (de:escherichia coli k-12  
 mg1655 section 267 of 400 of the completegenome.) (nt:f306; 100 pct  
 identical to speb\_ecoli sw: p16936;) (le:1195) (re:2115) (di:complement)  
 AE000377 AE000377 g1789306 Escherichia coli 562 -11533136 5000690356  
 (de:(ecoli\_2859) (pn:agmatinase) (gn:speb) (gtcfc:5.10) (ec:3.5.3.11)  
 (speb\_ecoli) (keggfc:5.10) (rileyfc:1.5.0) (db:gtc-escherichia coli))  
 ECOLI\_2859 ECOLI\_2859 Escherichia coli 562 10041094



ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501827815	8009	30165	441	146

Description

6500729279 spec:b2965 ornithine decarboxylase:constitutive (gtcfc:5.10:5.16) (ec:4.1.1.17) (keggfc:5.10:5.16) (rileyfc:1.5.0) (db:gtc-escherichia coli) b2965 b2965 Escherichia coli 562 -11533137 68084 spec (ec:4.1.1.17) (de:ornithine decarboxylase, constitutive,) (db:swissprot) DCOR\_ECOLI P21169 ESCHERICHIA COLI 562 -11533137 164210 spec ornithine decarboxylase (ec:4.1.1.17) (db:pir2.dat) I60729 I60729 Escherichia coli 562 -11533137 239179 (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli (clone plc20-5) ornithine decarboxylase (spec) and cyclicamp receptor protein genes, complete cds.) (nt:ornithine decarboxylase (spec) (ec 4.1.1.17)) (le:86) (re:2281) (di:direct) ECOSPEC M33766 g147861 Escherichia coli 562 -11533137 7500880066 spec (fn:ornithine decarboxylase) (db:genpept-bct1) (ec:4.1.1.17) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:cg site no. 159) (le:61414) (re:63609) (di:complement) ECU28377 U28377 g882495 Escherichia coli 562 -11533137 236022 spec ornithine decarboxylase isozyme (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:4.1.1.17) (de:escherichia coli k-12 mg1655 section 269 of 400 of the completegenome.) (nt:f731; 100 pct identical to dcor\_ecoli sw: p21169;) (le:2651) (re:4846) (di:complement) AE000379 AE000379 g1789337 Escherichia coli 562 -11533137 5000690358 (de:(ecoli\_2888) (pn:ornithine decarboxylase isozyme) (gn:spec) (gtcfc:5.10:5.16) (ec:4.1.1.17) (dcor\_ecoli) (keggfc:5.10:5.16) (rileyfc:1.5.0) (db:gtc-escherichia coli)) ECOLI\_2888 ECOLI\_2888 Escherichia coli 562 10010677

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501827822	8010	30166	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827824	8011	30167	531	176

#### Description

6500729280 ygjg:b3073 probable ornithine aminotransferase  
 (gtcfc:5.10:5.16:14.3) (ec:2.6.1.13) (keggfc:5.10:5.16) (rileyfc:5.8.0)  
 (db:gtc-escherichia coli) b3073 b3073 Escherichia coli 562 -11533138  
 7000691875 ygjg ornithine--oxo-acid transaminase (ec:2.6.1.13)  
 (db:pir2.dat) F65095 F65095 Escherichia coli 562 -11533138 7500960402  
 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to  
 76.0 minutes.) (nt:orf\_o496) (le:136) (re:1626) (di:direct) ECOUW67 U18997  
 g606011 Escherichia coli 562 -11533138 236310 ygjg probable ornithine  
 aminotransferase (fn:putative enzyme; amino acid biosynthesis:)  
 (db:genpept-bct2) (ec:2.6.1.13) (de:escherichia coli k-12 mg1655 section 279  
 of 400 of the completegenome.) (nt:o496; 100 pct identical to 429 amino  
 acids of) (le:2778) (re:4268) (di:direct) AE000389 AE000389 g1789454  
 Escherichia coli 562 -11533138 5000690359 (de:(ecoli\_2995) (pn:probable  
 ornithine aminotransferase) (gn:ygjg) (gtcfc:5.10:5.16) (ec:2.6.1.13)  
 (oat\_ecoli) (keggfc:5.10:5.16) (rileyfc:5.7.0) (db:gtc-escherichia coli))  
 ECOLI\_2995 ECOLI\_2995 Escherichia coli 562 10123970

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827835	8012	30168	186	61

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827841	8013	30169	1200	399

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827843	8014	30170	459	152

Description

6500729281 ygjh:b3074 hypothetical 12.3 kd protein in ilex-ebgr intergenic region (gtcfc:5.10:5.16:14.1) (ec:2.6.1.13) (keggfc:5.10:5.16) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3074 b3074 Escherichia coli 562 -11533139 112420 ygjh (de:hypothetical 12.3 kd protein in ilex-ebgr intergenic region) (db:swissprot) YGJH\_ECOLI P42589 ESCHERICHIA COLI 562 -11533139 7000687868 ygjh hypothetical 12.3 kd protein in ilex-ebgr intergenic region (db:pir2.dat) G65095 G65095 Escherichia coli 562 -11533139 7500924295 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf\_f110) (le:1668) (re:2000) (di:complement) ECOUW67 U18997 g606012 Escherichia coli 562 -11533139 236311 ygjh putative trna synthetase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 279 of 400 of the completegenome.) (nt:f110; 100 pct identical to ygjh\_ecoli sw: p42589) (le:4310) (re:4642) (di:complement) AE000389 AE000389 g1789455 Escherichia coli 562 -11533139 5000690360 (de:(ecoli\_2996) (pn:probable ornithine aminotransferase:ornithine--oxo-acid aminotransferase) (gn:ygjh) (gtcfc:5.10:5.16) (ec:2.6.1.13) (ygjh\_ecoli) (keggfc:5.10:5.16) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2996 ECOLI\_2996 Escherichia coli 562 10054148

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827850	8015	30171	1005	334

Description

6500729282 agaa:b3135 putative n-acetylgalactosamine-6-phosphate deacetylase (gtcfc:5.10:5.11:7.1:9.4:9.5:14.2) (ec:3.5.1.-) (keggfc:4.4:5.10:5.11:9.4:9.5) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3135 b3135 Escherichia coli 562 -11533140 7500876657 agaa (ec:3.5.1.-) (de:putative n-acetylgalactosamine-6-phosphate deacetylase,) (db:swissprot) AGAA\_ECOLI P42906 ESCHERICHIA COLI 562 -11533140 7000690852 agaa agaa protein (ec:3.5.1.-) (db:pir2.dat) C65103 C65103 Escherichia coli 562 -11533140 7500876659 agaa putative n-acetylgalactosamine-6-phosphate (fn:putative enzyme; not classified) (db:genpept-bct2) (ec:3.5.1.-) (de:escherichia coli k-12 mg1655 section 284 of 400 of the completegenome.) (nt:o167; c-terminal differs from earlier version;) (le:11520) (re:12023) (di:direct) AE000394 AE000394 g2367198 Escherichia coli 562 -11533140

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501827851	8016	30172	324	107

#### Description

6500729283 cstc:b1748 hypothetical  
protein:n-:alpha-acetylornithine-:delta-aminotransferase:carbon starvation  
protein c (gtcfc:5.11:5.8:14.1) (ec:2.6.1.-) (keggfc:5.8:5.11)  
(rileyfc:5.7.0) (db:gtc-escherichia coli) b1748 b1748 Escherichia coli 562  
-11533141 1500685837 astc:argm:cstc (ec:2.6.1.-) (de:aminotransferase)  
(carbon starvation protein c)) (db:swissprot) ASTC\_ECOLI P77581 ESCHERICHIA  
COLI 562 -11533141 7000684933 hypothetical protein b1748 (db:pir2.dat)  
D64934 D64934 Escherichia coli 562 -11533141 224219 acetylornithine  
aminotransferase ec 2.6.1.11 (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #327(39.2-39.5 min.)) (nt:orf\_id:o327#5; similar to (swissprot  
accession) (le:10490) (re:11710) (di:complement) D90818 D90818 g1742857  
Escherichia coli 562 -11533141 300865 acetylornithine aminotransferase ec  
2.6.1.11 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda  
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#328(39.4-39.8 min.)) (nt:orf\_id:o327#5; similar to (swissprot accession)  
(le:2277) (re:3497) (di:complement) D90819 D90819 g1742862 Escherichia coli  
562 -11533141 300861 cstc acetylornithine delta-aminotransferase  
(fn:enzyme; amino acid biosynthesis: arginine) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 159 of 400 of the completegenome.)  
(nt:f406; this 406 aa orf is 60 pct identical (0 gaps)) (le:9536) (re:10756)  
(di:complement) AE000269 AE000269 g1788044 Escherichia coli 562 -11533141  
224223 acetylornithine aminotransferase ec 2.6.1.11 (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #328(39.4-39.8 min.))  
(nt:orf\_id:o327#5; similar to (swissprot accession) (le:2277) (re:3497)  
(di:complement) D90819 D90819 g1742862 Escherichia coli 562 -11533141  
5000692466 (de:(ecoli\_1705) (pn:function not assigned) (gtcfc:13.7:14.1)  
(ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_1705  
ECOLI\_1705 Escherichia coli 562 10059254

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501827876	8017	30173	327	108

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827886	8018	30174	1230	409

Description

GTC ORF with score 285 to: (gtcfc:8.5:9.4:12.13:12.8:12.9) (ec:2.7.1.-)  
(keggfc:8.5:9.4:13.1:13.3) (sgdfc:3.2.0:3.3.0:9.2.0:10.1.4:15.0.0)  
(db:gtc-saccharomyces cerevisiae) (keggfc:metabolism of complex  
lipids-sphingoglycolipid metabolism:nicotinate ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827897	8019	30175	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827908	8020	30176	249	82

Description

6500729284 hisg:b2019 atp phosphoribosyltransferase (gtcfc:5.11)  
(ec:2.4.2.17) (keggfc:5.11) (rileyfc:1.4.5) (db:gtc-escherichia coli) b2019  
b2019 Escherichia coli 562 -11533142 232427 hisg (ec:2.4.2.17) (de:atp  
phosphoribosyltransferase,) (db:swissprot) HIS1\_ECOLI P10366 ESCHERICHIA  
COLI 562 -11533142 162766 hisg atp  
phosphoribosyltransferase::phosphoribosyl-atp pyrophosphohydrolase (cl:atp  
phosphoribosyltransferase) (ec:2.4.2.17) (db:pir1.dat) (mp:44 min) XREC  
B64967 Escherichia coli 562 -11533142 301173 hisg atp  
phosphoribosyltransferase ec 2.4.2.17 . (sr:escherichia coli (strain:k12)  
dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic  
dna, kohara clone #350(44.9-45.2 min.)) (nt:orf\_id:o350#5; similar to  
(swissprot accession) (le:7534) (re:8433) (di:direct) D90840 D90840 g1736697  
Escherichia coli 562 -11533142 238448 atp-phosphoribosyl transferase  
(db:genpept-bct1) (de:e.coli gene for atp-phosphoribosyl transferase.)  
(le:1) (re:900) (di:direct) ECATPPHTR X63697 g41022 Escherichia coli 562  
-11533142 5000690377 hisg atp phosphoribosyltransferase (db:genpept-bct1)  
(de:escherichia coli k-12 atp phosphoribosyltransferase (hisg) gene,complete  
cds.) (le:1) (re:900) (di:direct) ECU02070 U02070 g509817 Escherichia coli  
562 -11533142 224533 hisg atp phosphoribosyltransferase (fn:enzyme; amino  
acid biosynthesis: histidine) (db:genpept-bct2) (ec:2.4.2.17)  
(de:escherichia coli k-12 mg1655 section 183 of 400 of the completegenome.)  
(nt:o299; 99 pct identical to his1\_ecoli sw: p10366; cg) (le:4608) (re:5507)  
(di:direct) AE000293 AE000293 g1788330 Escherichia coli 562 -11533142 76991  
hisg (ec:2.4.2.17) (de:atp phosphoribosyltransferase,) (db:swissprot)  
HIS1\_ECOLI P10366 ESCHERICHIA COLI 562 -11533142 7000685528 hisg atp  
phosphoribosyltransferase::phosphoribosyl-atp pyrophosphohydrolase (cl:atp  
phosphoribosyltransferase) (ec:2.4.2.17) (db:pir) (mp:44 min) XREC JS0131  
Escherichia coli 562 -11533142

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827909	8021	30177	666	221

Description

6500729285 hisd:b2020 histidinol dehydrogenase:hdh (gtcfc:5.11)  
(ec:1.1.1.23) (keggfc:5.11) (rileyfc:1.4.5) (db:gtc-escherichia coli) b2020  
b2020 Escherichia coli 562 -11533143 7000688841 hisd histidinol  
dehydrogenase (cl:histidinol dehydrogenase:histidinol dehydrogenase  
homology) (ec:1.1.1.23) (db:pir1.dat) (mp:44 min) DEECHO C64967 Escherichia  
coli 562 -11533143 7500953169 hisd l-histidinal:nad+ oxidoreductase  
(fn:enzyme; amino acid biosynthesis: histidine) (db:genpept-bct2)  
(ec:1.1.1.23) (de:escherichia coli k-12 mg1655 section 183 of 400 of the  
completeness.) (nt:o434; 99 pct identical to hisx\_ecoli sw: p06988; cg)  
(le:5513) (re:6817) (di:direct) AE000293 AE000293 gl788331 Escherichia coli  
562 -11533143 5000690378 (de:(ecoli\_1968) (pn:l-histidinal:nad) (gn:hisd)  
(gtcfc:5.11) (ec:1.1.1.23) (hisx\_ecoli) (keggfc:5.11) (rileyfc:1.4.5)  
(db:gtc-escherichia coli)) ECOLI\_1968 ECOLI\_1968 Escherichia coli 562  
10123544

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827924	8022	30178	585	194

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827925	8023	30179	549	182

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501827928	8024	30180	693	230
<u>Description</u>				
6500729286 hisc:b2021 imidazole:histidinol-phosphate aminotransferase:imidazole acetol-phosphate transaminase (gtcfc:5.11) (ec:2.6.1.9) (keggfc:5.11) (rileyfc:1.4.5) (db:gtc-escherichia coli) b2021 b2021 Escherichia coli 562 -11533144 77053 hisc (ec:2.6.1.9) (de:phosphate transaminase)) (db:swissprot) HIS8_ECOLI P06986 ESCHERICHIA COLI 562 -11533144 163202 hisc histidinol-phosphate transaminase::histidinol-phosphate aminotransferase:imidazolylacetolphosphate aminotransferase (cl:histidinol-phosphate aminotransferase) (ec:2.6.1.9) (db:pir1.dat) (mp:44 min) XNECHC D64967 Escherichia coli 562 -11533144 301175 hisc histidinol-phosphate aminotransferase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #350(44.9-45.2 min.)) (nt:orf_id:o350#7; similar to (swissprot accession) (le:9740) (re:10810) (di:direct) D90840 D90840 g1736699 Escherichia coli 562 -11533144 238449 hisc histidinol-phosphate aminotransferase (db:genpept-bct1) (de:escherichia coli k-12 histidinol-phosphate aminotransferase (hisc)gene, complete cds.) (le:1) (re:1071) (di:direct) ECU02071 U02071 g509819 Escherichia coli 562 -11533144 224535 hisc histidinol-phosphate aminotransferase (fn:enzyme; amino acid biosynthesis: histidine) (db:genpept-bct2) (ec:2.6.1.9) (de:escherichia coli k-12 mg1655 section 183 of 400 of the completegenome.) (nt:o356; 100 pct identical to his8_ecoli sw: p06986;) (le:6814) (re:7884) (di:direct) AE000293 AE000293 g1788332 Escherichia coli 562 -11533144 7000685530 hisc histidinol-phosphate transaminase::histidinol-phosphate aminotransferase:imidazolylacetolphosphate aminotransferase (cl:histidinol-phosphate aminotransferase) (ec:2.6.1.9) (db:pir) (mp:44 min) XNECHC I73527 Escherichia coli 562 -11533144 5000690379 (de:(ecoli_1969) (pn:histidinol-phosphate aminotransferase) (gn:hisc) (gtcfc:5.11) (ec:2.6.1.9) (his8_ecoli) (keggfc:5.11) (rileyfc:1.4.5) (db:gtc-escherichia coli)) ECOLI_1969 ECOLI_1969 Escherichia coli 562 10019415				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827931	8025	30181	519	172

Description

6500729287 hisb:b2022 histidinol phosphatase:imidazoleglycerol-phosphate dehydratase:igpd / histidinol-phosphatase (gtcfc:5.11) (keggfc:5.11) (rileyfc:1.4.5) (db:gtc-escherichia coli) b2022 b2022 Escherichia coli 562 -11533145 7000688894 hisb hisb bifunctional enzyme (cl:hisb bifunctional enzyme:imidazoleglycerol-phosphate dehydratase homology) (db:pir1.dat) (mp:44 min) DWECHB E64967 Escherichia coli 562 -11533145 7500953342 hisb imidazoleglycerolphosphate dehydratase and (fn:enzyme; amino acid biosynthesis: histidine) (db:genpept-bct2) (ec:3.1.3.15:4.2.1.19) (de:escherichia coli k-12 mgl655 section 183 of 400 of the completegenome.) (nt:o356; uug start;100 pct identical to his7\_ecoli) (le:7881) (re:8951) (di:direct) AE000293 AE000293 g1788333 Escherichia coli 562 -11533145 5000690380 (de:(ecoli\_1970) (pn:imidazoleglycerolphosphate dehydratase and histidinol phosphate phosphatase) (gn:hisb) (gtcfc:5.11) (ec:4.2.1.19) (his7\_ecoli) (keggfc:5.11) (rileyfc:1.4.5) (db:gtc-escherichia coli)) ECOLI\_1970 ECOLI\_1970 Escherichia coli 562 10123545

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827941	8026	30182	489	162

Description

6500729288 hish:b2023 amidotransferase:amidotransferase hish (gtcfc:5.11) (ec:2.4.2.-) (keggfc:5.11) (rileyfc:1.4.5) (db:gtc-escherichia coli) b2023 b2023 Escherichia coli 562 -11533146 301177 hish (ec:2.4.2.-) (de:amidotransferase hish,) (db:swissprot) HIS5\_ECOLI P10375 ESCHERICHIA COLI 562 -11533146 123453 hish amidotransferase hish (cl:amidotransferase hish) (ec:2.4.2.-) (db:pir1.dat) (mp:44 min) XQECHH JS0132 Escherichia coli 562 -11533146 224537 hish amidotransferase hish ec 2.4.2.- (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #350(44.9-45.2 min.)) (nt:orf\_id:o350#9; similar to (pir accession number) (le:11877) (re:12467) (di:direct) D90840 D90840 g1736701 Escherichia coli 562 -11533146 301185 hish amidotransferase hish ec 2.4.2.- (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #351(45.1-45.5 min.)) (nt:orf\_id:o350#9; similar to (pir accession number) (le:835) (re:1425) (di:direct) D90841 D90841 g1736710 Escherichia coli 562 -11533146 5000690381 (db:genpept-bct1) (de:escherichia coli dna for histidin operon genes hisgdcbhafie.) (nt:hish orf (aa 1-196)) (le:4617) (re:5207) (di:direct) ECHISOP X13462 g41712 Escherichia coli 562 -11533146 233104 hish glutamine amidotransferase subunit of (fn:enzyme; amino acid biosynthesis: histidine) (db:genpept-bct2) (ec:2.4.2.-) (de:escherichia coli k-12 mg1655 section 183 of 400 of the completegenome.) (nt:o196; 100 pct identical to his5\_ecoli sw: p10375;) (le:8951) (re:9541) (di:direct) AE000293 AE000293 g1788334 Escherichia coli 562 -11533146 77022 hish (ec:2.4.2.-) (de:amidotransferase hish,) (db:swissprot) HIS5\_ECOLI P10375 ESCHERICHIA COLI 562 -11533146 224545 hish amidotransferase hish ec 2.4.2.- (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #351(45.1-45.5 min.)) (nt:orf\_id:o350#9; similar to (pir accession number) (le:835) (re:1425) (di:direct) D90841 D90841 g1736710 Escherichia coli 562 -11533146

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827945	8027	30183	1038	346

Description

6500729289 hisa:b2024 phosphoribosylformimino-5-aminoimidazole carboxamide ribotide:phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase (gtcfc:5.11) (ec:5.3.1.16) (keggfc:5.11) (rileyfc:1.4.5) (db:gtc-escherichia coli) b2024 b2024 Escherichia coli 562 -11533147  
7000688904 hisa n-5-phospho-d-ribosylformimino -5-amino-1- 5-phosphoribosyl -4-imidazolecarboxamide isomerase::compound iii isomerase (cl:n-(5'-phospho-d-ribosylformimino)-5-amino-1-(5''-phosphoribosyl)-4-imidazolecarboxamide isomerase) (ec:5.3.1.16) (db:pir1.dat) (mp:44 min) ISECIC G64967 Escherichia coli 562 -11533147  
7500953354 hisa n-5-phospho-l-ribosyl-formimino -5-amino-1- (fn:enzyme; amino acid biosynthesis: histidine) (db:genpept-bct2) (ec:5.3.1.16) (de:escherichia coli k-12 mg1655 section 183 of 400 of the completegenome.) (nt:o246; 99 pct identical to his4\_ecoli sw: p10371; cg) (le:9538) (re:10278) (di:direct) AE000293 AE000293 g1788335 Escherichia coli 562 -11533147 5000690382 (de:(ecoli\_1972) (pn:n-:5"-phospho-l-ribosyl-formimino-5-amino-1-:5"-phosphoribosyl-4-imidazolecarboxamide isomerase) (gn:hisa) (gtcfc:5.11) (ec:5.3.1.16) (his4\_ecoli) (keggfc:5.11) (rileyfc:1.4.5) (db:gtc-escherichia coli)) ECOLI\_1972 ECOLI\_1972 Escherichia coli 562 10123546

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827947	8028	30184	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501827955	8029	30185	396	131

#### Description

6500729290 hisi:hisie:b2026 phosphoribosyl-amp cyclohydrolase /  
phosphoribosyl-atp pyrophosphohydrolase (gtcfc:5.11:14.3) (keggfc:5.11)  
(rileyfc:5.8.0) (db:gtc-escherichia coli) b2026 b2026 Escherichia coli 562  
-11533148 77001 hisi:hisie (ec:3.5.4.19:3.6.1.31)  
(de:pyrophosphohydrolase,) (db:swissprot) HIS2\_ECOLI P06989 ESCHERICHIA COLI  
562 -11533148 301181 hisi:hisie phosphoribosyl-amp cyclohydrolase ec  
3.5.4.19 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda  
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#350(44.9-45.2 min.)) (nt:orf\_id:o350#13; similar to (swissprot accession)  
(le:13956) (re:14567) (di:direct) D90840 D90840 g1736705 Escherichia coli  
562 -11533148 301189 hisi:hisie phosphoribosyl-amp cyclohydrolase ec  
3.5.4.19 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda  
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#351(45.1-45.5 min.)) (nt:orf\_id:o350#13; similar to (swissprot accession)  
(le:2914) (re:3525) (di:direct) D90841 D90841 g1736714 Escherichia coli 562  
-11533148 238450 hisi phosphoribosyl-atp (db:genpept-bct1) (de:escherichia  
coli k-12 phosphoribosyl-atp pyrophosphohydrolase:phosphoribosyl-amp  
cyclohydrolase (hisi) gene, complete cds.) (le:1) (re:612) (di:direct)  
ECU02072 U02072 g509821 Escherichia coli 562 -11533148 224549 hisi  
phosphoribosyl-amp cyclohydrolase (fn:enzyme; amino acid biosynthesis:  
histidine) (db:genpept-bct2) (ec:3.5.4.19:3.6.1.31) (de:escherichia coli  
k-12 mg1655 section 183 of 400 of the completegenome.) (nt:o203; 100 pct  
identical to his2\_ecoli sw: p06989;) (le:11030) (re:11641) (di:direct)  
AE000293 AE000293 g2367128 Escherichia coli 562 -11533148 224541 hisi:hisie  
phosphoribosyl-amp cyclohydrolase ec 3.5.4.19 (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #351(45.1-45.5 min.))  
(nt:orf\_id:o350#13; similar to (swissprot accession) (le:2914) (re:3525)  
(di:direct) D90841 D90841 g1736714 Escherichia coli 562 -11533148 164315  
(de:phosphoribosyl-atp pyrophosphohydrolase/phosphoribosyl-ampcyclohydrolase  
- escherichia coli) I73528 I73528 Escherichia coli 562 10019363

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501827960	8030	30186	219	72

#### Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501827983	8031	30187	786	261

Description

6500729291 hiss:b2514 histidyl-trna synthetase:histidine--trna ligase:hisrs (gtcfc:10.6:5.11) (ec:6.1.1.21) (keggfc:5.11:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli) b2514 b2514 Escherichia coli 562 -11533149 125939 hiss histidine--trna ligase::histidyl-trna synthetase (cl:histidine--trna ligase:amino acid--trna ligase repeat homology:histidine--trna ligase homology) (ec:6.1.1.21) (db:pir1.dat) (mp:54 min) SYECH A23890 Escherichia coli 562 -11533149 225089 hiss histidine--trna ligase ec 6.1.1.21 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #427(56.5-56.9 min.)) (nt:similar to (pir accession number a23890)) (le:14140) (re:15414) (di:complement) D90880 D90880 g1805574 Escherichia coli 562 -11533149 7500953376 hiss histidine-trna synthetase (sr:escherichia coli dna, clones pse411 and pse421) (db:genpept-bct1) (de:e. coli hiss gene coding for histidine-trna synthetase, completecds.) (nt:gtg start codon; protein n-terminus sequenced) (le:204) (re:1478) (di:direct) ECOHISS M11843 g146372 Escherichia coli 562 -11533149 234666 hiss histidine trna synthetase (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:6.1.1.21) (de:escherichia coli k-12 mg1655 section 227 of 400 of the completegenome.) (nt:f424; 100 pct identical to syh\_ecoli sw: p04804) (le:10217) (re:11491) (di:complement) AE000337 AE000337 g1788861 Escherichia coli 562 -11533149 5000690384 (de:(ecoli\_2454) (pn:histidine trna synthetase) (gn:hiss) (gtcfc:5.11:10.6) (ec:6.1.1.21) (syh\_ecoli) (keggfc:5.11:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli)) ECOLI\_2454 ECOLI\_2454 Escherichia coli 562 10066493

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501827985	8032	30188	288	95

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501827997	8033	30189	1203	400

Description

6500729292 yrbm:mtga:b3208 hypothetical 27.3 kd protein in ptso-archb intergenic region:monofunctional biosynthetic peptidoglycan transglycosylase (gtcfc:5.11:14.1) (ec:2.4.2.-) (keggfc:5.11) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3208 b3208 Escherichia coli 562 -11533150 116117 mtga (ec:2.4.2.-) (de:(ec 2.4.2.-) (monofunctional tgase)) (db:swissprot) MTGA\_ECOLI P46022 ESCHERICHIA COLI 562 -11533150 7000685875 yrbm hypothetical 27.3 kd protein in ptso-archb intergenic region (db:pir2.dat) B65112 B65112 Escherichia coli 562 -11533150 7500886027 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf\_f242) (le:129832) (re:130560) (di:complement) ECOUW67 U18997 g606147 Escherichia coli 562 -11533150 236446 mtga putative peptidoglycan enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 290 of 400 of the completegenome.) (nt:f242; formerly designated yrbm) (le:2611) (re:3339) (di:complement) AE000400 AE000400 g1789601 Escherichia coli 562 -11533150 5000693446 (de:(ecoli\_3131) (pn:hypothetical 27) (gn:yrbm) (gtcfc:13.7:14.1) (ec:) (yrbm\_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_3131 ECOLI\_3131 Escherichia coli 562 10057843

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828020	8034	30190	393	130

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501828023	8035	30191	213	70

# Description

6500729293 hisl:b2018 his operon leader peptide:attenuator peptide (gtcfc:5.11) (keggfc:14.2) (rileyfc:1.4.5) (db:gtc-escherichia coli) b2018 b2018 Escherichia coli 562 -11533151 262777 hisl (de:his operon leader peptide (attenuator peptide)) (db:swissprot) LPHI\_ECOLI P03058 ESCHERICHIA COLI 562 -11533151 7502851885 hisl (de:his operon leader peptide (attenuator peptide)) (db:swissprot) LPHI\_ECOLI P03058 SALMONELLA TYPHIMURIUM 602 -11533151 131590 hisl his operon leader peptide (cl:his leader peptide) (db:pir1.dat) LFECH A03594 Escherichia coli 562 -11533151 233090 hisg (db:genpept-bct1) (de:e. coli hisg gene regulatory region and start of reading frame.hisg codes for atp phosphoribosyltransferase (e.c.2.4.2.17).) (nt:regulatory peptide. (525 is 2nd base in codon)) (le:478) (re:525) (di:direct) ECHIS1 V00284 g581104 Escherichia coli 562 -11533151 233096 (db:genpept-bct1) (de:e. coli hisg gene coding for phosphoribosyl transferase.) (nt:attenuator peptide) (le:1) (re:51) (di:direct) ECHISG V00285 g41702 Escherichia coli 562 -11533151 233099 (db:genpept-bct1) (de:escherichia coli dna for histidin operon genes hisgdcbhafie.) (nt:hisl orf (aa 1-16)) (le:79) (re:129) (di:direct) ECHISOP X13462 g41707 Escherichia coli 562 -11533151 262773 (db:genpept-bct1) (de:s. typhimurium hisg gene encoding atp phosphoribosyl transferase.) (nt:reading frame (attenuator peptide)) (le:58) (re:108) (di:direct) STHISG V01371 g47713 Salmonella typhimurium 602 -11533151 264276 (db:genpept-bct1) (de:salmonella typhimurium dna for histidin operon genes hisgdcbhafie.) (nt:hisl orf (aa 1-16)) (le:79) (re:129) (di:direct) STHISOP X13464 g47720 Salmonella typhimurium 602 -11533151 7502851886 (sr:salmonella typhimurium (strain lt2) dna) (db:genpept-bct1) (de:s.typhimurium his operon encoding atp phosphoribosyl transferase(hisg), histidinol dehydrogenase (hisd), histidinol phosphateaminotransferase (hisc) complete cds, and imidazole-glycerol... STYHISOGD J01804 g154117 Salmonella typhimurium 602 -11533151 7500885119 hisl his operon leader peptide (fn:leader; amino acid biosynthesis: histidine) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 183 of 400 of the completegenome.) (nt:ol6; 100 pct identical to lphi\_ecoli sw: p03058) (le:4412) (re:4462) (di:direct) AE000293 AE000293 g1788329 Escherichia coli 562 -11533151 82389 hisl (de:his operon leader peptide (attenuator peptide)) (db:swissprot) LPHI\_ECOLI P03058 ESCHERICHIA COLI 562 -11533151 7502851887 hisl (de:his operon leader peptide (attenuator peptide)) (db:swissprot) LPHI\_ECOLI P03058 SALMONELLA TYPHIMURIUM 602 -11533151 82390 hisl (de:his operon leader peptide (attenuator peptide)) (db:swissprot) LPHI\_ECOLI P03058 ESCHERICHIA COLI 562 -11533151 7502851888 hisl (de:his operon leader peptide (attenuator peptide)) (db:swissprot) LPHI\_ECOLI P03058 SALMONELLA TYPHIMURIUM 602 -11533151

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828024	8036	30192	639	212

Description

6500729294 hisf:b2025 hisf protein:cyclase (gtcfc:5.11) (keggfc:14.2) (rileyfc:1.4.5) (db:gtc-escherichia coli) b2025 b2025 Escherichia coli 562 -11533152 301180 hisf (de:hisf protein (cyclase)) (db:swissprot) HIS6\_ECOLI P10373 ESCHERICHIA COLI 562 -11533152 125733 hisf cyclase hisf (cl:cyclase hisf) (db:pir1.dat) (mp:44 min) OYECHF JS0134 Escherichia coli 562 -11533152 224540 hisf cyclase hisf (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #350(44.9-45.2 min.)) (nt:orf\_id:o350#12; similar to (pir accession number) (le:13186) (re:13962) (di:direct) D90840 D90840 g1736704 Escherichia coli 562 -11533152 301188 hisf cyclase hisf (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #351(45.1-45.5 min.)) (nt:orf\_id:o350#12; similar to (pir accession number) (le:2144) (re:2920) (di:direct) D90841 D90841 g1736713 Escherichia coli 562 -11533152 7502851889 (db:genpept-bct1) (de:escherichia coli dna for histidin operon genes hisgdcbhafie.) (nt:hisf orf (aa 1-258)) (le:5926) (re:6702) (di:direct) ECHISOP X13462 g41714 Escherichia coli 562 -11533152 233106 hisf imidazole glycerol phosphate synthase subunit in (fn:enzyme; amino acid biosynthesis: histidine) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 183 of 400 of the completegenome.) (nt:o258; 100 pct identical to his6\_ecoli sw: p10373;) (le:10260) (re:11036) (di:direct) AE000293 AE000293 g1788336 Escherichia coli 562 -11533152 77029 hisf (de:hisf protein (cyclase)) (db:swissprot) HIS6\_ECOLI P10373 ESCHERICHIA COLI 562 -11533152 224548 hisf cyclase hisf (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #351(45.1-45.5 min.)) (nt:orf\_id:o350#12; similar to (pir accession number) (le:2144) (re:2920) (di:direct) D90841 D90841 g1736713 Escherichia coli 562 -11533152

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828025	8037	30193	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828028	8038	30194	219	72

Description

6500729295 ybjv:b0870 hypothetical protein:probable l-allo-threonine aldolase:l-allo-ta:l-allo-threonine acetaldehyde-lyase (gtcfc:5.12:5.13:5.9:8.5:14.1) (ec:4.1.2.-) (keggfc:5.9:5.12:5.13:8.5) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0870 b0870 Escherichia coli 562 -11533153 5500685531 ybjv (ec:4.1.2.-) (de:acetaldehyde-lyase)) (db:swissprot) LTAA\_ECOLI P75823 ESCHERICHIA COLI 562 -11533153 7000685769 ybjv l-allo-threonine aldolase (ec:4.1.2.-) (db:pir2.dat) F64825 F64825 Escherichia coli 562 -11533153 7500885180 threonine aldolase (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct2) (de:escherichia coli gene for threonine aldolase, complete cds.) (le:61) (re:1062) (di:direct) AB005050 AB005050 g2225892 Escherichia coli 562 -11533153 4000713619 ybjv putative arylsulfatase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 78 of 400 of the completegenome.) (nt:f333) (le:8579) (re:9580) (di:complement) AE000188 AE000188 g1787095 Escherichia coli 562 -11533153 5000691849 gly1 protein (sr:escherichia coli (strain:k12) dna, clone:kohara clone #211) (db:genpept) (de:escherichia coli genomic dna. (19.4 - 19.8 min).) (nt:orf\_id:o211#13; similar to pir accession number) (le:10572) (re:11573) (di:complement) D90724 D90724 g4062450 Escherichia coli 562 -11533153

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828033	8039	30195	279	92

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828035	8040	30196	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828056	8041	30197	186	61

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828061	8042	30198	936	311

Description

GTC ORF with score 200 to: (sr:pseudomonas fluorescens (strain:ip01) dna, clone:e. coli jm10) (db:genpept-bct1) (de:pseudomonas fluorescens dna for outer membrane protein,2-hydroxy-6-oxo-7-methylocta-2,4-dienoate hydrolase, complete cds.) (le:1897) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828068	8043	30199	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828071	8044	30200	549	182

Description

6500729296 gaty:b2096 tagatose-bisphosphate aldolase gaty  
(gtcfc:5.12:5.13:5.9:8.5:14.3) (ec:4.1.2.-) (keggfc:5.9:5.12:5.13:8.5)  
(rileyfc:5.8.0) (db:gtc-escherichia coli) b2096 b2096 Escherichia coli 562  
-11533154 73177 gaty (ec:4.1.2.-) (de:tagatose-bisphosphate aldolase gaty,)  
(db:swissprot) GATY\_ECOLI P37192 ESCHERICHIA COLI 562 -11533154 7000685368  
gaty tagatose-bisphosphate aldolase gaty (cl:fructose-bisphosphate aldolase  
ii) (ec:4.1.2.-) (db:pir2.dat) G64976 G64976 Escherichia coli 562 -11533154  
224650 gaty tagatose-bisphosphate aldolase gaty ec (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #359(46.8-47.2 min.).)  
(nt:orf\_id:o359#6; similar to (swissprot accession) (le:4274) (re:5134)  
(di:complement) D90848 D90848 g1736822 Escherichia coli 562 -11533154  
301290 gaty tagatose-bisphosphate aldolase 1 (fn:enzyme; degradation of  
small molecules: carbon) (db:genpept-bct2) (ec:4.1.2.-) (de:escherichia coli  
k-12 mg1655 section 188 of 400 of the completegenome.) (nt:f286; 98 pct  
identical to gaty\_ecoli sw: p37192) (le:11304) (re:12164) (di:complement)  
AE000298 AE000298 g1788412 Escherichia coli 562 -11533154 5000690385  
(de:(ecoli\_2044) (pn:tagatose-bisphosphate aldolase) (gn:gaty)  
(gtcfc:5.12:5.13:5.9:8.4:8.5) (ec:4.1.2.-) (gaty\_ecoli)  
(keggfc:5.9:5.12:5.13:8.5) (rileyfc:5.7.0) (db:gtc-escherichia coli))  
ECOLI\_2044 ECOLI\_2044 Escherichia coli 562 10120009

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828083	8045	30201	573	190

# Description

6500729297 agay:kba:b3137 tagatose-bisphosphate  
aldolase:tagatose-bisphosphate aldolase agay (gtcfc:5.12:5.13:5.9:8.5:14.3)  
(ec:4.1.2.-) (keggfc:5.9:5.12:5.13:8.5) (rileyfc:5.8.0) (db:gtc-escherichia  
coli) b3137 b3137 Escherichia coli 562 -11533155 58936 agay:kba  
(ec:4.1.2.-) (de:tagatose-bisphosphate aldolase agay,) (db:swissprot)  
AGAY\_ECOLI P42908 ESCHERICHIA COLI 562 -11533155 7000684537 agay  
tagatose-bisphosphate aldolase agay (cl:fructose-bisphosphate aldolase ii)  
(ec:4.1.2.-) (db:pir2.dat) E65103 E65103 Escherichia coli 562 -11533155  
7500876664 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region  
from 67.4 to 76.0 minutes.) (nt:orf\_o286) (le:63895) (re:64755) (di:direct)  
ECOUW67 U18997 g606077 Escherichia coli 562 -11533155 236376 agay  
tagatose-bisphosphate aldolase 2 (fn:enzyme; central intermediary  
metabolism: pool,) (db:genpept-bct2) (ec:4.1.2.-) (de:escherichia coli k-12  
mg1655 section 285 of 400 of the completegenome.) (nt:o286; 100 pct  
identical amino acid sequence and) (le:1378) (re:2238) (di:direct) AE000395  
AE000395 g1789526 Escherichia coli 562 -11533155 5000690386  
(de:(ecoli\_3061) (pn:tagatose-bisphosphate aldolase) (gn:agay)  
(gtcfc:5.12:5.13:5.9:8.4:8.5) (ec:4.1.2.-) (agay\_ecoli)  
(keggfc:5.9:5.12:5.13:8.5) (rileyfc:5.7.0) (db:gtc-escherichia coli))  
ECOLI\_3061 ECOLI\_3061 Escherichia coli 562 10001680

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828086	8046	30202	402	133

Description

6500729298 yiaq:sgbh:b3581 hypothetical 23.4 kd protein in avta-selb intergenic region:probable hexulose-6-phosphate synthase:humps:d-arabino 3-hexulose 6-phosphate formaldehyde lyase (gtcfc:5.12:5.13:5.9:8.5:14.1) (ec:4.1.2.-) (keggfc:5.9:5.12:5.13:8.5) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3581 b3581 Escherichia coli 562 -11533156 113139 sgbh (ec:4.1.2.-) (de:3-hexulose 6-phosphate formaldehyde lyase)) (db:swissprot) SGBH\_ECOLI P37678 ESCHERICHIA COLI 562 -11533156 163772 yiaq hypothetical 23.4k protein avta-selb intergenic region:hypothetical protein o220 (cl:hypothetical protein hi1024) (db:pir2.dat) S47802 S47802 Escherichia coli 562 -11533156 7500891593 (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:162830) (re:163492) (di:direct) ECOUW76 U00039 g466719 Escherichia coli 562 -11533156 236818 sgbh probable 3-hexulose 6-phosphate synthase (fn:putative enzyme; central intermediary) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 325 of 400 of the completegenome.) (nt:o220; formerly designated yiaq) (le:7615) (re:8277) (di:direct) AE000435 AE000435 g1790006 Escherichia coli 562 -11533156 5000693665 (de:(ecoli\_3501) (pn:hypothetical 23) (gn:yiaq) (gtcfc:13.7:14.1) (ec:) (yiaq\_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_3501 ECOLI\_3501 Escherichia coli 562 10054867

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501828103	8047	30203	456	152

Description

6500729299 tyrb:b4054 tyrosine aminotransferase:aromatic-amino-acid  
aminotransferase (gtcfc:5.12:5.13:5.15) (keggfc:5.12:5.13:5.15)  
(rileyfc:1.4.4) (db:gtc-escherichia coli) b4054 b4054 Escherichia coli 562  
-11533157 238439 tyrb (ec:2.6.1.57) (de:aromatic-amino-acid  
aminotransferase, (aroat) (arat)) (db:swissprot) TYRB\_ECOLI P04693  
ESCHERICHIA COLI 562 -11533157 123495 tyrb tyrosine transaminase::tyrosine  
aminotransferase (cl:aspartate aminotransferase) (ec:2.6.1.5) (db:pir1.dat)  
(mp:92 min) XNECY A30379 Escherichia coli 562 -11533157 237260 tyrb  
tyrosine aminotransferase (sr:e.coli dna) (db:genpept-bct1) (ec:2.6.1.5)  
(de:e.coli k12 tyrb gene encoding aminotransferase, complete cds.) (le:376)  
(re:1569) (di:direct) ECOTYRBA M12047 g148085 Escherichia coli 562 -11533157  
5000690412 (db:genpept-bct1) (de:e. coli tyr b gene for aromatic  
aminotransferase.) (nt:aromatic aminotransferase (tyrb)) (le:276) (re:1469)  
(di:direct) ECTYRB X03628 g581243 Escherichia coli 562 -11533157 236231  
tyrb tyrosine aminotransferase:tyrosine repressible (fn:enzyme; amino acid  
biosynthesis: tyrosine) (db:genpept-bct2) (ec:2.6.1.57) (de:escherichia coli  
k-12 mg1655 section 368 of 400 of the completegenome.) (nt:o397; 100 pct  
identical to tyrb\_ecoli sw: p04693;) (le:7953) (re:9146) (di:direct)  
AE000478 AE000478 g1790488 Escherichia coli 562 -11533157 324400 tyrb  
tyrosine aminotransferase (sr:escherichia coli (sub\_strain mg1655, strain  
k-12) (library: lambda) (db:genpept-bct2) (ec:2.6.1.5) (de:e. coli  
chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 57)  
(le:132355) (re:133548) (di:direct) ECOUW89 U00006 g409800 Escherichia coli  
562 -11533157 7502851890 tyrb aromatic transaminase (db:genpept-pat)  
(de:e.coli tyrb gene.) (le:378) (re:1571) (di:direct) A01447 A01447 g580653  
Escherichia coli 562 -11533157 102909 tyrb (ec:2.6.1.57)  
(de:aromatic-amino-acid aminotransferase,) (db:swissprot) TYRB\_ECOLI P04693  
ESCHERICHIA COLI 562 -11533157

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828108	8048	30204	261	86

Description

6500729300 yjfv:sgah:b4196 hypothetical 23.6 kd protein in aidb-rpsf intergenic region:probable hexulose-6-phosphate synthase:humps:d-arabino 3-hexulose 6-phosphate formaldehyde lyase (gtcfc:5.12:5.13:5.9:8.5:14.1) (ec:4.1.2.-) (keggfc:5.9:5.12:5.13:8.5) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4196 b4196 Escherichia coli 562 -11533158 113733 sgah (ec:4.1.2.-) (de:3-hexulose 6-phosphate formaldehyde lyase)) (db:swissprot) SGAH\_ECOLI P39304 ESCHERICHIA COLI 562 -11533158 163768 yjfv hypothetical 23.6k protein aidb-rpsf intergenic region:hypothetical protein o216 (cl:hypothetical protein hil024) (db:pir2.dat) S56421 S56421 Escherichia coli 562 -11533158 7500891583 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf\_o216) (le:113018) (re:113668) (di:direct) ECOUW93 U14003 g537037 Escherichia coli 562 -11533158 237401 sgah probable hexulose-6-phosphate synthase (fn:putative enzyme; central intermediary) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 381 of 400 of the completegenome.) (nt:o216; formerly designated yjfv) (le:5852) (re:6502) (di:direct) AE000491 AE000491 g1790640 Escherichia coli 562 -11533158 5000693935 (de:(ecoli\_4079) (pn:hypothetical 23) (gn:yjfv) (gtcfc:13.7:14.1) (ec:) (yjfv\_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_4079 ECOLI\_4079 Escherichia coli 562 10055461

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828110	8049	30205	582	193

Description

6500729301 mhp:b0348 2:3-dihydroxyphenylpropionate 1:2-dioxygenase  
(gtcfc:5.13:5.14:9.13:14.3) (ec:1.13.11.-) (keggfc:5.13:5.14:9.14)  
(rileyfc:5.8.0) (db:gtc-escherichia coli) b0348 b0348 Escherichia coli 562  
-11533159 239965 mhp (ec:1.13.11.-) (de:2,3-dihydroxyphenylpropionate  
1,2-dioxygenase,) (db:swissprot) MHPB\_ECOLI P54711 ESCHERICHIA COLI 562  
-11533159 7000685841 mhp 2:3-dihydroxyphenylpropionate 1:2-dioxygenase  
(ec:1.13.11.-) (db:pir2.dat) D64762 D64762 Escherichia coli 562 -11533159  
5000690387 mhp 3-2:3-dihydroxyphenylpropionate 1 (db:genpept-bct1)  
(de:e.coli mhp cluster for 3-hydroxy-phenylpropionic acid degradation.)  
(le:2709) (re:3653) (di:direct) ECMHP Y09555 g1702882 Escherichia coli 562  
-11533159 7500885608 (db:genpept-bct1) (de:escherichia coli chromosome  
minutes 6-8.) (nt:similar to mcp1 gene (catechol 2,3-dioxygenase) of)  
(le:78072) (re:79016) (di:direct) ECU73857 U73857 g1657544 Escherichia coli  
562 -11533159 233385 mhp 2:3-dihydroxyphenylpropionate 1:2-dioxygenase  
(fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2)  
(ec:1.13.11.-) (de:escherichia coli k-12 mg1655 section 32 of 400 of the  
completegenome.) (nt:o314; 98 pct identical to mhp\_ecoli sw: p54711)  
(le:1735) (re:2679) (di:direct) AE000142 AE000142 g1786544 Escherichia coli  
562 -11533159 83675 mhp (ec:1.13.11.-) (de:2,3-dihydroxyphenylpropionate  
1,2-dioxygenase,) (db:swissprot) MHPB\_ECOLI P54711 ESCHERICHIA COLI 562  
-11533159

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828111	8050	30206	276	91

Description

6500729302 hema:b1210 glutamyl-trna reductase:glutr (gtcfc:10.6:5.1)  
(ec:1.2.1.-) (keggfc:5.13:5.14:9.10) (rileyfc:1.7.12) (db:gtc-escherichia  
coli) b1210 b1210 Escherichia coli 562 -11533160 76460 hema (ec:1.2.1.-)  
(de:glutamyl-trna reductase, (glutr)) (db:swissprot) HEM1\_ECOLI P13580  
ESCHERICHIA COLI 562 -11533160 7000685504 hema glutamyl-trna  
reductase::hema protein:hema protein (cl:glutamyl-trna reductase) (sr:strain  
k-12, , strain k-12) (sr:strain k-12, ) (ec:1.2.1.-) (db:pir1.dat) (mp:27  
min) BVECHA A45918 Escherichia coli 562 -11533160 223412 hema glutamyl-trna  
reductase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #247)  
(db:genpept-bct1) (de:escherichia coli genomic dna.(27.0 -27.4 min).)  
(le:7976) (re:9232) (di:direct) D90756 D90756 g1651600 Escherichia coli 562  
-11533160 7500883135 hema (sr:escherichia coli (strain k12), dna)  
(db:genpept-bct1) (de:e.coli delta-aminolevulinic synthase (hema) gene,  
complete cds.) (nt:delta-aminolevulinic synthase (ec 2.3.1.37)) (le:221)  
(re:1477) (di:direct) ECOHEMAA M25323 g146333 Escherichia coli 562 -11533160  
234629 hema enzyme in alternate path of synthesis of (fn:enzyme;  
biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:1.2.1.-)  
(de:escherichia coli k-12 mg1655 section 109 of 400 of the completegenome.)  
(nt:o418; 100 pct identical to hem1\_ecoli sw: p13580) (le:7408) (re:8664)  
(di:direct) AE000219 AE000219 g1787461 Escherichia coli 562 -11533160  
5000690389 hema glutamyl-trna reductase ec 1.2.1.- glutr . (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #247) (db:genpept) (de:escherichia  
coli genomic dna. (27.1 - 27.5 min).) (nt:orf\_id:o247#8; similar to  
swissprot accession) (le:7976) (re:9232) (di:direct) D90756 D90756 g1651600  
Escherichia coli 562 -11533160

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501828113	8051	30207	507	168

# Description

6500729303 feab:pada:maob:b1385 hypothetical protein:phenylacetaldehyde dehydrogenase:pad (gtcfc:5.13) (ec:1.2.1.39) (keggfc:5.13) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1385 b1385 Escherichia coli 562 -11533161

7000691270 probable phenylacetaldehyde dehydrogenase (cl:aldehyde dehydrogenase (nad+):aldehyde dehydrogenase homology) (ec:1.2.1.39) (db:pir2.dat) D64889 D64889 Escherichia coli 562 -11533161 223665 aldehyde dehydrogenase:mitochondrial 3 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #265(30.9-31.2 min.)) (nt:orf\_id:o265#6; similar to (swissprot accession) (le:11593) (re:13095) (di:direct) D90776 D90776 g1742261 Escherichia coli 562 -11533161 300441 aldehyde dehydrogenase:mitochondrial 3 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #266(31.1-31.5 min.)) (nt:orf\_id:o265#6; similar to (swissprot accession) (le:3734) (re:5236) (di:direct) D90777 D90777 g1742265 Escherichia coli 562 -11533161 300438 feab phenylacetaldehyde dehydrogenase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 125 of 400 of the completegenome.) (nt:o500; this 500 aa orf is 39 pct identical (8 gaps)) (le:6494) (re:7996) (di:direct) AE000235 AE000235 g1787650 Escherichia coli 562 -11533161 223668 aldehyde dehydrogenase:mitochondrial 3 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #266(31.1-31.5 min.)) (nt:orf\_id:o265#6; similar to (swissprot accession) (le:3734) (re:5236) (di:direct) D90777 D90777 g1742265 Escherichia coli 562 -11533161 5000692190 (de:(ecoli\_1345) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_1345 ECOLI\_1345 Escherichia coli 562 10119572



ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501828115	8052	30208	198	65

Description

6500729304 epd:gapb:b2927 d-erythrose 4-phosphate dehydrogenase:e4pdh  
 (gtcfc:5.13:5.14:9.10:14.3) (ec:1.2.1.-) (keggfc:5.13:5.14:9.10)  
 (rileyfc:5.8.0) (db:gtc-escherichia coli) b2927 b2927 Escherichia coli 562  
 -11533162 122645 epd:gapb glyceraldehyde-3-phosphate dehydrogenase:b  
 (cl:glyceraldehyde-3-phosphate dehydrogenase) (ec:1.2.1.12) (db:pir1.dat)  
 (mp:63 min) DEECGB S04732 Escherichia coli 562 -11533162 239140  
 (db:genpept-bct1) (de:escherichia coli fda, pgk and gapb genes for  
 fructose1,6-biphosphate aldolase (class ii), phosphoglycerate kinase  
 andglyceraldehyde 3-phosphate dehydrogenase.) (nt:glyceraldehyde 3-phosphate  
 dehydrogenase (aa) (le:1954) (re:2973) ... ECFDAPGK X14436 g41421  
 Escherichia coli 562 -11533162 7500953188 gapb glyceraldehyde 3-phosphate  
 dehydrogenase (db:genpept-bct1) (de:escherichia coli k-12 genome;  
 approximately 65 to 68 minutes.) (le:27063) (re:28082) (di:complement)  
 ECU28377 U28377 g882456 Escherichia coli 562 -11533162 232834 epd  
 d-erythrose 4-phosphate dehydrogenase (fn:enzyme; central intermediary  
 metabolism) (db:genpept-bct2) (ec:1.2.1.-) (de:escherichia coli k-12 mg1655  
 section 266 of 400 of the completegenome.) (nt:f339; 100 pct identical to  
 e4pd\_ecoli sw: p11603) (le:2716) (re:3735) (di:complement) AE000376 AE000376  
 g1789295 Escherichia coli 562 -11533162 5000690390 (de:(ecoli\_2849)  
 (pn:d-erythrose 4-phosphate dehydrogenase) (gn:epd) (gtcfc:5.13:5.14:9.10)  
 (ec:1.2.1.-) (e4pd\_ecoli) (keggfc:5.13:5.14:9.10) (rileyfc:5.7.0)  
 (db:gtc-escherichia coli)) ECOLI\_2849 ECOLI\_2849 Escherichia coli 562  
 10065572

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828126	8053	30209	405	134

Description

6500729305 caic:b0037 probable crotonobetaine/carnitine-coa ligase  
 (gtcfc:8.1:3.1:5.9) (ec:6.3.2.-) (keggfc:5.9:5.14) (rileyfc:5.8.0)  
 (db:gtc-escherichia coli) b0037 b0037 Escherichia coli 562 -11533163 62522  
 caic (ec:6.3.2.-) (de:probable crotonobetaine/carnitine-coa ligase,)  
 (db:swissprot) CAIC\_ECOLI P31552 ESCHERICHIA COLI 562 -11533163 163374 caic  
 probable crotonobetaine/carnitine-coa ligase (cl:acetate--coa ligase  
 homology) (ec:6.3.2.-) (db:pir2.dat) S40558 E64724 Escherichia coli 562  
 -11533163 233572 orf (sr:escherichia coli (strain:k-12) dna)  
 (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.)  
 (nt:4-coumarate-coa homolog(pir:s01667)) (le:35928) (re:37496)  
 (di:complement) ECO110K D10483 g216462 Escherichia coli 562 -11533163  
 7500878115 caic probable crotonobetaine/carnitine-coa ligase (fn:putative  
 enzyme; central intermediary) (db:genpept-bct2) (ec:6.3.2.-) (de:escherichia  
 coli k-12 mg1655 section 4 of 400 of the completegenome.) (nt:f522; 100 pct  
 identical to caic\_ecoli sw: p31552) (le:2185) (re:3753) (di:complement)  
 AE000114 AE000114 g1786221 Escherichia coli 562 -11533163 7000684744 caic  
 probable crotonobetaine/carnitine-coa ligase (ec:6.3.2.-) (db:pir) S40558  
 S40558 Escherichia coli 562 -11533163 5000690481 (de:(ecoli\_37)  
 (pn:probable crotonobetaine) (gn:caic) (gtcfc:5.9) (ec:6.3.2.-) (caic\_ecoli)  
 (keggfc:5.9) (rileyfc:5.7.0) (db:gtc-escherichia coli) ECOLI\_37 ECOLI\_37  
 Escherichia coli 562 10005220

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828128	8054	30210	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828145	8055	30211	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828150	8056	30212	558	185

Description

6500729306 ente:b0594 2:3-dihydroxybenzoate-amp ligase:dihydroxybenzoic acid-activating enzyme:enterobactin synthetase component e:enterochelin synthase e (gtcfc:5.14:5.9:9.13) (ec:6.3.2.-) (keggfc:5.9:5.14) (rileyfc:1.7.14) (db:gtc-escherichia coli) b0594 b0594 Escherichia coli 562 -11533164 70234 ente (ec:6.3.2.-) (de:synthase e)) (db:swissprot) ENTE\_ECOLI P10378 ESCHERICHIA COLI 562 -11533164 7000685164 ente 2:3-dihydroxybenzoate--carrier protein ligase, ente:2,3-dihydroxybenzoate--amp ligase (misnomer):dihydroxybenzoic acid-activating enzyme component e:enterobactin synthetase component e:enterochelin synthetase component e) (cl:4-coumarate--coa ligase:acetate--coa ligase homology) (ec:6.2.1.-... SYCEB H64792 Escherichia coli 562 -11533164 7500881065 ente 2:3-dihydroxybenzoate-amp ligase (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (le:66701) (re:68311) (di:direct) ECU82598 U82598 g1778511 Escherichia coli 562 -11533164 240107 ente 2:3-dihydroxybenzoate-amp ligase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:6.3.2.-) (de:escherichia coli k-12 mg1655 section 55 of 400 of the completegenome.) (nt:o536; 98 pct identical to ente\_ecoli sw: p10378) (le:1403) (re:3013) (di:direct) AE000165 AE000165 g1786810 Escherichia coli 562 -11533164 5000690484 (de:(ecoli\_575) (pn:2,3-dihydroxybenzoate-amp ligase) (gn:ente) (gtcfc:5.9) (ec:6.3.2.-) (ente\_ecoli) (keggfc:5.9) (rileyfc:1.7.14) (db:gtc-escherichia coli)) ECOLI\_575 ECOLI\_575 Escherichia coli 562 10122916

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828154	8057	30213	522	173

Description

6500729307 trps:b3384 tryptophanyl-trna synthetase:tryptophan--trna  
ligase:trprs (gtcfc:10.6:5.14) (ec:6.1.1.2) (keggfc:5.14:10.1:10.2)  
(rileyfc:3.1.5) (db:gtc-escherichia coli) b3384 b3384 Escherichia coli 562  
-11533165 7000688906 trps tryptophan--trna ligase::tryptophanyl-trna  
synthetase (cl:tryptophan--trna ligase) (ec:6.1.1.2) (db:pir1.dat) (mp:74  
min) YWEC C65133 Escherichia coli 562 -11533165 7500953358 trps  
(fn:tryptophanyl-trna synthetase) (db:genpept-bct1) (ec:6.1.1.2)  
(de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.)  
(nt:cg site no. 67) (le:293382) (re:294386) (di:complement) ECOUW67 U18997  
g606318 Escherichia coli 562 -11533165 236617 trps tryptophan trna  
synthetase (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2)  
(ec:6.1.1.2) (de:escherichia coli k-12 mg1655 section 304 of 400 of the  
completegenome.) (nt:f334; cg site no. 67; n-ter of this 334 aa orf is)  
(le:1646) (re:2650) (di:complement) AE000414 AE000414 g1789786 Escherichia  
coli 562 -11533165 5000690391 (de:(ecoli\_3302) (pn:tryptophan trna  
synthetase) (gn:trps) (gtcfc:5.14:10.6) (ec:6.1.1.2) (syw\_ecoli)  
(keggfc:5.14:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli))  
ECOLI\_3302 ECOLI\_3302 Escherichia coli 562 10124020

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501828156	8058	30214	450	149

#### Description

6500729308 arol:b0388 shikimate kinase ii:skii (gtcfc:5.15) (ec:2.7.1.71) (keggfc:5.15) (rileyfc:1.4.4) (db:gtc-escherichia coli) b0388 b0388 Escherichia coli 562 -11533166 233862 arol (ec:2.7.1.71) (de:shikimate kinase ii, (skii)) (db:swissprot) AROL\_ECOLI P08329 ESCHERICHIA COLI 562 -11533166 123823 arol shikimate kinase:ii:atp:shikimate 3-phosphotransferase (cl:shikimate kinase:shikimate kinase homology) (ec:2.7.1.71) (db:pir1.dat) (mp:9 min) KIECS A90333 Escherichia coli 562 -11533166 5000690392 (db:genpept-bct1) (de:e.coli arol gene for shikimate kinase ii (ec 2.7.1.71).) (nt:shikimate kinase ii) (le:286) (re:810) (di:direct) ECAROL X04064 g40984 Escherichia coli 562 -11533166 240005 arol shikimate kinase ii (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (ec:2.7.1.71) (de:escherichia coli k-12 arol and arom genes encoding shikimate kinaseii and a 26 kd protein respectively, complete cds.) (nt:precursor) (le:230) (re:754) (di:direct) ECOAROLM M13045 g145382 Escherichia coli 562 -11533166 7500877194 arol shikimate kinase ii (db:genpept-bct1) (ec:2.7.1.71) (de:escherichia coli chromosome minutes 6-8.) (le:113995) (re:114519) (di:direct) ECU73857 U73857 g1657584 Escherichia coli 562 -11533166 232398 arol shikimate kinase ii (fn:enzyme; amino acid biosynthesis: chorismate) (db:genpept-bct2) (ec:2.7.1.71) (de:escherichia coli k-12 mg1655 section 35 of 400 of the completegenome.) (nt:o174; 100 pct identical to arol\_ecoli sw: p08329) (le:5281) (re:5805) (di:direct) AE000145 AE000145 g1786587 Escherichia coli 562 -11533166 60226 arol (ec:2.7.1.71) (de:shikimate kinase ii, (skii)) (db:swissprot) AROL\_ECOLI P08329 ESCHERICHIA COLI 562 -11533166

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501828160	8059	30215	447	149

#### Description

GTC ORF with score 310 to: (or:Candida albicans) (sr:candida albicans (strain b792) dna) (db:genpept-pln1) (ec:4.1.2.15) (de:candida albicans 3-deoxy-d-arabinoheptulosonate-7-phosphatesynthase (aro3) gene, complete cds.) (le:336) (re:1442) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501828165	8060	30216	498	165

#### Description

GTC ORF with score 274 to: (db:genpept-bct1) (ec:4.1.2.15) (de:erwinia herbicola phosphoenolpyruvate synthase (ppsa) gene, partialcds, and hypothetical 32.1 kda protein (ydia) and3-deoxy-d-arabinoheptulosonate 7-phosphate synthase (aroh) genes,complete ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828167	8061	30217	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828169	8062	30218	891	296

Description

6500729309 arog:b0754 phospho-2-dehydro-3-deoxyheptonate aldolase:dahp synthetase phenylalanine repressible:phospho-2-dehydro-3-deoxyheptonate aldolase:phe-sensitive:phospho-2-keto-3-deoxyheptonate aldolase:dahp synthetase:3-deoxy-d-arabino-heptulosonate 7-phosphate synthase (gtcfc:5.15) (ec:4.1.2.15) (keggfc:5.15) (rileyfc:1.4.4) (db:gtc-escherichia coli) b0754 b0754 Escherichia coli 562 -11533167 60214 arog (ec:4.1.2.15) (de:synthetase) (3-deoxy-d-arabino-heptulosonate 7-phosphate synthase)) (db:swissprot) AROG\_ECOLI P00886 ESCHERICHIA COLI 562 -11533167 125515 arog 2-dehydro-3-deoxyphosphoheptonate aldolase:phe-sensitive:phospho-2-dehydro-3-deoxyheptonate aldolase:phospho-2-keto-3-deoxyheptonate aldolase (cl:phospho-2-dehydro-3-deoxyheptonate aldolase) (ec:4.1.2.15) (db:pir1.dat) (mp:17 min) ADECHF A01106 Escherichia coli 562 -11533167 223189 arog phospho-2-dehydro-3-deoxyheptonate aldolase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #179) (db:genpept-bct1) (de:escherichia coli genomic dna.(16.8 - 17.1 min).) (le:5697) (re:6749) (di:direct) D90714 D90714 g1651339 Escherichia coli 562 -11533167 7500877186 (sr:escherichia coli k12 dna) (db:genpept-bct1) (de:e.coli arog gene coding for dahp synthetase (phenylalaninerepressible).) (nt:dahp synthetase (arog)) (le:507) (re:1559) (di:direct) ECOAROG J01591 g145368 Escherichia coli 562 -11533167 233854 arog 3-deoxy-d-arabinoheptulosonate-7-phosphate (fn:enzyme; amino acid biosynthesis: phenylalanine) (db:genpept-bct2) (ec:4.1.2.15) (de:escherichia coli k-12 mg1655 section 68 of 400 of the completgenome.) (nt:o350; 100 pct identical to arog\_ecoli sw: p00886) (le:783) (re:1835) (di:direct) AE000178 AE000178 g1786969 Escherichia coli 562 -11533167 5000690393 arog phospho-2-dehydro-3-deoxyheptonate aldolase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #179) (db:genpept) (de:escherichia coli genomic dna.(16.8 - 17.1 min).) (nt:orf\_id:o179#5; similar to swissprot accession) (le:5697) (re:6749) (di:direct) D90714 D90714 g1651339 Escherichia coli 562 -11533167

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501828176	8063	30219	399	132

# Description

6500729310 *aroa*:b0908 3-phosphoshikimate  
1-carboxyvinyltransferase:5-enolpyruvylshikimate-3-phosphate synthase:epsp  
synthase (gtcfc:5.15) (ec:2.5.1.19) (keggfc:5.15) (rileyfc:1.4.4)  
(db:gtc-escherichia coli) b0908 b0908 Escherichia coli 562 -11533168 60159  
*aroa* (ec:2.5.1.19) (de:enolpyruvylshikimate-3-phosphate synthase) (epsp  
synthase)) (db:swissprot) AROA\_ECOLI P07638 ESCHERICHIA COLI 562 -11533168  
7000684621 *aroa* 3-phosphoshikimate  
1-carboxyvinyltransferase::5-enolpyruvylshikimate-3-phosphate synthase:epsp  
synthase (cl:3-phosphoshikimate 1-carboxyvinyltransferase:3-phosphoshikimate  
1-carboxyvinyltransferase homology) (ec:2.5.1.19) (db:pir1.dat) (mp:20 min)  
XUECVS C64830 Escherichia coli 562 -11533168 223267 *aroa* 3-phosphoshikimate  
1-carboxyvinyltransferase (sr:escherichia coli(strain:k12) dna, clone:kohara  
clone #216) (db:genpept-bct1) (de:escherichia coli genomic dna. (20.3 - 20.7  
min).) (le:14505) (re:15788) (di:direct) D90728 D90728 g1651430 Escherichia  
coli 562 -11533168 223273 *aroa* 3-phosphoshikimate 1-carboxyvinyltransferase  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #217)  
(db:genpept-bct1) (de:escherichia coli genomic dna. (20.4 - 20.8 min).)  
(le:6972) (re:8255) (di:direct) D90729 D90729 g1651437 Escherichia coli 562  
-11533168 7500877163 *aroa* 5-enolpyruvylshikimate-3-phosphate synthetase  
(fn:enzyme; amino acid biosynthesis: chorismate) (db:genpept-bct2)  
(ec:2.5.1.19) (de:escherichia coli k-12 mg1655 section 83 of 400 of the  
completeness genome.) (nt:o427; 99 pct identical to *aroa\_ecoli* sw: p07638)  
(le:2141) (re:3424) (di:direct) AE000193 AE000193 g1787137 Escherichia coli  
562 -11533168 5000690394 *aroa* 3-phosphoshikimate 1-carboxyvinyltransferase  
ec (sr:escherichia coli(strain:k12) dna, clone:kohara clone #216)  
(db:genpept) (de:escherichia coli genomic dna. (20.4 - 20.8 min).)  
(nt:orf\_id:o217#5; similar to pir accession number) (le:14505) (re:15788)  
(di:direct) D90728 D90728 g1651430 Escherichia coli 562 -11533168  
7502851891 *aroa* 3-phosphoshikimate 1-carboxyvinyltransferase ec  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #217) (db:genpept)  
(de:escherichia coli genomic dna. (20.5 - 20.9 min).) (nt:orf\_id:o217#5;  
similar to pir accession number) (le:6972) (re:8255) (di:direct) D90729  
D90729 g1651437 Escherichia coli 562 -11533168

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501828178	8064	30220	498	165

# Description

6500729311 trpa:b1260 tryptophan synthase alpha chain (gtcfc:5.15) (ec:4.2.1.20) (keggfc:5.15) (rileyfc:1.4.4) (db:gtc-escherichia coli) b1260 b1260 Escherichia coli 562 -11533169 238778 trpa (ec:4.2.1.20) (de:tryptophan synthase alpha chain,) (db:swissprot) TRPA\_ECOLI P00928 ESCHERICHIA COLI 562 -11533169 125656 trpa tryptophan synthase:alpha chain (cl:tryptophan synthase alpha chain:tryptophan synthase alpha chain homology) (ec:4.2.1.20) (db:pir1.dat) (mp:28 min) TSECA E93746 Escherichia coli 562 -11533169 223466 trpa tryptophan synthase a chain ec 4.2.1.20 . (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #252(28.1-28.4 min.)) (nt:orf\_id:o252#18; similar to (swissprot accession) (le:14737) (re:15543) (di:complement) D90763 D90763 g1742049 Escherichia coli 562 -11533169 238412 trpa tryptophan synthase alpha subunit (sr:escherichia coli rna and dna) (db:genpept-bct1) (de:escherichia coli tryptophan operon (trpabcde) genes, complete.) (le:6207) (re:7013) (di:direct) ECOTGP J01714 g147959 Escherichia coli 562 -11533169 238426 (db:genpept-bct1) (de:e. coli trpa gene (codes for tryptophan synthetase alpha-su.) (nt:reading frame trpa) (le:72) (re:878) (di:direct) ECTRPA V00364 g43184 Escherichia coli 562 -11533169 5000690395 (db:genpept-bct1) (de:e. coli trp operon with the genes trpe, trpd, trpc, trpb and trpa.genetic map position approximately 27.5 minutes. these genes codefor the following enzymes: trpe - anthranilate synthetase (e.c.4.1.3.27) trpd - glutamine amidotran... ECTRPX V00372 g43206 Escherichia coli 562 -11533169 238784 trpa tryptophan synthase alpha subunit (db:genpept-bct1) (de:escherichia coli k12 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:2578) (re:3384) (di:direct) ECU23489 U23489 g775126 Escherichia coli 562 -11533169 238790 trpa tryptophan synthase alpha subunit (db:genpept-bct1) (de:escherichia coli ecor 1 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:2578) (re:3384) (di:direct) ECU23490 U23490 g775133 Escherichia coli 562 -11533169 238796 trpa tryptophan synthase alpha subunit (db:genpept-bct1) (de:escherichia coli ecor 4 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:2578) (re:3384) (di:direct) ECU23491 U23491 g775140 Escherichia coli 562 -11533169 238808 trpa tryptophan synthase alpha subunit (db:genpept-bct1) (de:escherichia coli ecor 16 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:2578) (re:3384) (di:direct) ECU23492 U23492 g775147 Escherichia coli 562 -11533169 238949 trpa tryptophan synthase alpha subunit (db:genpept-bct1) (de:escherichia coli ecor 31 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:2578)



subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:2578)  
 (re:3384) (di:direct) FCU23494 U23494 g775161 Escherichia coli 562 -11533169

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828183	8065	30221	219	72

Description

GTC ORF with score 181 to: (sr:pyrococcus horikoshii (strain:ot3) dna)  
 (db:genpept-bct2) (de:pyrococcus horikoshii ot3 genomic dna, 544001-777000  
 nt. position(3/7).) (nt:motif=prokaryotic membrane lipoprotein lipid)  
 (le:67676) (re:68116) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828201	8066	30222	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501828208	8067	30223	1386	461

# Description

6500729312 trpb:b1261 tryptophan synthase beta chain (gtcfc:5.15) (ec:4.2.1.20) (keggfc:5.15) (rileyfc:1.4.4) (db:gtc-escherichia coli) b1261 b1261 Escherichia coli 562 -11533170 7000688895 trpb tryptophan synthase:beta chain (cl:tryptophan synthase beta chain:tryptophan synthase beta chain homology) (ec:4.2.1.20) (db:pirl.dat) (mp:28 min) TSECB H64873 Escherichia coli 562 -11533170 238425 trpb tryptophan synthase beta subunit (sr:escherichia coli rna and dna) (db:genpept-bct1) (de:escherichia coli tryptophan operon (trpabcde) genes, complete.) (le:5014) (re:6207) (di:direct) ECOTGP J01714 g147958 Escherichia coli 562 -11533170 238777 (db:genpept-bct1) (de:e. coli trp operon with the genes trpe, trpd, trpc, trpb and trpa.genetic map position approximately 27.5 minutes. these genes codefor the following enzymes: trpe - anthranilate synthetase (e.c.4.1.3.27) trpd - glutamine amidotran... ECTRPX V00372 g43205 Escherichia coli 562 -11533170 238783 trpb tryptophan synthase beta subunit (db:genpept-bct1) (de:escherichia coli k12 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:1385) (re:2578) (di:direct) ECU23489 U23489 g775125 Escherichia coli 562 -11533170 238795 trpb tryptophan synthase beta subunit (db:genpept-bct1) (de:escherichia coli ecor 1 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:1385) (re:2578) (di:direct) ECU23490 U23490 g775132 Escherichia coli 562 -11533170 238801 trpb tryptophan synthase beta subunit (db:genpept-bct1) (de:escherichia coli ecor 16 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:1385) (re:2578) (di:direct) ECU23492 U23492 g775146 Escherichia coli 562 -11533170 238838 trpb tryptophan synthase beta subunit (db:genpept-bct1) (de:escherichia coli ecor 28 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:1385) (re:2578) (di:direct) ECU23493 U23493 g775153 Escherichia coli 562 -11533170 238948 trpb tryptophan synthase beta subunit (db:genpept-bct1) (de:escherichia coli ecor 71 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:1385) (re:2578) (di:direct) ECU23500 U23500 g775197 Escherichia coli 562 -11533170 238954 trpb tryptophan synthase beta subunit (db:genpept-bct1) (de:escherichia coli ecor 8 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:1385) (re:2578) (di:direct) ECU25417 U25417 g924763 Escherichia coli 562 -11533170 238960 trpb tryptophan synthase beta subunit (db:genpept-bct1) (de:escherichia coli ecor 15 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:1385)

subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:1385)  
(re:2578) (di:direct) ECU25418 U25418 g924770 Escherichia coli 562 -11533170

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828213	8068	30224	234	77
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828229	8069	30225	558	186
<u>Description</u>				

GTC ORF with score 118 to: (fn:ensures cocoon cohesion by sticking silk)  
(sr:greater wax moth) (db:genpept-inv) (de:galleria mellonella sericin-2  
(ser-2) mrna, partial cds.) (nt:similar to bombyx mori sericins;  
water-soluble silk) (le:<1) (re:664) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828245	8070	30226	666	221
<u>Description</u>				

6500729313 trpc:b1262 indole-3-glycerol phosphate synthase:igps /  
n-:5-phospho-ribosylanthranilate isomerase:prai (gtcfc:5.15) (keggfc:5.15)  
(rileyfc:1.4.4) (db:gtc-escherichia coli) b1262 b1262 Escherichia coli 562  
-11533171 7000688889 trpc-trpf indole-3-glycerol-phosphate  
synthase:phosphoribosylanthranilate isomerase (cl:trpc-trpf bifunctional  
enzyme:trpc homology:trpf homology) (ec:4.1.1.48:5.3.1.24) (db:pir1.dat)  
(mp:28 min) GWEC A64874 Escherichia coli 562 -11533171 7500953334 trpc  
n-5-phosphoribosyl anthranilate isomerase and (fn:enzyme; amino acid  
biosynthesis: tryptophan) (db:genpept-bct2) (ec:4.1.1.48) (de:escherichia  
coli k-12 mg1655 section 114 of 400 of the completegenome.) (nt:f453; 99 pct  
identical to trpc\_ecoli sw: p00909) (le:4616) (re:5977) (di:complement)  
AE000224 AE000224 g1787516 Escherichia coli 562 -11533171 5000690397  
(de:(ecoli\_1222) (pn:n-:5-phosphoribosylanthranilate isomerase and indole-3-  
glycerolphosphate synthetase) (gn:trpc) (gtcfc:5.15) (ec:4.1.1.48)  
(trpc\_ecoli) (keggfc:5.15) (rileyfc:1.4.4) (db:gtc-escherichia coli))  
ECOLI\_1222 ECOLI\_1222 Escherichia coli 562 10123247

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828247	8071	30227	228	75

Description

6500729314 trpd:trpgd:b1263 anthranilate synthase component  
ii:contains:glutamine amidotransferase:anthranilate  
phosphoribosyltransferase (gtcfc:5.15:9.12) (keggfc:5.15:9.13)  
(rileyfc:1.4.4) (db:gtc-escherichia coli) b1263 b1263 Escherichia coli 562  
-11533172 7000688888 trpg-trpd anthranilate synthase:component ii  
(cl:trpg-trpd bifunctional enzyme:trpd homology:trpg homology) (ec:4.1.3.27)  
(db:pir1.dat) (mp:28 min) NNEC2 B64874 Escherichia coli 562 -11533172  
223472 trpd anthranilate synthase ec 4.1.3.27 component (sr:escherichia  
coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #253(28.4-28.7 min.).)  
(nt:orf\_id:o253#1; similar to (pir accession number) (le:2409) (re:4004)  
(di:complement) D90764 D90764 g1742056 Escherichia coli 562 -11533172  
300275 trpd anthranilate synthase component ii:glutamine (fn:enzyme; amino  
acid biosynthesis: tryptophan) (db:genpept-bct2) (ec:4.1.3.27:2.4.2.18)  
(de:escherichia coli k-12 mg1655 section 114 of 400 of the completegenome.)  
(nt:f531; 99 pct identical to trpg\_ecoli sw: p00904; cg) (le:5978) (re:7573)  
(di:compl... AE000224 AE000224 g1787517 Escherichia coli 562 -11533172  
5000690398 (de:(ecoli\_1223) (pn:anthranilate synthase component ii,  
glutamine amidotransferase and phosphoribosylanthranilate transferase)  
(gn:trpd) (gtcfc:5.15:9.12) (ec:4.1.3.27) (trpg\_ecoli) (keggfc:5.15:9.13)  
(rileyfc:1.4.4) (db:gtc-es) ECOLI\_1223 ECOLI\_1223 Escherichia coli 562  
10119487

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828249	8072	30228	447	148

Description

6500729315 trpe:b1264 anthranilate synthase component i (gtcfc:5.15:9.12) (ec:4.1.3.27) (keggfc:5.15:9.13) (rileyfc:1.4.4) (db:gtc-escherichia coli) b1264 b1264 Escherichia coli 562 -11533173 102398 trpe (ec:4.1.3.27) (de:anthranilate synthase component i,) (db:swissprot) TRPE\_ECOLI P00895 ESCHERICHIA COLI 562 -11533173 7000686832 trpe anthranilate synthase:component i (cl:anthranilate synthase component i) (ec:4.1.3.27) (db:pir1.dat) (mp:28 min) NNEC1 C64874 Escherichia coli 562 -11533173 223473 trpe anthranilate synthase component i ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #253(28.4-28.7 min.).) (nt:orf\_id:o253#2; similar to (swissprot accession) (le:4004) (re:5566) (di:complement) D90764 D90764 g1742057 Escherichia coli 562 -11533173 300291 trpe anthranilate synthase component i ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #254(28.4-28.9 min.).) (nt:orf\_id:o253#2; similar to (swissprot accession) (le:1510) (re:3072) (di:complement) D90765 D90765 g1742073 Escherichia coli 562 -11533173 300276 trpe anthranilate synthase component i (fn:enzyme; amino acid biosynthesis: tryptophan) (db:genpept-bct2) (ec:4.1.3.27) (de:escherichia coli k-12 mg1655 section 114 of 400 of the completegenome.) (nt:f520; 99 pct identical to trpe\_ecoli sw: p00895; cg) (le:7573) (re:9135) (di:complement) AE000224 AE000224 g1787518 Escherichia coli 562 -11533173 223488 trpe anthranilate synthase component i ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #254(28.4-28.9 min.).) (nt:orf\_id:o253#2; similar to (swissprot accession) (le:1510) (re:3072) (di:complement) D90765 D90765 g1742073 Escherichia coli 562 -11533173 5000690399 (de:(ecoli\_1224) (pn:anthranilate synthase component i) (gn:trpe) (gtcfc:5.15:9.12) (ec:4.1.3.27) (trpe\_ecoli) (keggfc:5.15:9.13) (rileyfc:1.4.4) (db:gtc-escherichia coli)) ECOLI\_1224 ECOLI\_1224 Escherichia coli 562 10119488

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828250	8073	30229	375	124

Description

6500729316 tyrs:b1637 tyrosyl-trna synthetase:tyrosine--trna ligase:tyrrs  
 (gtcfc:10.6:5.12) (ec:6.1.1.1) (keggfc:5.15:10.1:10.2) (rileyfc:3.1.5)  
 (db:gtc-escherichia coli) b1637 b1637 Escherichia coli 562 -11533174 125871  
 tyrs tyrosine--trna ligase::tyrosyl-trna synthetase (cl:tyrosine--trna  
 ligase) (ec:6.1.1.1) (db:pir1.dat) (mp:36 min) SYECYT A01178 Escherichia  
 coli 562 -11533174 7500953357 (sr:escherichia coli k12 dna)  
 (db:genpept-bct1) (de:e.coli tyrs gene coding for tyrosyl-trna synthetase.)  
 (nt:tyrosyl-trna synthetase (tyrs)) (le:1) (re:1275) (di:direct) ECOTYRS  
 J01719 g148094 Escherichia coli 562 -11533174 236235 tyrs tyrosine trna  
 synthetase (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2)  
 (ec:6.1.1.1) (de:escherichia coli k-12 mgl655 section 149 of 400 of the  
 completegenome.) (nt:f424; 100 pct identical to syy\_ecoli sw: p00951; cg)  
 (le:3555) (re:4829) (di:complement) AE000259 AE000259 g1787925 Escherichia  
 coli 562 -11533174 5000690400 (de:(ecoli\_1596) (pn:tyrosine trna  
 synthetase) (gn:tyrs) (gtcfc:5.15:10.6) (ec:6.1.1.1) (syy\_ecoli)  
 (keggfc:5.15:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli))  
 ECOLI\_1596 ECOLI\_1596 Escherichia coli 562 10066467

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828251	8074	30230	270	89

Description

6500729317 arod:b1693 3-dehydroquinate dehydratase:3-dehydroquinase  
 (gtcfc:5.15) (ec:4.2.1.10) (keggfc:5.15) (rileyfc:1.4.4) (db:gtc-escherichia  
 coli) b1693 b1693 Escherichia coli 562 -11533175 300795 arod (ec:4.2.1.10)  
 (de:3-dehydroquinate dehydratase, (3-dehydroquinase)) (db:swissprot)  
 AROD\_ECOLI P05194 ESCHERICHIA COLI 562 -11533175 125631 arod  
 3-dehydroquinate dehydratase::3-dehydroquinase (cl:3-dehydroquinate  
 dehydratase:3-dehydroquinate dehydratase homology) (ec:4.2.1.10)  
 (db:pir1.dat) (mp:37 min) DWECDO S14750 Escherichia coli 562 -11533175  
 224126 arod 3-dehydroquinate dehydratase ec 4.2.1.10 (sr:escherichia coli  
 (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
 (de:e.coli genomic dna, kohara clone #320(37.9-38.3 min..))  
 (nt:orf\_id:o320#3; similar to (pir accession number) (le:2104) (re:2862)  
 (di:complement) D90811 D90811 g1742757 Escherichia coli 562 -11533175  
 5000690401 arod 3-dehydroquinate dehydratase (fn:biosynthesis of aromatic  
 amino acids) (db:genpept-bct1) (ec:4.2.1.10) (de:e.coli arod gene for  
 3-dehydroquinase.) (nt:3-dehydroquinase) (le:1) (re:759) (di:direct) ECARODG  
 X59503 g40975 Escherichia coli 562 -11533175 232392 arod 3-dehydroquinate  
 dehydratase (fn:enzyme; amino acid biosynthesis: chorismate)  
 (db:genpept-bct2) (ec:4.2.1.10) (de:escherichia coli k-12 mg1655 section 154  
 of 400 of the completegenome.) (nt:o252; 100 pct identical to arod\_ecoli sw:  
 p05194;) (le:5932) (re:6690) (di:direct) AE000264 AE000264 g1787984  
 Escherichia coli 562 -11533175 60191 arod (ec:4.2.1.10)  
 (de:3-dehydroquinate dehydratase, (3-dehydroquinase)) (db:swissprot)  
 AROD\_ECOLI P05194 ESCHERICHIA COLI 562 -11533175

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828257	8075	30231	615	204

Description

6500729318 aroh:b1704 3-deoxy-d-arabinoheptulosonate 7-phosphate  
synthase:phospho-2-dehydro-3-deoxyheptonate  
aldolase:trp-sensitive:phospho-2-keto-3-deoxyheptonate aldolase:dahp  
synthetase:3-deoxy-d-arabino-heptulosonate 7-phosphate synthase (gtcfc:5.15)  
(ec:4.1.2.15) (keggfc:5.15) (rileyfc:1.4.4) (db:gtc-escherichia coli) b1704  
b1704 Escherichia coli 562 -11533176 7000688883 aroh  
2-dehydro-3-deoxyphosphoheptonate  
aldolase:trp-sensitive:3-deoxy-d-arabino-heptulosonate-7-phosphate  
synthase:phospho-2-dehydro-3-deoxyheptonate  
aldolase:phospho-2-keto-3-deoxyheptonate aldolase  
(cl:phospho-2-dehydro-3-deoxyheptonate aldolase) (ec:4.1.2.15) (db:pir1.dat)  
(mp:37 min) ADECH H64928 Escherichia coli 562 -11533176 224152 aroh  
phospho-2-dehydro-3-deoxyheptonate aldolase (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #322(38.4-38.8 min.).)  
(nt:orf\_id:o322#5; similar to (swissprot accession) (le:5180) (re:6226)  
(di:direct) D90813 D90813 g1742785 Escherichia coli 562 -11533176 300821  
aroh 3-deoxy-d-arabinoheptulosonate-7-phosphate (fn:enzyme; amino acid  
biosynthesis: tryptophan) (db:genpept-bct2) (ec:4.1.2.15) (de:escherichia  
coli k-12 mg1655 section 155 of 400 of the completegenome.) (nt:o348; 99 pct  
identical to aroh\_ecoli sw: p00887; cg) (le:9054) (re:10100) (di:direct)  
AE000265 AE000265 g1787996 Escherichia coli 562 -11533176 5000690402  
(de:(ecoli\_1661) (pn:phospho-2-dehydro-3-deoxyheptonate aldolase:dahp  
synthetase, tryptophan repressible) (gn:aroh) (gtcfc:5.15) (ec:4.1.2.15)  
(aroh\_ecoli) (keggfc:5.15) (rileyfc:1.4.4) (db:gtc-escherichia coli))  
ECOLI\_1661 ECOLI\_1661 Escherichia coli 562 10119783



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828263	8076	30232	432	143

Description

6500729319 phet:b1713 phenylalanyl-trna synthetase beta chain:phenylalanine--trna ligase beta chain:phers (gtcfc:10.6:5.15) (ec:6.1.1.20) (keggfc:5.15:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli) b1713 b1713 Escherichia coli 562 -11533177 100034 phet (ec:6.1.1.20) (de:trna ligase beta chain) (phers)) (db:swissprot) SYFB\_ECOLI P07395 ESCHERICHIA COLI 562 -11533177 164277 phet phenylalanine--trna ligase:beta chain:phenylalanyl-trna synthetase beta chain (cl:phenylalanine--trna ligase beta chain) (ec:6.1.1.20) (db:pir1.dat) (mp:38 min) SYECFB I41284 Escherichia coli 562 -11533177 224160 phet phenylalanine--trna ligase ec 6.1.1.20 b (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #322(38.4-38.8 min.)) (nt:orf\_id:o322#14; similar to (pir accession number) (le:12302) (re:14689) (di:complement) D90813 D90813 g1742793 Escherichia coli 562 -11533177 224172 phet phenylalanine--trna ligase ec 6.1.1.20 b (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #323(38.6-39.0 min.)) (nt:orf\_id:o322#14; similar to (pir accession number) (le:5142) (re:7529) (di:complement) D90814 D90814 g1742806 Escherichia coli 562 -11533177 300829 phet phenylalanyl-trna synthetase beta-subunit (sr:e.coli dna, clone lambda-hima) (db:genpept-bct1) (ec:6.1.1.20) (de:e.coli infc, rplt, phes, phet and hima genes encoding initiationfactor if3, ribosomal protein 120, beta- and alpha-subunits ofphenylalanyl-trna synthetase and the alpha-subunit of i... ECOHIMA K02844 g146346 Escherichia coli 562 -11533177 234650 phet phenylalanine trna synthetase:beta-subunit (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:6.1.1.20) (de:escherichia coli k-12 mg1655 section 156 of 400 of the completegenome.) (nt:f795; 98 pct identical to syfb\_ecoli sw: p07395; cg) (le:6040) (re:8427) (di:complement) AE000266 AE000266 g1788006 Escherichia coli 562 -11533177 5000690403 (de:(ecoli\_1670) (pn:phenylalanine trna synthetase, beta-subunit) (gn:phet) (gtcfc:5.15:10.6) (ec:6.1.1.20) (syfb\_ecoli) (keggfc:5.15:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli)) ECOLI\_1670 ECOLI\_1670 Escherichia coli 562 10072856

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828271	8077	30233	207	68

Description

6500729320 phes:b1714 phenylalanyl-trna synthetase alpha chain:phenylalanine--trna ligase alpha chain:phers (gtcfc:10.6:5.15) (ec:6.1.1.20) (keggfc:5.15:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli) b1714 b1714 Escherichia coli 562 -11533178 100028 phes (ec:6.1.1.20) (de:-trna ligase alpha chain) (phers)) (db:swissprot) SYFA\_ECOLI P08312 ESCHERICHIA COLI 562 -11533178 7000686710 phes phenylalanine--trna ligase:alpha chain:phenylalanyl-trna synthetase alpha chain (cl:phenylalanine--trna ligase alpha chain) (ec:6.1.1.20) (db:pir1.dat) (mp:37 min) SYECFA B64930 Escherichia coli 562 -11533178 7500892384 phes phenylalanine trna synthetase:alpha-subunit (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:6.1.1.20) (de:escherichia coli k-12 mg1655 section 156 of 400 of the completegenome.) (nt:f327; 100 pct identical to syfa\_ecoli sw: p08312;) (le:8442) (re:9425) (di:complement) AE000266 AE000266 g1788007 Escherichia coli 562 -11533178 5000690404 (de:(ecoli\_1671) (pn:phenylalanine trna synthetase, alpha-subunit) (gn:phes) (gtcfc:5.15:10.6) (ec:6.1.1.20) (syfa\_ecoli) (keggfc:5.15:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli)) ECOLI\_1671 ECOLI\_1671 Escherichia coli 562 10041882

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828273	8078	30234	1428	476

Description

6500729321 aroc:b2329 chorismate synthase:5-enolpyruvylshikimate-3-phosphate phospholyase (gtcfc:5.15) (ec:4.6.1.4) (keggfc:5.15) (rileyfc:1.4.4) (db:gtc-escherichia coli) b2329 b2329 Escherichia coli 562 -11533179 7000688901 aroc chorismate synthase::5-enolpyruvylshikimate-3-phosphate phospholyase (cl:chorismate synthase) (ec:4.6.1.4) (db:pir1.dat) (mp:51 min) SYECKR G65005 Escherichia coli 562 -11533179 7500953349 (sr:e.coli (strain k12) isolate c600 dna) (db:genpept-bct1) (de:e.coli chorismate synthase (aroc) gene, complete cds.) (nt:chorismate synthase (ec 4.6.1.4)) (le:455) (re:1540) (di:direct) ECOAROC M27714 g145358 Escherichia coli 562 -11533179 233849 aroc chorismate synthase (fn:enzyme; amino acid biosynthesis: chorismate) (db:genpept-bct2) (ec:4.6.1.4) (de:escherichia coli k-12 mg1655 section 211 of 400 of the completegenome.) (nt:f361; 100 pct identical aroc\_ecoli sw: p12008 but) (le:9736) (re:10821) (di:complement) AE000321 AE000321 g1788669 Escherichia coli 562 -11533179 5000690405 (de:(ecoli\_2278) (pn:chorismate synthase) (gn:aroc) (gtcfc:5.15) (ec:4.6.1.4) (aroc\_ecoli) (keggfc:5.15) (rileyfc:1.4.4) (db:gtc-escherichia coli)) ECOLI\_2278 ECOLI\_2278 Escherichia coli 562 10123639

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828309	8079	30235	1788	595

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828340	8080	30236	789	262

Description

6500729322 phea:b2599 chorismate mutase-p/prephenate dehydratase:chorismate mutase:cm / prephenate dehydratase:pdt:p-protein (gtcfc:5.15) (keggfc:5.15) (rileyfc:1.4.4) (db:gtc-escherichia coli) b2599 b2599 Escherichia coli 562 -11533180 89522 phea (ec:5.4.99.5:4.2.1.51) (de:(ec 4.2.1.51) (pdt) (p-protein)) (db:swissprot) PHEA\_ECOLI P07022 ESCHERICHIA COLI 562 -11533180 125843 phea chorismate mutase:p / prephenate dehydratase (cl:phea bifunctional enzyme:prephenate dehydratase homology) (ec:5.4.99.5:4.2.1.51) (db:pir1.dat) (mp:57 min) KMECPW A30261 Escherichia coli 562 -11533180 225174 phea chorismate mutase ec 5.4.99.5 p / prephenate (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #438(58.9-59.3 min.).) (nt:similar to (pir accession number a30261)) (le:628) (re:1788) (di:direct) D90888 D90888 g1800004 Escherichia coli 562 -11533180 7500888016 phea chorismate mutase/prephenate dehydratase (sr:e.coli k12 dna, clone pmu1000) (db:genpept-bct1) (de:e.coli phe and tyr operons: phea and phe genes coding forchorismate mutase/prephenate dehydratase and phe leader peptide;and arof and tyra genes encoding dhap synthetase and chorismatemutase/prep... ECOPHEAB M10431 g147175 Escherichia coli 562 -11533180 235407 phea chorismate mutase-p and prephenate dehydratase (fn:enzyme; amino acid biosynthesis: phenylalanine) (db:genpept-bct2) (ec:5.4.99.5:4.2.1.51) (de:escherichia coli k-12 mg1655 section 236 of 400 of the completegenome.) (nt:o386; 100 pct identical to phea\_ecoli sw: p07022;) (le:3537) (re:4697) (di:direct) AE000346 AE000346 g1788951 Escherichia coli 562 -11533180 5000690406 (de:(ecoli\_2535) (pn:chorismate mutase-p - prephenate dehydratase) (gn:phea) (gtcfc:5.15) (ec:5.4.99.5) (phea\_ecoli) (keggfc:5.15) (rileyfc:1.4.4) (db:gtc-escherichia coli)) ECOLI\_2535 ECOLI\_2535 Escherichia coli 562 10031644

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828351	8081	30237	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828366	8082	30238	240	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828368	8083	30239	636	211

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828369	8084	30240	810	269

Description

6500729323 tyra:b2600 chorismate mutase/prephenate dehydrogenase:chorismate mutase:cm / prephenate dehydrogenase:pdh:t-protein (gtcfc:5.15) (keggfc:5.15) (rileyfc:1.4.4) (db:gtc-escherichia coli) b2600 b2600 Escherichia coli 562 -11533181 102905 tyra (ec:5.4.99.5:1.3.1.12) (de:(ec 1.3.1.12) (pdh) (t-protein)) (db:swissprot) TYRA\_ECOLI P07023 ESCHERICHIA COLI 562 -11533181 125840 tyra chorismate mutase:t / prephenate dehydrogenase (cl:tyra bifunctional enzyme) (ec:5.4.99.5:1.3.1.12) (db:pir1.dat) (mp:57 min) KMECTD A30274 Escherichia coli 562 -11533181 7500893606 tyra chorismate mutase/prephenate dehydratase (sr:e.coli k12 dna, clone pmu1000) (db:genpept-bct1) (de:e.coli phe and tyr operons: pheA and phe genes coding forchorismate mutase/prephenate dehydratase and phe leader peptide;and arof and tyra genes encoding dhap synthetase and chorismatemutase/prep... ECOPHEAB M10431 g457110 Escherichia coli 562 -11533181 235408 tyra chorismate mutase-t and prephenate (fn:enzyme; amino acid biosynthesis: tyrosine) (db:genpept-bct2) (ec:5.4.99.5:1.3.1.12) (de:escherichia coli k-12 mg1655 section 236 of 400 of the completegenome.) (nt:f373; 100 pct identical to tyra\_ecoli sw: p07023;) (le:4740) (re:5861) (di:complement) AE000346 AE000346 g1788952 Escherichia coli 562 -11533181 5000690407 (de:(ecoli\_2536) (pn:chorismate mutase t - prephenate dehydrogenase) (gn:tyra) (gtcfc:5.15) (ec:5.4.99.5) (tyra\_ecoli) (keggfc:5.15) (rileyfc:1.4.4) (db:gtc-escherichia coli)) ECOLI\_2536 ECOLI\_2536 Escherichia coli 562 10044717

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828373	8085	30241	192	63
<u>Description</u>				
6500729324 arof:b2601 phospho-2-dehydro-3-deoxyheptonate aldolase:tyr-sensitive:phospho-2-keto-3-deoxyheptonate aldolase:dahp synthetase:3-deoxy-d-arabino-heptulosonate 7-phosphate synthase (gtcfc:5.15) (ec:4.1.2.15) (keggfc:5.15) (rileyfc:1.4.4) (db:gtc-escherichia coli) b2601 b2601 Escherichia coli 562 -11533182 60204 arof (ec:4.1.2.15) (de:synthetase) (3-deoxy-d-arabino-heptulosonate 7-phosphate synthase)) (db:swissprot) AROF_ECOLI P00888 ESCHERICHIA COLI 562 -11533182 164795 arof 2-dehydro-3-deoxyphosphoheptonate aldolase:tyr-sensitive:phospho-2-dehydro-3-deoxyheptonate aldolase:phospho-2-keto-3-deoxyheptonate aldolase (cl:phospho-2-dehydro-3-deoxyheptonate aldolase) (ec:4.1.2.15) (db:pir1.dat) (mp:57 min) ADECHY I41141 Escherichia coli 562 -11533182 225177 arof phospho-2-dehydro-3-deoxyheptonate aldolase (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #438(58.9-59.3 min.)) (nt:similar to (swissprot accession number p00888)) (le:2964) (re:4034) (di:complement) D90888 D90888 g1800007 Escherichia coli 562 -11533182 235409 (sr:e.coli dna, clone pkb45) (db:genpept-bct1) (de:e.coli arof gene for dahp synthase (tyr), complete coding sequence.) (nt:tyrosine-sensitive dahp synthase (arof)) (le:1) (re:1071) (di:direct) ECOAROF K01989 g145362 Escherichia coli 562 -11533182 7500877184 arof dhap synthetase (sr:e.coli k12 dna, clone pmu1000) (db:genpept-bct1) (ec:4.1.2.15) (de:e.coli phe and tyr operons: pheA and phe genes coding for chorismate mutase/prephenate dehydratase and phe leader peptide; and arof and tyra genes encoding dhap synthetase and chorism... ECOPHEAB M10431 g457111 Escherichia coli 562 -11533182 233851 arof 3-deoxy-d-arabinoheptulosonate-7-phosphate (fn:enzyme; amino acid biosynthesis: tyrosine) (db:genpept-bct2) (ec:4.1.2.15) (de:escherichia coli k-12 mg1655 section 236 of 400 of the complete genome.) (nt:f356; 100 pct identical to arof_ecoli sw: p00888;) (le:5872) (re:6942) (di:complement) AE000346 AE000346 g1788953 Escherichia coli 562 -11533182 5000690408 (de:(ecoli_2537) (pn:phospho-2-dehydro-3-deoxyheptonate aldolase:dahp synthetase, tyrosine repressible) (gn:arof) (gtcfc:5.15) (ec:4.1.2.15) (arof_ecoli) (keggfc:5.15) (rileyfc:1.4.4) (db:gtc-escherichia coli)) ECOLI_2537 ECOLI_2537 Escherichia coli 562 10002930				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828377	8086	30242	372	123

Description

6500729325 aroe:b3281 shikimate dehydrogenase:shikimate 5-dehydrogenase (gtcfc:5.15) (ec:1.1.1.25) (keggfc:5.15) (rileyfc:1.4.4) (db:gtc-escherichia coli) b3281 b3281 Escherichia coli 562 -11533183 236514 aroe (ec:1.1.1.25) (de:shikimate 5-dehydrogenase,) (db:swissprot) AROE\_ECOLI P15770 ESCHERICHIA COLI 562 -11533183 136180 aroe shikimate 5-dehydrogenase (cl:shikimate dehydrogenase:shikimate dehydrogenase homology) (ec:1.1.1.25) (db:pir2.dat) (mp:72 min) S00252 S00252 Escherichia coli 562 -11533183 5000690409 (db:genpept-bct1) (de:escherichia coli aroe gene for shikimate dehydrogenase (ec1.1.1.25).) (nt:shikimate dehydrogenase) (le:1) (re:819) (di:direct) ECAROE1 Y00710 g40978 Escherichia coli 562 -11533183 7500877181 aroe shikimate dehydrogenase (db:genpept-bct1) (ec:1.1.1.25) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 1004) (le:210766) (re:211584) (di:complement) ECOUW67 U18997 g606215 Escherichia coli 562 -11533183 232394 aroe dehydroshikimate reductase (fn:enzyme; amino acid biosynthesis: chorismate) (db:genpept-bct2) (ec:1.1.1.25) (de:escherichia coli k-12 mg1655 section 296 of 400 of the completegenome.) (nt:f272; cg site no. 1004; 100 pct identical amino) (le:8779) (re:9597) (di:complement) AE000406 AE000406 g1789675 Escherichia coli 562 -11533183 60198 aroe (ec:1.1.1.25) (de:shikimate 5-dehydrogenase,) (db:swissprot) AROE\_ECOLI P15770 ESCHERICHIA COLI 562 -11533183

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828385	8087	30243	354	118

Description

6500729326 arob:b3389 3-dehydroquinate synthase (gtcfc:5.15) (ec:4.6.1.3) (keggfc:5.15) (rileyfc:1.4.4) (db:gtc-escherichia coli) b3389 b3389  
Escherichia coli 562 -11533184 236622 arob (ec:4.6.1.3)  
(de:3-dehydroquinate synthase,) (db:swissprot) AROB\_ECOLI P07639 ESCHERICHIA COLI 562 -11533184 125735 arob 3-dehydroquinate synthase  
(cl:3-dehydroquinate synthase:3-dehydroquinate synthase homology) (ec:4.6.1.3) (db:pir1.dat) (mp:75 min) SYECQ A24863 Escherichia coli 562 -11533184 232635 (db:genpept-bct1) (de:e. coli arob gene for 3-dehydroquinate synthase (ec 4.6.1.3).) (nt:3-dehydroquinate synthase (aa 1-362)) (le:456) (re:1544) (di:direct) ECAROB X03867 g40968 Escherichia coli 562 -11533184 5000690410 (db:genpept-bct1) (de:e.coli dam operon.) (nt:orf, arob. millar g., coggins j.r.; febs lett.) (le:2451) (re:3539) (di:direct) ECDAMOPRA Z19601 g41225 Escherichia coli 562 -11533184 7500877168 arob 3-dehydroquinate synthase (db:genpept-bct1) (ec:4.6.1.3) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 1007) (le:298146) (re:299234) (di:complement) ECOUW67 U18997 g606323 Escherichia coli 562 -11533184 232388 arob 3-dehydroquinate synthase (fn:enzyme; amino acid biosynthesis: chorismate) (db:genpept-bct2) (ec:4.6.1.3) (de:escherichia coli k-12 mg1655 section 304 of 400 of the completegenome.) (nt:f362; cg site no. 1007; 100 pct identical amino) (le:6410) (re:7498) (di:complement) AE000414 AE000414 g1789791 Escherichia coli 562 -11533184 60175 arob (ec:4.6.1.3) (de:3-dehydroquinate synthase,) (db:swissprot) AROB\_ECOLI P07639 ESCHERICHIA COLI 562 -11533184

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828390	8088	30244	510	169

Description

6500729327 arok:b3390 shikimic acid kinase i (gtcfc:5.15) (ec:2.7.1.71) (keggfc:5.15) (rileyfc:1.4.4) (db:gtc-escherichia coli) b3390 b3390 Escherichia coli 562 -11533185 7000689099 arok shikimate kinase:i (cl:shikimate kinase:shikimate kinase homology) (ec:2.7.1.71) (db:pir2.dat) (mp:27 min) A65134 A65134 Escherichia coli 562 -11533185 7500954128 arok shikimic acid kinase i (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:gtg start, many differences from ecoarok) (le:299291) (re:300013) (di:complement) ECOUW67 U18997 g606324 Escherichia coli 562 -11533185 236623 arok shikimate kinase i (fn:enzyme; amino acid biosynthesis: chorismate) (db:genpept-bct2) (ec:2.7.1.71) (de:escherichia coli k-12 mg1655 section 304 of 400 of the completegenome.) (nt:f240; gtg start, many differences from ecoarok; 100) (le:7555) (re:8277) (di:complement) AE000414 AE000414 g1789792 Escherichia coli 562 -11533185 5000690411 (de:(ecoli\_3308) (pn:shikimate kinase i) (gn:arok) (gtcfc:5.15) (ec:2.7.1.71) (arok\_ecoli) (keggfc:5.15) (rileyfc:1.4.4) (db:gtc-escherichia coli)) ECOLI\_3308 ECOLI\_3308 Escherichia coli 562 10124022

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828392	8089	30245	954	317

Description

GTC ORF with score 351 to: (fn:probable involvement with glycolysis) (db:genpept) (ec:4.1.2.13) (de:giardia intestinalis putative fructose-1,6-bisphosphate aldolase(ald) gene, complete cds.) (nt:class ii aldolase) (le:134) (re:1105) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828393	8090	30246	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828435	8091	30247	216	71

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828442	8092	30248	231	76
<u>Description</u>				
6500729328 arom:b0390 arom protein (gtcfc:5.15) (keggfc:14.2) (rileyfc:1.4.4) (db:gtc-escherichia coli) b0390 b0390 Escherichia coli 562 -11533186 60229 arom (de:arom protein) (db:swissprot) AROM_ECOLI P08403 ESCHERICHIA COLI 562 -11533186 7000684635 arom membrane protein arom (cl:arom protein) (db:pir1.dat) (mp:9 min) BVECAM F64767 Escherichia coli 562 -11533186 7500877195 arom arom protein (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (le:115018) (re:115695) (di:direct) ECU73857 U73857 g1657586 Escherichia coli 562 -11533186 240007 arom protein of aro operon:regulated by aror (fn:phenotype; amino acid biosynthesis: chorismate) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 35 of 400 of the completegenome.) (nt:o225; 99 pct identical to arom_ecoli sw: p08403) (le:6304) (re:6981) (di:direct) AE000145 AE000145 g1786589 Escherichia coli 562 -11533186				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828443	8093	30249	324	108
<u>Description</u>				
6500729329 wrba:b1004 trp repressor binding protein (gtcfc:5.15) (keggfc:14.2) (rileyfc:1.4.4) (db:gtc-escherichia coli) b1004 b1004 Escherichia coli 562 -11533187 7000691927 wrba trp repressor-binding protein:tryptophan repressor-binding protein (cl:conserved hypothetical protein ycr004c) (db:pir2.dat) B64842 B64842 Escherichia coli 562 -11533187 7500960475 wrba trp repressor binding protein:affects (fn:regulator; amino acid biosynthesis: tryptophan) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 92 of 400 of the completegenome.) (nt:f198; 99 pct identical to wrba_ecoli sw: p30849) (le:4668) (re:5264) (di:complement) AE000202 AE000202 g1787239 Escherichia coli 562 -11533187 7502851892 trp repressor binding protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #227) (db:genpept) (de:escherichia coli genomic dna. (22.8 - 23.1 min).) (nt:orf_id:o228#2; similar to pir accession number) (le:12609) (re:13205) (di:complement) D90737 D90737 g4062558 Escherichia coli 562 -11533187 7502851893 trp repressor binding protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #228) (db:genpept) (de:escherichia coli genomic dna. (23.0 - 23.4 min).) (nt:orf_id:o228#2; similar to pir accession number) (le:1073) (re:1669) (di:complement) D90738 D90738 g4062567 Escherichia coli 562 -11533187				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828444	8094	30250	1632	543

Description

6500729330 trpl:trpee:b1265 trp operon leader peptide (gtcfc:5.15)  
(keggfc:14.2) (rileyfc:1.4.4) (db:gtc-escherichia coli) b1265 b1265  
Escherichia coli 562 -11533188 82445 trpl:trpee (de:trp operon leader  
peptide) (db:swissprot) LPW\_ECOLI P03053 ESCHERICHIA COLI 562 -11533188  
131584 trpl:trpee trp operon leader peptide (cl:trp leader peptide)  
(db:pir1.dat) (mp:27 min) LFECW A03589 Escherichia coli 562 -11533188  
324575 (sr:escherichia coli rna and dna) (db:genpept-bct1) (de:escherichia  
coli tryptophan operon (trpabcde) genes, complete.) (nt:trp operon leader  
peptide (putative); putative) (le:347) (re:391) (di:direct) ECOTGP J01714  
g147954 Escherichia coli 562 -11533188 236079 trpl trp operon leader  
peptide (fn:leader; amino acid biosynthesis: tryptophan) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 114 of 400 of the completegenome.)  
(nt:f14; 100 pct identical to lpw\_ecoli sw: p03053) (le:9227) (re:9271)  
(di:complement) AE000224 AE000224 g1787519 Escherichia coli 562 -11533188  
408455 (db:genpept-pat) (de:nucleotide sequence 8 from patent number  
wo8400380.) (nt:unnamed protein product) (le:67) (re:111) (di:direct) A04494  
A04494 g410992 unclassified 32644 -11533188 7502851894 (sr:escherichia coli  
k-12 (strain hb101) dna, clone pwt511) (db:genpept-syn) (de:e.coli  
tryptophan promoter-operator region.) (nt:trp attenuator peptide) (le:117)  
(re:161) (di:direct) SYNTRPPO K01155 g209530 artificial sequence 81077  
-11533188

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501828445	8095	30251	420	139

Description

6500729331 phel:pheae:b2598 phe leader peptide:attenuator peptide  
 (gtcfc:5.15) (keggfc:14.2) (rileyfc:1.4.4) (db:gtc-escherichia coli) b2598  
 b2598 Escherichia coli 562 -11533189 7500885117 phel:pheae (de:phe leader  
 peptide (attenuator peptide)) (db:swissprot) LPF\_ECOLI P03057 ESCHERICHIA  
 COLI 562 -11533189 131589 phel:pheae phe operon leader peptide:attenuator  
 peptide (cl:phea leader peptide) (db:pir1.dat) (mp:56 min) LFECF A03593  
 Escherichia coli 562 -11533189 235406 (sr:escherichia coli dna)  
 (db:genpept-bct1) (de:e.coli phe operon, phea gene coding for  
 chorismatmutase-p-prephenate dehydratase.) (nt:attenuator peptide) (le:22)  
 (re:69) (di:direct) ECOPHEA J01658 g147170 Escherichia coli 562 -11533189  
 235411 phe leader peptide (sr:e.coli k12 dna, clone pmu1000)  
 (db:genpept-bct1) (de:e.coli phe and tyr operons: phea and phe genes coding  
 forchorismat mutase/prephenate dehydratase and phe leader peptide;and arof  
 and tyra genes encoding dhap synthetase and chorismatmutase/prep...  
 ECOPHEAB M10431 g147174 Escherichia coli 562 -11533189 237797 phel leader  
 peptide (sr:e.coli k-12 dna, clones pmu(1130,1131,1132)) (db:genpept-bct1)  
 (de:e.coli chorismat mutase/prephenate dehydratase (phea) gene, 5' endof  
 cds, and leader peptide, complete cds.) (le:218) (re:265) (di:direct)  
 ECOPHEAC M58024 g147180 Escherichia coli 562 -11533189 7502851895  
 (db:genpept-bct1) (de:e. coli phea gene.) (nt:attenuator peptide) (le:22)  
 (re:69) (di:direct) ECPHEA V00314 g42379 Escherichia coli 562 -11533189  
 235403 phel leader peptide of chorismat mutase-p-prephenate (fn:leader;  
 amino acid biosynthesis: phenylalanine) (db:genpept-bct2) (de:escherichia  
 coli k-12 mg1655 section 236 of 400 of the completegenome.) (nt:o15; 100 pct  
 identical to lpf\_ecoli sw: p03057) (le:3391) (re:3438) (di:direct) AE000346  
 AE000346 g1788950 Escherichia coli 562 -11533189 82386 phel:pheae (de:phe  
 leader peptide (attenuator peptide)) (db:swissprot) LPF\_ECOLI P03057  
 ESCHERICHIA COLI 562 -11533189

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828455	8096	30252	267	88

Description

6500729332 trpr:rtry:b4393 trpr:trp operon repressor (gtcfc:5.15)  
(keggfc:14.2) (rileyfc:1.4.4) (db:gtc-escherichia coli) b4393 b4393  
Escherichia coli 562 -11533190 131525 trpr trp operon repressor (cl:trp  
repressor) (db:pir1.dat) (mp:100 min) RPECW A03568 Escherichia coli 562  
-11533190 237598 (sr:escherichia coli dna (1), (2) and mrna (2))  
(db:genpept-bct1) (de:e.coli trpr gene coding for the trp operon repressor  
protein.) (nt:trp operon repressor protein (trpr)) (le:385) (re:711)  
(di:direct) ECOTRPR J01715 g148060 Escherichia coli 562 -11533190  
7500953665 trpr (fn:regulation of trp operon and aroh; trp)  
(db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to  
00.1 minutes.) (nt:cg site no. 68; alternate gene name rtry) (le:323593)  
(re:323919) (di:direct) ECOUW93 U14003 g537233 Escherichia coli 562  
-11533190 236148 trpr regulator for trp operon and aroh:trp (fn:regulator;  
amino acid biosynthesis: tryptophan) (db:genpept-bct2) (de:escherichia coli  
k-12 mg1655 section 399 of 400 of the completegenome.) (nt:ol08; cg site no.  
68; alternate gene name rtry) (le:7948) (re:8274) (di:direct) AE000509  
AE000509 g1790854 Escherichia coli 562 -11533190

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828456	8097	30253	384	127

Description

6500729333 pand:b0131 aspartate 1-decarboxylase:aspartate 1-decarboxylase  
precursor:aspartate alpha-decarboxylase (gtcfc:5.2:6.1:9.5) (ec:4.1.1.11)  
(keggfc:5.2:6.1) (rileyfc:1.7.5) (db:gtc-escherichia coli) b0131 b0131  
Escherichia coli 562 -11533191 88579 pand (ec:4.1.1.11) (de:decarboxylase))  
(db:swissprot) PAND\_ECOLI P31664 ESCHERICHIA COLI 562 -11533191 7000686083  
pand aspartate 1-decarboxylase (cl:aspartate 1-decarboxylase) (ec:4.1.1.11)  
(db:pir2.dat) C64736 C64736 Escherichia coli 562 -11533191 7500887649 pand  
aspartate-1-decarboxylase (fn:aspartate -- beta-alanine) (sr:escherichia  
coli (sub\_strain w3110, strain k-12) dna) (db:genpept-bct1) (de:e. coli  
alpha-ketopantoate hydroxymethyl transferase (panb),pantothenate synthetase  
(panc), aspartate-1-decarboxylase (pand),and two unidenti... ECOPANBCD  
L17086 g304930 Escherichia coli 562 -11533191 235332 pand aspartate  
1-decarboxylase (fn:enzyme; biosynthesis of cofactors, carriers:)  
(db:genpept-bct2) (ec:4.1.1.11) (de:escherichia coli k-12 mg1655 section 12  
of 400 of the completegenome.) (nt:f126; 100 pct identical to pand\_ecoli sw:  
p31664) (le:7610) (re:7990) (di:complement) AE000122 AE000122 g1786323  
Escherichia coli 562 -11533191 5000690420 (de:(ecoli\_131) (pn:aspartate  
1-decarboxylase) (gn:pand) (gtcfc:5.2:6.1) (ec:4.1.1.11) (pand\_ecoli)  
(keggfc:5.2:6.1) (rileyfc:1.7.5) (db:gtc-escherichia coli)) ECOLI\_131  
ECOLI\_131 Escherichia coli 562 10030706

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828457	8098	30254	186	62
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828463	8099	30255	282	93
<u>Description</u>				

6500729334 asns:tss:b0930 asparaginyl-trna synthetase:asparagine--trna  
 ligase:asnrs (gtcfc:10.6:5.2) (ec:6.1.1.22) (keggfc:5.2:10.1:10.2)  
 (rileyfc:3.1.5) (db:gtc-escherichia coli) b0930 b0930 Escherichia coli 562  
 -11533192 125899 asns:tss asparagine--trna ligase::asparaginyl-trna  
 synthetase (cl:lysine--trna ligase) (ec:6.1.1.22) (db:pirl.dat) (mp:21 min)  
 SYECNT JS0396 Escherichia coli 562 -11533192 223289 asns asparagine-trna  
 ligase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #219)  
 (db:genpept-bct1) (de:escherichia coli genomic dna. (21.1 - 21.4 min).)  
 (le:4738) (re:6138) (di:complement) D90731 D90731 g1651455 Escherichia coli  
 562 -11533192 236078 asns asparaginyl-trna synthetase (db:genpept-bct1)  
 (de:e.coli asns gene for asparaginyl-trna synthetase.) (le:91) (re:1491)  
 (di:direct) ECASNS X68192 g41000 Escherichia coli 562 -11533192 7500953364  
 (sr:e.coli dna) (db:genpept-bct1) (de:e.coli asparaginyl-trna synthetase  
 (asns) gene, complete cds.) (nt:asparaginyl-trna synthetase (asns)) (le:382)  
 (re:1782) (di:direct) ECOTGASNS M33145 g147935 Escherichia coli 562  
 -11533192 232412 asns asparagine trna synthetase (fn:enzyme; aminoacyl trna  
 synthetases, trna) (db:genpept-bct2) (ec:6.1.1.22) (de:escherichia coli k-12  
 mg1655 section 85 of 400 of the completengenome.) (nt:f466; 100 pct identical  
 to syn\_ecoli sw: p17242 but) (le:4631) (re:6031) (di:complement) AE000195  
 AE000195 g1787161 Escherichia coli 562 -11533192 5000690421 asns  
 asparaginyl-trna synthetase ec 6.1.1.22 (sr:escherichia coli(strain:k12)  
 dna, clone:kohara clone #219) (db:genpept) (de:escherichia coli genomic dna.  
 (21.2 - 21.5 min).) (nt:orf\_id:o219#5; similar to swissprot accession)  
 (le:4738) (re:6138) (di:complement) D90731 D90731 g1651455 Escherichia coli  
 562 -11533192

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828465	8100	30256	315	104

Description

6500729335 dadx:dadb:alnb:b1190 alanine racemase:catabolic precursor  
 (gtcfc:5.2:6.15:6.6) (ec:5.1.1.1) (keggfc:5.2:6.8) (rileyfc:1.1.2)  
 (db:gtc-escherichia coli) b1190 b1190 Escherichia coli 562 -11533193 59224  
 dadx:dadb:alnb (ec:5.1.1.1) (de:alanine racemase, catabolic,) (db:swissprot)  
 ALR2\_ECOLI P29012 ESCHERICHIA COLI 562 -11533193 7000684564 dadx:dadb:alnb  
 alanine racemase:precursor:catabolic (cl:alanine racemase) (ec:5.1.1.1)  
 (db:pir1.dat) C53383 C64865 Escherichia coli 562 -11533193 223406 dadb  
 alanine racemase:catabolic precursor (sr:escherichia coli(strain:k12) dna,  
 clone:kohara clone #244) (db:genpept-bct1) (de:escherichia coli genomic dna.  
 (26.4 - 26.7 min).) (le:10625) (re:11695) (di:direct) D90753 D90753 g1651592  
 Escherichia coli 562 -11533193 7500876777 dadx alanine racemase 2:catabolic  
 (fn:enzyme; degradation of small molecules: amino) (db:genpept-bct2)  
 (ec:5.1.1.1) (de:escherichia coli k-12 mg1655 section 107 of 400 of the  
 completegenome.) (nt:o356; 98 pct identical to alr2\_ecoli sw: p29012)  
 (le:5806) (re:6876) (di:direct) AE000217 AE000217 g1787439 Escherichia coli  
 562 -11533193 5000690422 alnb alanine racemase:catabolic precursor ec  
 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #244) (db:genpept)  
 (de:escherichia coli genomic dna. (26.5 - 26.8 min).) (nt:orf\_id:o244#10;  
 similar to swissprot accession) (le:10625) (re:11695) (di:direct) D90753  
 D90753 g1651592 Escherichia coli 562 -11533193

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828469	8101	30257	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828473	8102	30258	360	119

#### Description

6500729336 asps:tls:b1866 aspartyl-trna synthetase:aspartate--trna ligase:asprs (gtcfc:10.6:5.2) (ec:6.1.1.12) (keggfc:5.2:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli) b1866 b1866 Escherichia coli 562 -11533194 301000 asps:tls (ec:6.1.1.12) (de:(asprs)) (db:swissprot) SYD\_ECOLI P21889 ESCHERICHIA COLI 562 -11533194 125904 asps:tls aspartate--trna ligase::aspartyl-trna synthetase (cl:lysine--trna ligase) (ec:6.1.1.12) (db:pir1.dat) SYECD JT0942 Escherichia coli 562 -11533194 224360 asps:tls aspartate--trna ligase ec 6.1.1.12 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #337(41.9-42.3 min).) (nt:orf\_id:o337#7; similar to (pir accession number) (le:5552) (re:7324) (di:complement) D90829 D90829 g1736513 Escherichia coli 562 -11533194 5000690423 asps aspartate-trna ligase (db:genpept-bct1) (ec:6.1.1.12) (de:e. coli asps gene for aspartyl-trna synthetase (ec 6.1.1.12).) (le:1372) (re:3144) (di:direct) ECASPS X53863 g41015 Escherichia coli 562 -11533194 232423 asps aspartate trna synthetase (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:6.1.1.12) (de:escherichia coli k-12 mg1655 section 170 of 400 of the completegenome.) (nt:f590; 100 pct identical to syd\_ecoli sw: p21889; cg) (le:7169) (re:8941) (di:complement) AE000280 AE000280 g1788173 Escherichia coli 562 -11533194 100005 asps:tls (ec:6.1.1.12) (de:(asprs)) (db:swissprot) SYD\_ECOLI P21889 ESCHERICHIA COLI 562 -11533194

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828489	8103	30259	429	142

#### Description

6500729337 nadb:nicb:b2574 l-aspartate oxidase:quinolinate synthetase b (gtcfc:5.2:9.4) (ec:1.4.3.16) (keggfc:5.2:9.4) (rileyfc:1.7.7) (db:gtc-escherichia coli) b2574 b2574 Escherichia coli 562 -11533195 7000688845 nadb l-aspartate oxidase::quinolinate synthetase b (cl:fumarate reductase flavoprotein:3-oxosteroid 1-dehydrogenase homology:fumarate reductase flavoprotein homology) (ec:1.4.3.16) (db:pir1.dat) (mp:56 min) OXECLD E65035 Escherichia coli 562 -11533195 7500953196 nadb quinolinate synthetase:b protein (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:1.4.3.16) (de:escherichia coli k-12 mg1655 section 234 of 400 of the completegenome.) (nt:o540; 99 pct identical to nadb\_ecoli sw: p10902) (le:234) (re:1856) (di:direct) AE000344 AE000344 g1788928 Escherichia coli 562 -11533195 5000690424 (de:(ecoli\_2514) (pn:quinolinate synthetase, b protein) (gn:nadb) (gtcfc:5.2:9.4) (ec:1.4.3.16) (nadb\_ecoli) (keggfc:5.2:9.4) (rileyfc:1.7.7) (db:gtc-escherichia coli)) ECOLI\_2514 ECOLI\_2514 Escherichia coli 562 10123734

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828522	8104	30260	2970	990

Description

6500729338 alas:lovb:b2697 alanyl-trna synthetase:alanine--trna ligase:alars (gtcfc:10.6:5.2) (ec:6.1.1.7) (keggfc:5.2:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli) b2697 b2697 Escherichia coli 562 -11533196 99977 alas:lovb (ec:6.1.1.7) (de:alanyl-trna synthetase, (alanine--trna ligase) (alars)) (db:swissprot) SYA\_ECOLI P00957 ESCHERICHIA COLI 562 -11533196 7000686703 alas alanine--trna ligase::alanyl-trna synthetase (cl:alanine--trna ligase) (ec:6.1.1.7) (db:pir1.dat) (mp:58 min) SYECAT E65049 Escherichia coli 562 -11533196 225249 alas alanyl-trna synthetase ec 6.1.1.7 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #446(60.5-60.9 min.)) (nt:similar to (swissprot accession number p00957)) (le:8287) (re:10917) (di:complement) D90892 D90892 gl800083 Escherichia coli 562 -11533196 7500892316 alas alanyl-trna synthetase (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:6.1.1.7) (de:escherichia coli k-12 mg1655 section 243 of 400 of the completegenome.) (nt:f876; 98 pct identical to sya\_ecoli sw: p00957; cg) (le:9857) (re:12487) (di:complement) AE000353 AE000353 g1789048 Escherichia coli 562 -11533196 5000690425 (de:(ecoli\_2625) (pn:alanyl-trna synthetase) (gn:alas) (gtcfc:5.2:10.6) (ec:6.1.1.7) (sya\_ecoli) (keggfc:5.2:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli)) ECOLI\_2625 ECOLI\_2625 Escherichia coli 562 10120329

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828528	8105	30261	240	79

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828532	8106	30262	339	112

Description

6500729339 alr:b4053 alanine racemase:alanine racemase:biosynthetic  
 (gtcfc:5.2:6.15) (ec:5.1.1.1) (keggfc:5.2:6.8) (rileyfc:1.4.6)  
 (db:gtc-escherichia coli) b4053 b4053 Escherichia coli 562 -11533197 59222  
 alr (ec:5.1.1.1) (de:alanine racemase, biosynthetic,) (db:swissprot)  
 ALR1\_ECOLI P29743 ESCHERICHIA COLI 562 -11533197 7000684563 alr alanine  
 racemase::biosynthetic (cl:alanine racemase) (ec:5.1.1.1) (db:pir1.dat)  
 (mp:92 min) PC1296 D65213 Escherichia coli 562 -11533197 7500876775 alr  
 alanine racemase 1 (fn:enzyme; amino acid biosynthesis: alanine)  
 (db:genpept-bct2) (ec:5.1.1.1) (de:escherichia coli k-12 mg1655 section 368  
 of 400 of the completegenome.) (nt:o359; ??? pct identical amino acid  
 sequence and) (le:6621) (re:7700) (di:direct) AE000478 AE000478 g1790487  
 Escherichia coli 562 -11533197 5000690426 (de:(ecoli\_3939) (pn:alanine  
 racemase 1) (gn:alr) (gtcfc:5.2:6.15) (ec:5.1.1.1) (alr1\_ecoli)  
 (keggfc:5.2:6.8) (rileyfc:1.4.6) (db:gtc-escherichia coli)) ECOLI\_3939  
 ECOLI\_3939 Escherichia coli 562 10124140

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501828547	8107	30263	690	230

# Description

6500729340 thr1:b0001 thr operon leader peptide:thr operon attenuator (gtcfc:5.2) (keggfc:14.2) (rileyfc:1.4.2) (db:gtc-escherichia coli) b0001 b0001 Escherichia coli 562 -11533198 7500885141 thr1 (de:thr operon leader peptide (thr operon attenuator)) (db:swissprot) LPT\_ECOLI P03059 ESCHERICHIA COLI 562 -11533198 131591 thr1 thr operon leader peptide (cl:thr leader peptide) (db:pir1.dat) LFECT A03595 Escherichia coli 562 -11533198 236098 thr leader peptide (sr:escherichia coli (strain k-12) (clone: pip2.) dna) (db:genpept-bct1) (de:e.coli threonine operon with thra, thrb and thrc genes coding for aspartokinase i-homoserine dehydrogenase i, homoserine kinase and threonine synthase.) (nt:thr operon) (le:50) ... ECOTHR J01706 g147978 Escherichia coli 562 -11533198 237609 thr1 (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli threonine operon (thrpla) genes, complete cds.) (le:175) (re:240) (di:direct) ECOTHRIPA M28570 g290477 Escherichia coli 562 -11533198 238345 thr1 thr operon leader peptide (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:332675) (re:332740) (di:direct) ECOUW93 U14003 g537244 Escherichia coli 562 -11533198 238355 (db:genpept-bct1) (de:part of the e. coli thra gene coding for aspartokinase i-homoserine dehydrogenase i.) (nt:reading frame (attenuator peptide)) (le:32) (re:97) (di:direct) ECTHR1 V00360 g43061 Escherichia coli 562 -11533198 5000690521 thr leader peptide (db:genpept-bct1) (de:e.coli thr operon-controlling elements.) (le:173) (re:238) (di:direct) ECTHRPRO X68872 g43074 Escherichia coli 562 -11533198 236091 thr1 thr operon leader peptide (fn:leader; amino acid biosynthesis: threonine) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 1 of 400 of the complete genome.) (nt:o21; 100 pct identical to lpt\_ecoli sw: p03059) (le:190) (re:255) (di:direct) AE000111 AE000111 g1786182 Escherichia coli 562 -11533198 82440 thr1 (de:thr operon leader peptide (thr operon attenuator)) (db:swissprot) LPT\_ECOLI P03059 ESCHERICHIA COLI 562 -11533198

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828548	8108	30264	204	67

Description

6500729341 thra:thra1:thra2:b0002 aspartokinase i/homoserine dehydrogenase i:aspartokinase i / homoserine dehydrogenase i (gtcfc:5.2:5.3:5.8) (keggfc:5.3:5.8) (rileyfc:1.4.2) (db:gtc-escherichia coli) b0002 b0002 Escherichia coli 562 -11533199 7000688867 thra:thra1:thra2 thra bifunctional enzyme:aspartokinase i / homoserine dehydrogenase i:protein f132 (cl:thra bifunctional enzyme:aspartate kinase homology:homoserine dehydrogenase homology) (db:pir1.dat) (mp:0 min) DEECK B64720 Escherichia coli 562 -11533199 7500953265 thra aspartokinase i-homoserine dehydrogenase i (db:genpept-bct1) (ec:2.7.2.4:1.1.1.3) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 111) (le:332822) (re:335284) (di:direct) ECOUW93 U14003 g537245 Escherichia coli 562 -11533199 237610 thra aspartokinase i:homoserine dehydrogenase i (fn:enzyme; amino acid biosynthesis: threonine) (db:genpept-bct2) (ec:2.7.2.4) (de:escherichia coli k-12 mg1655 section 1 of 400 of the completegenome.) (nt:o820; 99 pct identical to ak1h\_ecoli sw: p00561; cg) (le:337) (re:2799) (di:direct) AE000111 AE000111 g1786183 Escherichia coli 562 -11533199 5000690427 (de:(ecoli\_2) (pn:aspartokinase i-homoserine dehydrogenase i) (gn:thra) (gtcfc:5.3:5.8) (ec:2.7.2.4) (ak1h\_ecoli) (keggfc:5.3:5.8) (rileyfc:1.4.2) (db:gtc-escherichia coli)) ECOLI\_2 ECOLI\_2 Escherichia coli 562 10122617

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828549	8109	30265	1032	343

Description

6500729342 thrb:b0003 homoserine kinase:hk (gtcfc:5.2:5.3) (ec:2.7.1.39) (keggfc:5.3) (rileyfc:1.4.2) (db:gtc-escherichia coli) b0003 b0003 Escherichia coli 562 -11533200 80667 thrb (ec:2.7.1.39) (de:homoserine kinase, (hk)) (db:swissprot) KHSE\_ECOLI P00547 ESCHERICHIA COLI 562 -11533200 138849 thrb homoserine kinase (cl:homoserine kinase) (ec:2.7.1.39) (db:pir1.dat) (mp:0 min) KIECM S56630 Escherichia coli 562 -11533200 237611 thrb (sr:escherichia coli (strain pc 0542) dna) (db:genpept-bct1) (ec:2.7.1.39) (de:escherichia coli thrb gene sequence.) (nt:homoserine kinase) (le:1) (re:933) (di:direct) ECOTHRBUPD L13601 g529240 Escherichia coli 562 -11533200 7500884607 thrb homoserine kinase (db:genpept-bct1) (ec:2.7.1.39) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 110) (le:335286) (re:336218) (di:direct) ECOUW93 U14003 g537246 Escherichia coli 562 -11533200 236097 thrb homoserine kinase (fn:enzyme; amino acid biosynthesis: threonine) (db:genpept-bct2) (ec:2.7.1.39) (de:escherichia coli k-12 mg1655 section 1 of 400 of the completegenome.) (nt:o310; 100 pct identical to khse\_ecoli sw: p00547;) (le:2801) (re:3733) (di:direct) AE000111 AE000111 g1786184 Escherichia coli 562 -11533200 5000690428 (de:(ecoli\_3) (pn:homoserine kinase) (gn:thrb) (gtcfc:5.3) (ec:2.7.1.39) (khse\_ecoli) (keggfc:5.3) (rileyfc:1.4.2) (db:gtc-escherichia coli)) ECOLI\_3 ECOLI\_3 Escherichia coli 562 10022908

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501828551	8110	30266	303	100

Description

6500729343 thrc:b0004 threonine synthase (gtcfc:5.2:5.3:9.3) (ec:4.2.99.2) (keggfc:5.3:9.3) (rileyfc:1.4.2) (db:gtc-escherichia coli) (gtcfc:l-amino acid metabolism-alanine and aspartate metabolism:l-amino acid metabolism-glycine--serine and threonine metabolism:metabolism of cofactors and vi... b0004 b0004 Escherichia coli 562 -11533201 101440 thrc (ec:4.2.99.2) (de:threonine synthase,) (db:swissprot) THRC\_ECOLI P00934 ESCHERICHIA COLI 562 -11533201 125692 thrc threonine synthase (cl:threonine synthase) (ec:4.2.99.2) (db:pir1.dat) (mp:0 min) SYECR A01157 Escherichia coli 562 -11533201 236094 thrc threonine synthase (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (ec:4.2.99.2) (de:e.coli k12 genome, 0-2.4min. region.) (le:3395) (re:4681) (di:direct) ECO110K D10483 g216437 Escherichia coli 562 -11533201 237612 thrc threonine synthase (sr:escherichia coli (strain k-12) (clone: pip2.) dna) (db:genpept-bct1) (ec:4.2.99.2) (de:e.coli threonine operon with thra, thrb and thrc genes coding foraspartokinase i-homoserine dehydrogenase i, homoserine kinase andthreonine synthase.) (le:3591) ... ECOTHR J01706 g147981 Escherichia coli 562 -11533201 7500893112 thrc threonine synthase (db:genpept-bct1) (ec:4.2.99.2) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 109) (le:336219) (re:337505) (di:direct) ECOUW93 U14003 g537247 Escherichia coli 562 -11533201 233547 thrc threonine synthase (fn:enzyme; amino acid biosynthesis: threonine) (db:genpept-bct2) (ec:4.2.99.2) (de:escherichia coli k-12 mg1655 section 1 of 400 of the completegenome.) (nt:o428; 100 pct identical to thrc\_ecoli sw: p00934;) (le:3734) (re:5020) (di:direct) AE000111 AE000111 g1786185 Escherichia coli 562 -11533201 5000690429 (de:(ecoli\_4) (pn:threonine synthase) (gn:thrc) (gtcfc:5.3:9.3) (ec:4.2.99.2) (thrc\_ecoli) (keggfc:5.3:9.3) (rileyfc:1.4.2) (db:gtc-escherichia coli)) ECOLI\_4 ECOLI\_4 Escherichia coli 562 10043279

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828562	8111	30267	933	310

Description

6500729344 dapb:b0031 dihydrodipicolinate reductase (gtcfc:5.2:5.8) (ec:1.3.1.26) (keggfc:5.8) (rileyfc:1.4.2) (db:gtc-escherichia coli) b0031 b0031 Escherichia coli 562 -11533202 67873 dapb (ec:1.3.1.26) (de:dihydrodipicolinate reductase,) (db:swissprot) DAPB\_ECOLI P04036 ESCHERICHIA COLI 562 -11533202 122673 dapb dihydrodipicolinate reductase (cl:dihydrodipicolinate reductase) (ec:1.3.1.26) (db:pir1.dat) (mp:1 min) RDECPD A00375 Escherichia coli 562 -11533202 234126 dapb dehydrodipicolinate reductase (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (ec:1.3.1.26) (de:e.coli k12 genome, 0-2.4min. region.) (le:28028) (re:28849) (di:direct) ECO110K D10483 g216458 Escherichia coli 562 -11533202 7500879994 dapb (sr:e.coli k12 dna, clone pdb17) (db:genpept-bct1) (de:e.coli dapb gene coding for dihydrodipicolinate reductase, completecds.) (nt:dihydrodipicolinate reductase) (le:135) (re:956) (di:direct) ECODAPB M10611 g145710 Escherichia coli 562 -11533202 233568 dapb dihydrodipicolinate reductase (fn:enzyme; amino acid biosynthesis: lysine) (db:genpept-bct2) (ec:1.3.1.26) (de:escherichia coli k-12 mg1655 section 3 of 400 of the completegenome.) (nt:o273; 100 pct identical to dapb\_ecoli sw: p04036) (le:7715) (re:8536) (di:direct) AE000113 AE000113 g1786214 Escherichia coli 562 -11533202 5000690470 (de:(ecoli\_31) (pn:dihydrodipicolinate reductase) (gn:dapb) (gtcfc:5.8) (ec:1.3.1.26) (dapb\_ecoli) (keggfc:5.8) (rileyfc:1.4.2) (db:gtc-escherichia coli)) ECOLI\_31 ECOLI\_31 Escherichia coli 562 10010469

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828569	8112	30268	321	106

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828579	8113	30269	819	272

Description

6500729345 dapd:b0166 2:3:4:5-tetrahydropyridine-2-carboxylate  
n-succinyltransferase:2:3:4:5-tetrahydropyridine-2-carboxylate  
n-succinyltransferase:tetrahydrodipicolinate n-succinyltransferase:thp  
succinyltransferase:tetrahydropicolinate succinylase (gtcfc:5.2:5.8)  
(ec:2.3.1.117) (keggfc:5.8) (rileyfc:1.4.2) (db:gtc-escherichia coli) b0166  
b0166 Escherichia coli 562 -11533203 67879 dapd (ec:2.3.1.117) (de:(thp  
succinyltransferase) (tetrahydropicolinate succinylase)) (db:swissprot)  
DAPD\_ECOLI P03948 ESCHERICHIA COLI 562 -11533203 7000684984 dapd  
2:3:4:5-tetrahydropyridine-2-carboxylate  
n-succinyltransferase::succinyldiaminopimelate  
aminotransferase:succinyldiaminopimelate transferase:tetrahydrodipicolinate  
n-succinyltransferase (cl:2,3,4,5-tetrahydropyridine-2-carboxylate  
n-succinyltransferase) (ec:2.3.1.117) (db:pirl.dat) (mp:4 min) XNECSD F64740  
Escherichia coli 562 -11533203 239794 dapd tetrahydrodipicolinate  
n-succinyltransferase (sr:escherichia coli (sub\_strain w3110, strain k-12)  
(library: kohara') (db:genpept-bct1) (ec:2.6.1.17) (de:escherichia coli  
genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0 min).) (le:73718)  
(re:74542) (di:complement) ECO82K D26562 g473821 Escherichia coli 562  
-11533203 301632 dapd tetrahydrodipicolinate n-succinyltransferase  
(db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:16198)  
(re:17022) (di:complement) ECU70214 U70214 g1552743 Escherichia coli 562  
-11533203 233694 dapd 2:3:4:5-tetrahydropyridine-2-carboxylate (fn:enzyme;  
amino acid biosynthesis: lysine) (db:genpept-bct2) (ec:2.3.1.117)  
(de:escherichia coli k-12 mg1655 section 16 of 400 of the completegenome.)  
(nt:f274; 98 pct identical to dapd\_ecoli sw: p03948) (le:1489) (re:2313)  
(di:complement) AE000126 AE000126 g1786362 Escherichia coli 562 -11533203  
5000690473 (de:(ecoli\_166) (pn:tetrahydrapicolinate n-succinyltransferase)  
(gn:dapd) (gtcfc:5.8) (ec:2.3.1.117) (dapd\_ecoli) (keggfc:5.8)  
(rileyfc:1.4.2) (db:gtc-escherichia coli)) ECOLI\_166 ECOLI\_166 Escherichia  
coli 562 10122692

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828581	8114	30270	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828582	8115	30271	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828599	8116	30272	564	187

Description

GTC ORF with score 389 to: (fn:controls entry of the cell into the asexual)  
(db:genpept-pln2) (de:neurospora crassa protein kinase nrc-2 (nrc-2) gene,  
complete cds.) (nt:similar to kad5 from schizosaccharomyces pombe;)  
(le:81:953:1322:1766) ...

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828602	8117	30273	336	111

Description

Hypothetical protein

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501828615	8118	30274	282	93

#### Description

6500729346 dape:msgb:b2472 succinyl-diaminopimelate desuccinylase:sdap  
 (gtcfc:5.2:5.8) (ec:3.5.1.18) (keggfc:5.8) (rileyfc:1.4.2)  
 (db:gtc-escherichia coli) b2472 b2472 Escherichia coli 562 -11533204 258386  
 dape:msgb (ec:3.5.1.18) (de:succinyl-diaminopimelate desuccinylase, (sdap))  
 (db:swissprot) DAPE\_ECOLI P24176 ESCHERICHIA COLI 562 -11533204 164655  
 dape:msgb succinyl-diaminopimelate  
 desuccinylase::n-succinyl-l-diaminopimelic acid desuccinylase:sdap-deacylase  
 (ec:3.5.1.18) (db:pir2.dat) (mp:15 min) A42959 A42959 Escherichia coli 562  
 -11533204 225034 dape succinyl-diaminopimelate desuccinylase ec  
 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
 (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #422(55.5-55.8  
 min.)) (nt:similar to (pir accession number a42959)) (le:14700) (re:15827)  
 (di:direct) D90875 D90875 g1799895 Escherichia coli 562 -11533204 225038  
 dape succinyl-diaminopimelate desuccinylase ec (sr:escherichia coli  
 (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
 (de:e.coli genomic dna, kohara clone #423(55.7-56.1 min.)) (nt:similar to  
 (pir accession number a42959)) (le:2556) (re:3683) (di:direct) D90876 D90876  
 g1799900 Escherichia coli 562 -11533204 5000690474 dape  
 succinyldiaminopimelate desuccinylase (db:genpept-bct1) (ec:3.5.1.18)  
 (de:escherichia coli dape gene for succinyldiaminopimelatedesuccinylase.)  
 (le:1023) (re:2150) (di:direct) ECDAPE X57403 g41234 Escherichia coli 562  
 -11533204 7500879999 msgb/dape n-succinyl-l-diaminopimelic acid  
 desuccinylase (db:genpept-bct1) (de:msgb/dape=multicopy suppressor of grpe  
 (escherichia coli, genomic,1555 nt).) (nt:method: conceptual translation  
 with partial peptide) (le:326) (re:1453) (di:direct) S41760 S41760 g253061  
 Escherichia coli 562 -11533204 232644 dape n-succinyl-diaminopimelate  
 deacylase (fn:enzyme; amino acid biosynthesis: lysine) (db:genpept-bct2)  
 (ec:3.5.1.18) (de:escherichia coli k-12 mg1655 section 224 of 400 of the  
 completegenome.) (nt:o375; 99 pct identical to dape\_ecoli sw: p24176)  
 (le:4124) (re:5251) (di:direct) AE000334 AE000334 g1788816 Escherichia coli  
 562 -11533204 67882 dape:msgb (ec:3.5.1.18) (de:succinyl-diaminopimelate  
 desuccinylase, (sdap)) (db:swissprot) DAPE\_ECOLI P24176 ESCHERICHIA COLI 562  
 -11533204

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501828619	8119	30275	561	186

#### Description

GTC ORF with score 257 to: (sr:house mouse) (db:genpept-rod) (de:mus  
 musculus major histocompatibility locus class ii region;fas-binding protein  
 daxx (daxx) gene, partial cds; bing1 (bing1),tapasin (tapasin), ralgds-like  
 factor (rlf), ke2 (ke2), ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828625	8120	30276	240	79
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828630	8121	30277	267	88
<u>Description</u>				

GTC ORF with score 131 to: (sr:pyrococcus horikoshii (strain:ot3) dna)  
(db:genpept-bct1) (de:pyrococcus horikoshii ot3 genomic dna, 1485001-1738505  
nt. position(7/7).) (nt:similar to owl:zmgfo percent identity:28.788 in)  
(le:152170) (re:153177) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828631	8122	30278	750	249
<u>Description</u>				
6500729347 dapa:b2478 dihydrodipicolinate synthase:dhdps (gtcfc:5.2:5.8) (ec:4.2.1.52) (keggfc:5.8) (rileyfc:1.4.2) (db:gtc-escherichia coli) b2478 b2478 Escherichia coli 562 -11533205 67866 dapa (ec:4.2.1.52) (de:dihydrodipicolinate synthase, (dhdps)) (db:swissprot) DAPA_ECOLI P05640 ESCHERICHIA COLI 562 -11533205 7000684980 dapa dihydrodipicolinate synthase (cl:n-acetylneuraminate lyase) (ec:4.2.1.52) (db:pir1.dat) (mp:53 min) SYECDP E65023 Escherichia coli 562 -11533205 225043 dapa dihydrodipicolinate synthase ec 4.2.1.52 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #423(55.7-56.1 min.)) (nt:similar to (pir accession number a30381)) (le:9832) (re:10710) (di:complement) D90876 D90876 g1799905 Escherichia coli 562 -11533205 225053 dapa dihydrodipicolinate synthase ec 4.2.1.52 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #424(55.9-56.3 min.)) (nt:similar to (pir accession number a30381)) (le:2572) (re:3450) (di:complement) D90877 D90877 g1805536 Escherichia coli 562 -11533205 7500879990 dapa dihydrodipicolinate synthase (fn:enzyme; amino acid biosynthesis: lysine) (db:genpept-bct2) (ec:4.2.1.52) (de:escherichia coli k-12 mg1655 section 225 of 400 of the completegenome.) (nt:f292; 97 pct identical to dapa_ecoli sw: p05640) (le:1188) (re:2066) (di:complement) AE000335 AE000335 g1788823 Escherichia coli 562 -11533205 5000690475 (de:(ecoli_2418) (pn:dihydrodipicolinate synthase) (gn:dapa) (gtcfc:5.8) (ec:4.2.1.52) (dapa_ecoli) (keggfc:5.8) (rileyfc:1.4.2) (db:gtc-escherichia coli)) ECOLI_2418 ECOLI_2418 Escherichia coli 562 10120217				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828656	8123	30279	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828659	8124	30280	414	137

Description

6500729348 lysa:b2838 diaminopimelate decarboxylase:dap decarboxylase  
(gtcfc:5.2:5.8) (ec:4.1.1.20) (keggfc:5.8) (rileyfc:1.4.2)  
(db:gtc-escherichia coli) b2838 b2838 Escherichia coli 562 -11533206 67971  
lysa (ec:4.1.1.20) (de:diaminopimelate decarboxylase, (dap decarboxylase))  
(db:swissprot) DCDA\_ECOLI P00861 ESCHERICHIA COLI 562 -11533206 125305 lysa  
diaminopimelate decarboxylase (cl:diaminopimelate decarboxylase)  
(ec:4.1.1.20) (db:pirl.dat) (mp:61 min) DCECD A01078 Escherichia coli 562  
-11533206 239409 lysa diaminopimelate decarboxylase (sr:escherichia coli  
(1): k-12 bmh71-18(lac-pro)-del/f' pro-laci-q-zm1) (db:genpept-bct1)  
(de:e.coli galr, lysa, and lysr genes coding for galetk operonrepressor  
protein (gal repressor), diaminopimelate decarboxylaseand lysa activatory  
protein.) (le:11... ECOGALLYYS J01614 g455170 Escherichia coli 562 -11533206  
7500880047 lysa diaminopimelate decarboxylase (db:genpept-bct1)  
(ec:4.1.1.20) (de:escherichia coli k-12 genome; approximately 63 to 64  
minutes.) (nt:cg site no.540) (le:59192) (re:60454) (di:complement) ECU29581  
U29581 g882731 Escherichia coli 562 -11533206 234430 lysa diaminopimelate  
decarboxylase (fn:enzyme; amino acid biosynthesis: lysine) (db:genpept-bct2)  
(ec:4.1.1.20) (de:escherichia coli k-12 mg1655 section 257 of 400 of the  
completegenome.) (nt:f420; 100 pct identical to dcda\_ecoli sw: p00861;)  
(le:8348) (re:9610) (di:complement) AE000367 AE000367 g1789203 Escherichia  
coli 562 -11533206 5000690476 (de:(ecoli\_2766) (pn:diaminopimelate  
decarboxylase) (gn:lysa) (gtcfc:5.8) (ec:4.1.1.20) (dcda\_ecoli) (keggfc:5.8)  
(rileyfc:1.4.2) (db:gtc-escherichia coli)) ECOLI\_2766 ECOLI\_2766 Escherichia  
coli 562 10010564

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828666	8125	30281	816	271

Description

6500729349 lysr:b2839 transcriptional activator protein lysr  
 (gtcfc:5.2:10.2) (keggfc:14.2) (rileyfc:1.4.2) (db:gtc-escherichia coli)  
 b2839 b2839 Escherichia coli 562 -11533207 82770 lysr (de:transcriptional  
 activator protein lysr) (db:swissprot) LYSR\_ECOLI P03030 ESCHERICHIA COLI  
 562 -11533207 131501 lysr regulatory protein lysr (cl:regulatory protein  
 lysr) (db:pir1.dat) (mp:61 min) RGECK A03565 Escherichia coli 562 -11533207  
 7500885218 lysr activatory protein (sr:escherichia coli (1): k-12  
 bmh71-18(lac-pro)-del/f' pro-laci-q-zml) (db:genpept-bct1) (de:e.coli galr,  
 lysa, and lysr genes coding for galetk operonrepressor protein (gal  
 repressor), diaminopimelate decarboxylaseand lysa activatory protein.)  
 (le:25... ECOGALLYS J01614 gl46070 Escherichia coli 562 -11533207 234431  
 lysr positive regulator for lys (fn:regulator; amino acid biosynthesis:  
 lysine) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 257 of  
 400 of the completegenome.) (nt:o311; 99 pct identical to lysr\_ecoli sw:  
 p03030; cg) (le:9732) (re:10667) (di:direct) AE000367 AE000367 g1789204  
 Escherichia coli 562 -11533207 5000690522 (de:(ecoli\_2767) (pn:positive  
 regulator for lys) (gn:lysr) (gtcfc:6.9) (ec:) (lysr\_ecoli) (keggfc:11.2)  
 (rileyfc:1.4.2) (db:gtc-escherichia coli)) ECOLI\_2767 ECOLI\_2767 Escherichia  
 coli 562 10024990

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828675	8126	30282	456	151

#### Description

6500729350 asd:hom:b3433 aspartate semialdehyde dehydrogenase:aspartate-semialdehyde dehydrogenase:asa dehydrogenase (gtcfc:5.2:5.8) (ec:1.2.1.11) (keggfc:5.3:5.8) (rileyfc:1.4.2) (db:gtc-escherichia coli) b3433 b3433 Escherichia coli 562 -11533208 7500880236 asd:hom (ec:1.2.1.11) (de:dehydrogenase)) (db:swissprot) DHAS\_ECOLI P00353 ESCHERICHIA COLI 562 -11533208 122601 asd aspartate-semialdehyde dehydrogenase (cl:aspartate-semialdehyde dehydrogenase) (ec:1.2.1.11) (db:pir1.dat) DEECDA A00364 Escherichia coli 562 -11533208 5000690444 (db:genpept-bct1) (de:e. coli gene asd coding for aspartic semialdehyde dehydrogenase.) (nt:dehydrogenase) (le:240) (re:1343) (di:direct) ECASDX V00262 g40992 Escherichia coli 562 -11533208 232409 asd aspartate-semialdehyde dehydrogenase (fn:enzyme; amino acid biosynthesis: lysine) (db:genpept-bct2) (ec:1.2.1.11) (de:escherichia coli k-12 mg1655 section 310 of 400 of the completegenome.) (nt:f367; cg site no. 996; alternate names dap, hom; 99) (le:167) (re:1270) (di:complement) AE000420 AE000420 g1789841 Escherichia coli 562 -11533208 7502851896 asd aspartate semialdehyde dehydrogenase (db:genpept-bct2) (de:shigella sonnei aspartate semialdehyde dehydrogenase (asd) gene,complete cds.) (le:242) (re:1345) (di:direct) AF101226 AF101226 g3859587 Shigella sonnei 624 -11533208 68418 asd:hom (ec:1.2.1.11) (de:dehydrogenase)) (db:swissprot) DHAS\_ECOLI P00353 ESCHERICHIA COLI 562 -11533208

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828687	8127	30283	219	72

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828690	8128	30284	669	222

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828695	8129	30285	309	102

Description

6500729351 asnc:b3743 regulatory protein:regulatory protein asnc (gtcfc:5.2) (keggfc:14.2) (rileyfc:1.4.2) (db:gtc-escherichia coli) b3743 b3743  
Escherichia coli 562 -11533209 60372 asnc (de:regulatory protein asnc) (db:swissprot) ASNC\_ECOLI P03809 ESCHERICHIA COLI 562 -11533209 131515 asnc regulatory protein asnc (cl:regulatory protein asnc) (db:pir1.dat) (mp:84 min) QQECE1 A04434 Escherichia coli 562 -11533209 236980 (sr:escherichia coli, clone (minichromosome) pcm959, dna) (db:genpept-bct1) (de:e.coli replication origin (oric) and asna gene coding forasparagine synthetase a.) (nt:17k protein) (le:1501) (re:1959) (di:complement) ECOORIASN K00826 g455179 Escherichia coli 562 -11533209 7500877251 asnc::cg site no. 1... regulatory protein (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:115934) (re:116392) (di:complement) ECOUW82 L10328 g290592 Escherichia coli 562 -11533209 235310 asnc regulator for asna:asnc and gida (fn:regulator; amino acid biosynthesis: asparagine) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 341 of 400 of the completegenome.) (nt:f152; 100 pct identical to asnc\_ecoli sw: p03809) (le:3642) (re:4100) (di:complement) AE000451 AE000451 g1790182 Escherichia coli 562 -11533209 5000690523 (de:(ecoli\_3661) (pn:regulator for asna, and gida) (gn:asnc) (gtcfc:6.9) (ec:) (asnc\_ecoli) (keggfc:11.2) (rileyfc:1.4.2) (db:gtc-escherichia coli)) ECOLI\_3661 ECOLI\_3661 Escherichia coli 562 10003098

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828719	8130	30286	339	112

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828720	8131	30287	540	179

Description

6500729352 dapf:b3809 diaminopimelate epimerase (gtcfc:5.2:5.8) (ec:5.1.1.7) (keggfc:5.8) (rileyfc:1.4.2) (db:gtc-escherichia coli) b3809 b3809  
 Escherichia coli 562 -11533210 7000688916 dapf diaminopimelate epimerase (cl:diaminopimelate epimerase) (ec:5.1.1.7) (db:pir1.dat) (mp:85 min) S01913  
 B65185 Escherichia coli 562 -11533210 7500953395 dapf diaminopimelate epimerase (fn:enzyme; amino acid biosynthesis: lysine) (db:genpept-bct2) (ec:5.1.1.7) (de:escherichia coli k-12 mg1655 section 347 of 400 of the completegenome.) (nt:o275; 99 pct identical amino acid sequence and) (le:391) (re:1218) (di:direct) AE000457 AE000457 gl790242 Escherichia coli 562 -11533210 5000690478 (de:(ecoli\_3715) (pn:diaminopimelate epimerase) (gn:dapf) (gtcfc:5.8) (ec:5.1.1.7) (dapf\_ecoli) (keggfc:5.8) (rileyfc:1.4.2) (db:gtc-escherichia coli)) ECOLI\_3715 ECOLI\_3715 Escherichia coli 562 10124102

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828722	8132	30288	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828729	8133	30289	396	131

Description

GTC ORF with score 194 to: (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 220 of 400 of the completegenome.) (nt:o298; this 298 aa orf is 56 pct identical (0 gaps)) (le:4337) (re:5233) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828730	8134	30290	519	172

Description

6500729353 metr:b3828 trans-activator of mete and meth:transcriptional activator protein metr (gtcfc:5.2:10.2) (keggfc:14.2) (rileyfc:1.4.2) (db:gtc-escherichia coli) b3828 b3828 Escherichia coli 562 -11533211 83592 metr (de:transcriptional activator protein metr) (db:swissprot) METR\_ECOLI P19797 ESCHERICHIA COLI 562 -11533211 164068 metr trans-activator of mete and meth:metr protein (db:pir2.dat) (mp:86 min.) A36066 A36066 Escherichia coli 562 -11533211 7500885563 metr (sr:escherichia coli (clone psre562, strain k-12) dna) (db:genpept-bct1) (de:e.coli (clone prse562) metr gene, complete cds.) (le:40) (re:993) (di:direct) ECOMETR M37630 g146849 Escherichia coli 562 -11533211 235135 metr regulator for mete and meth (fn:regulator; amino acid biosynthesis: methionine) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 348 of 400 of the completegenome.) (nt:f317; 99 pct identical amino acid sequence and) (le:7061) (re:8014) (di:complement) AE000458 AE000458 g1790262 Escherichia coli 562 -11533211 5000690524 (de:(ecoli\_3734) (pn:regulator for mete and meth) (gn:metr) (gtcfc:6.9) (ec:) (metr\_ecoli) (keggfc:11.2) (rileyfc:1.4.2) (db:gtc-escherichia coli)) ECOLI\_3734 ECOLI\_3734 Escherichia coli 562 10025806

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828734	8135	30291	420	140

Description

6500729354 mete:b3829 5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase:5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase:methionine synthase:vitamin-b12 independent isozyme (gtcfc:5.2:5.4) (ec:2.1.1.14) (keggfc:5.4) (rileyfc:1.4.2) (db:gtc-escherichia coli) b3829 b3829 Escherichia coli 562 -11533212 7000688854 mete 5-methyltetrahydropteroyltriglutamate--homocysteine s-methyltransferase::cobalamin-independent methionine synthase:tetrahydropteroylglutamate methyltransferase (cl:cobalamin-independent methionine synthase) (ec:2.1.1.14) (db:pir1.dat) A42863 F65187 Escherichia coli 562 -11533212 7500953226 mete tetrahydropteroyltriglutamate methyltransferase (fn:enzyme; amino acid biosynthesis: methionine) (db:genpept-bct2) (ec:2.1.1.14) (de:escherichia coli k-12 mg1655 section 348 of 400 of the completegenome.) (nt:o753; 99 pct identical to mete\_ecoli sw: p25665; cg) (le:8251) (re:10512) (di:direct) AE000458 AE000458 g2367304 Escherichia coli 562 -11533212

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828743	8136	30292	237	78

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828744	8137	30293	1470	490
<u>Description</u>				
6500729355 metj:b3938 metf aporepressor:met repressor:met regulon regulatory protein metj (gtcfc:5.2) (keggfc:14.2) (rileyfc:1.4.2) (db:gtc-escherichia coli) b3938 b3938 Escherichia coli 562 -11533213 131517 metj met regulon regulatory protein metj (cl:metj protein) (db:pir1.dat) (mp:89 min) RGECMJ A22660 Escherichia coli 562 -11533213 235129 (sr:e.coli dna) (db:genpept-bct1) (de:e.coli regulon aporepressor mutant metj193 allele, complete cds.) (le:1) (re:318) (di:direct) ECOMETJ123 M38202 g146835 Escherichia coli 562 -11533213 237155 (sr:e.coli dna, clone pmad4) (db:genpept-bct1) (de:e.coli metj gene coding for a regulatory protein.) (nt:regulatory protein metj) (le:286) (re:603) (di:direct) ECOMETJA M12869 g146837 Escherichia coli 562 -11533213 7500953664 metj metf aporepressor (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 508) (le:89711) (re:90028) (di:complement) ECOUW87 L19201 g305041 Escherichia coli 562 -11533213 235128 metj repressor of all met genes but metf (fn:regulator; amino acid biosynthesis: methionine) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 357 of 400 of the completegenome.) (nt:f105; 100 pct identical to metj_ecoli sw: p08338;) (le:15204) (re:15521) (di:complement) AE000467 AE000467 g1790373 Escherichia coli 562 -11533213 5000690525 (de:(ecoli_3836) (pn:repressor of all met genes but metf) (gn:metj) (gtcfc:6.9) (ec:) (metj_ecoli) (keggfc:11.2) (rileyfc:1.4.2) (db:gtc-escherichia coli)) ECOLI_3836 ECOLI_3836 Escherichia coli 562 10068142				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828746	8138	30294	246	81
<u>Description</u>				
6500729356 metl:metm:b3940 aspartokinase ii/homoserine dehydrogenase ii:aspartokinase ii / homoserine dehydrogenase ii (gtcfc:5.2:5.3:5.8) (keggfc:5.3:5.8) (rileyfc:1.4.2) (db:gtc-escherichia coli) b3940 b3940 Escherichia coli 562 -11533214 123867 metl metl bifunctional enzyme:aspartokinase ii/homoserine dehydrogenase ii (cl:thra bifunctional enzyme:aspartate kinase homology:homoserine dehydrogenase homology) (db:pir1.dat) (mp:89 min) DEECK2 S40883 Escherichia coli 562 -11533214 7500953266 metl aspartokinase ii/homoserine dehydrogenase ii (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:bifunctional enzyme; cg site no. 506) (le:91468) (re:93900) (di:direct) ECOUW87 L19201 g305043 Escherichia coli 562 -11533214 237157 metl aspartokinase ii and homoserine dehydrogenase (fn:enzyme; amino acid biosynthesis: methionine) (db:genpept-bct2) (ec:2.7.2.4) (de:escherichia coli k-12 mg1655 section 358 of 400 of the completegenome.) (nt:o810; 100 pct identical to ak2h_ecoli sw:) (le:1386) (re:3818) (di:direct) AE000468 AE000468 g1790376 Escherichia coli 562 -11533214 5000690450 (de:(ecoli_3838) (pn:aspartokinase ii, and homoserine dehydrogenase ii) (gn:metl) (gtcfc:5.3:5.8) (ec:2.7.2.4) (ak2h_ecoli) (keggfc:5.3:5.8) (rileyfc:1.4.2) (db:gtc-escherichia coli)) ECOLI_3838 ECOLI_3838 Escherichia coli 562 10065979				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828752	8139	30295	612	203

Description

6500729357 meth:b4019 b12-dependent homocysteine-n5-methyltetrahydrofolate transmethyrase:5-methyltetrahydrofolate--homocysteine methyltransferase:methionine synthase:vitamin-b12 dependent isozyme (gtcfc:10.7:9.6:5.2:5.4) (ec:2.1.1.13) (keggfc:5.4:9.8) (rileyfc:1.4.2) (db:gtc-escherichia coli) (gtcfc:metabolism of macromolecules-protein translation and modification:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthes... b4019 b4019 Escherichia coli 562 -11533215 7000688853 meth 5-methyltetrahydrofolate--homocysteine s-methyltransferase::methionine synthase:tetrahydropteroylglutamate methyltransferase (cl:cobalamin-dependent methionine synthase) (ec:2.1.1.13) (db:pir1.dat) (mp:91 min) XYECPMH B65209 Escherichia coli 562 -11533215 7500953225 meth b12-dependent (fn:enzyme; amino acid biosynthesis: methionine) (db:genpept-bct2) (ec:2.1.1.13) (de:escherichia coli k-12 mg1655 section 365 of 400 of the completegenome.) (nt:ol227; 99 pct identical amino acid sequence and) (le:1184) (re:4867) (di:direct) AE000475 AE000475 g1790450 Escherichia coli 562 -11533215 5000690458 (de:(ecoli\_3905) (pn:b12-dependent homocysteine-n5-methyltetrahydrofolate transmethyrase, repressor of mete and metf) (gn:meth) (gtcfc:5.4:9.6) (ec:2.1.1.13) (meth\_ecoli) (keggfc:5.4:9.8) (rileyfc:1.4.2) (db:gtc-escherichia coli) ECOLI\_3905 ECOLI\_3905 Escherichia coli 562 10124134

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828753	8140	30296	369	123

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828757	8141	30297	327	108

#### Description

6500729358 lysc:apk:b4024 lysine-sensitive aspartokinase iii:aspartate kinase iii (gtcfc:5.2:5.3:5.8) (ec:2.7.2.4) (keggfc:5.3:5.8) (rileyfc:1.4.2) (db:gtc-escherichia coli) b4024 b4024 Escherichia coli 562 -11533216 59022 lysc:apk (ec:2.7.2.4) (de:iii) (db:swissprot) AK3\_ECOLI P08660 ESCHERICHIA COLI 562 -11533216 7000684547 lysc aspartate kinase:iii:lysine-sensitive:aspartokinase iii (cl:aspartate kinase:aspartate kinase homology) (ec:2.7.2.4) (db:pir1.dat) (mp:91 min) KIECD3 G65209 Escherichia coli 562 -11533216 237230 lysc aspartokinase iii:lysine sensitive (fn:enzyme; amino acid biosynthesis: lysine) (db:genpept-bct2) (ec:2.7.2.4) (de:escherichia coli k-12 mg1655 section 365 of 400 of the completegenome.) (nt:f449; 100 pct identical to ak3\_ecoli sw: p08660; cg) (le:9240) (re:10589) (di:complement) AE000475 AE000475 g1790455 Escherichia coli 562 -11533216 7500876712 lysc aspartokinase iii (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (ec:2.7.2.4) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 539) (le:97126) (re:98475) (di:complement) ECOUW89 U00006 g396359 Escherichia coli 562 -11533216 5000690451 (de:(ecoli\_3910) (pn:aspartokinase iii, lysine sensitive) (gn:lysc) (gtcfc:5.3:5.8) (ec:2.7.2.4) (ak3\_ecoli) (keggfc:5.3:5.8) (rileyfc:1.4.2) (db:gtc-escherichia coli)) ECOLI\_3910 ECOLI\_3910 Escherichia coli 562 10001766

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828771	8142	30298	201	66

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828773	8143	30299	228	75

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828780	8144	30300	468	155

Description

6500729359 avta:b3572 valine--pyruvate aminotransferase:transaminase  
c:alanine--valine transaminase (gtcfc:5.2:5.7) (ec:2.6.1.66) (keggfc:5.7)  
(rileyfc:1.4.6) (db:gtc-escherichia coli) b3572 b3572 Escherichia coli 562  
-11533217 61240 avta (ec:2.6.1.66) (de:(alanine--valine transaminase))  
(db:swissprot) AVTA\_ECOLI P09053 ESCHERICHIA COLI 562 -11533217 163835 avta  
valine--pyruvate transaminase::hypothetical protein o417 (ec:2.6.1.66)  
(db:pir2.dat) S47793 S47793 Escherichia coli 562 -11533217 7500877617  
(sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda)  
(db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.)  
(nt:o417) (le:153956) (re:155209) (di:direct) ECOUW76 U00039 g466710  
Escherichia coli 562 -11533217 236809 avta alanine-alpha-ketoisovalerate or  
(fn:enzyme; amino acid biosynthesis: alanine) (db:genpept-bct2)  
(ec:2.6.1.66) (de:escherichia coli k-12 mg1655 section 324 of 400 of the  
completeness genome.) (nt:o417; 100 pct identical amino acid sequence and)  
(le:8848) (re:10101) (di:direct) AE000434 AE000434 g1789996 Escherichia coli  
562 -11533217 5000690466 (de:(ecoli\_3492)  
(pn:alanine-alpha-ketoisovalerate:or valine-pyruvate transaminase,  
transaminase c) (gn:avta) (gtcfc:5.7) (ec:2.6.1.66) (avta\_ecoli)  
(keggfc:5.7) (rileyfc:1.4.6) (db:gtc-escherichia coli)) ECOLI\_3492  
ECOLI\_3492 Escherichia coli 562 10003951

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828806	8145	30301	282	93

Description

6500729360 beta:b0311 choline dehydrogenase:chd (gtcfc:5.3:12.11)  
(ec:1.1.99.1) (keggfc:5.3) (rileyfc:4.6.0) (db:gtc-escherichia coli) b0311  
b0311 Escherichia coli 562 -11533218 232448 beta (ec:1.1.99.1) (de:choline  
dehydrogenase, (chd)) (db:swissprot) BETA\_ECOLI P17444 ESCHERICHIA COLI 562  
-11533218 7500877758 beta choline dehydrogenase:beta (cl:alcohol oxidase)  
(ec:1.1.99.1) (db:pir1.dat) (mp:7.5 min) S10901 S15182 Escherichia coli 562  
-11533218 5000690430 (db:genpept-bct1) (de:escherichia coli bett, beti,  
betb and beta genes.) (nt:beta gene product (aa 1-556)) (le:5503) (re:7173)  
(di:direct) ECBET X52905 g581047 Escherichia coli 562 -11533218 7500877760  
beta choline dehydrogenase (fn:oxidation of choline) (sr:escherichia coli  
(strain k-12) dna) (db:genpept-bct1) (de:e.coli choline dehydrogenase (beta)  
gene, complete cds.) (le:64) (re:1734) (di:direct) ECOBETA M77738 g145402  
Escherichia coli 562 -11533218 233888 beta choline dehydrogenase:a  
flavoprotein (fn:enzyme; osmotic adaptation) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 28 of 400 of the completeness genome.)  
(nt:f556; 100 pct identical to beta\_ecoli sw:) (le:949) (re:2619)  
(di:complement) AE000138 AE000138 g1786503 Escherichia coli 562 -11533218  
61586 beta (ec:1.1.99.1) (de:choline dehydrogenase, (chd)) (db:swissprot)  
BETA\_ECOLI P17444 ESCHERICHIA COLI 562 -11533218

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828809	8146	30302	825	274
<u>Description</u>				
6500729361 betb:b0312 betaine aldehyde dehydrogenase:badh (gtcfc:5.3:12.11:1.4) (ec:1.2.1.8) (keggfc:5.3) (rileyfc:4.6.0) (db:gtc-escherichia coli) b0312 b0312 Escherichia coli 562 -11533219 162785 betb betaine-aldehyde dehydrogenase::betb protein (cl:aldehyde dehydrogenase (nad+):aldehyde dehydrogenase homology) (ec:1.2.1.8) (db:pir1.dat) (mp:7.5 min) S15181 S15181 Escherichia coli 562 -11533219 7500953184 (db:genpept-bct1) (de:escherichia coli bett, beti, betb and beta genes.) (nt:betb gene product (aa 1-490)) (le:4017) (re:5489) (di:direct) ECBET X52905 g48718 Escherichia coli 562 -11533219 232447 betb nad+-dependent betaine aldehyde dehydrogenase (fn:enzyme; osmotic adaptation) (db:genpept-bct2) (ec:1.2.1.8) (de:escherichia coli k-12 mg1655 section 28 of 400 of the completegenome.) (nt:f490; 100 pct identical to dhab_ecoli sw: p17445) (le:2633) (re:4105) (di:complement) AE000138 AE000138 g1786504 Escherichia coli 562 -11533219 5000690431 (de:(ecoli_296) (pn:nad) (gn:betb) (gtcfc:5.3) (ec:1.2.1.8) (dhab_ecoli) (keggfc:5.3) (rileyfc:4.6.0) (db:gtc-escherichia coli)) ECOLI_296 ECOLI_296 Escherichia coli 562 10065551				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828810	8147	30303	210	70

Description

6500729362 sers:b0893 seryl-trna synthetase:serine--trna ligase:serrs  
 (gtcfc:10.6:5.3) (ec:6.1.1.11) (keggfc:5.3:10.1:10.2) (rileyfc:3.1.5)  
 (db:gtc-escherichia coli) b0893 b0893 Escherichia coli 562 -11533220  
 7500892577 sers (ec:6.1.1.11) (de:seryl-trna synthetase, (serine--trna  
 ligase) (serrs)) (db:swissprot) SYS\_ECOLI P09156 ESCHERICHIA COLI 562  
 -11533220 125915 sers serine--trna ligase::seryl-trna synthetase  
 (cl:serine--trna ligase) (ec:6.1.1.11) (db:pir1.dat) (mp:20 min) YSEC A26400  
 Escherichia coli 562 -11533220 223258 sers serine-trna ligase  
 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #215)  
 (db:genpept-bct1) (de:escherichia coli genomic dna.(20.0 - 20.3 min).)  
 (le:8611) (re:9903) (di:direct) D90727 D90727 g1651420 Escherichia coli 562  
 -11533220 5000690432 (db:genpept-bct1) (de:e. coli sers gene for seryl-trna  
 synthetase.) (nt:seryl-trna synthetase) (le:337) (re:1629) (di:direct)  
 ECSERS X05017 g42950 Escherichia coli 562 -11533220 238242 sers serine trna  
 synthetase:also charges (fn:enzyme; aminoacyl trna synthetases, trna)  
 (db:genpept-bct2) (ec:6.1.1.11) (de:escherichia coli k-12 mg1655 section 81  
 of 400 of the completegenome.) (nt:o430; 100 pct identical to sys\_ecoli sw:  
 p09156) (le:7136) (re:8428) (di:direct) AE000191 AE000191 g1787120  
 Escherichia coli 562 -11533220 7502851897 sers serine-trna ligase ec  
 6.1.1.11 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #215)  
 (db:genpept) (de:escherichia coli genomic dna. (20.1 - 20.4 min).)  
 (nt:orf\_id:o215#6; similar to pir accession number) (le:8611) (re:9903)  
 (di:direct) D90727 D90727 g1651420 Escherichia coli 562 -11533220 100176  
 sers (ec:6.1.1.11) (de:seryl-trna synthetase, (serine--trna ligase) (serrs))  
 (db:swissprot) SYS\_ECOLI P09156 ESCHERICHIA COLI 562 -11533220

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828818	8148	30304	282	94

# Description

6500729363 serc:pdx:f:b0907 phosphoserine aminotransferase (gtcfc:5.3:9.3) (ec:2.6.1.52) (keggfc:5.3:9.3) (rileyfc:1.4.3) (db:gtc-escherichia coli) (gtcfc:l-amino acid metabolism-glycine--serine and threonine metabolism:metabolism of cofactors and vitamins-pyridoxine metabolism (vitamin b6)) (keggfc:amino acid... b0907 b0907 Escherichia coli 562 -11533221 7000689084 serc:pdx:f phosphoserine transaminase (cl:phosphoserine aminotransferase) (ec:2.6.1.52) (db:pir2.dat) B64830 B64830 Escherichia coli 562 -11533221 223266 serc phosphoserine transaminase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #216) (db:genpept-bct1) (de:escherichia coli genomic dna. (20.3 - 20.7 min).) (le:13346) (re:14434) (di:direct) D90728 D90728 g1651429 Escherichia coli 562 -11533221 223272 serc phosphoserine transaminase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #217) (db:genpept-bct1) (de:escherichia coli genomic dna. (20.4 - 20.8 min).) (le:5813) (re:6901) (di:direct) D90729 D90729 g1651436 Escherichia coli 562 -11533221 7500954060 serc 3-phosphoserine aminotransferase (fn:enzyme; amino acid biosynthesis: serine) (db:genpept-bct2) (ec:2.6.1.52) (de:escherichia coli k-12 mg1655 section 83 of 400 of the completegenome.) (nt:o362; 99 pct identical to serc\_ecoli sw: p23721) (le:982) (re:2070) (di:direct) AE000193 AE000193 g1787136 Escherichia coli 562 -11533221 5000690433 serc phosphoserine transaminase ec 2.6.1.52 . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #216) (db:genpept) (de:escherichia coli genomic dna. (20.4 - 20.8 min).) (nt:orf\_id:o217#4; similar to pir accession number) (le:13346) (re:14434) (di:direct) D90728 D90728 g1651429 Escherichia coli 562 -11533221 7502851898 serc phosphoserine transaminase ec 2.6.1.52 . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #217) (db:genpept) (de:escherichia coli genomic dna. (20.5 - 20.9 min).) (nt:orf\_id:o217#4; similar to pir accession number) (le:5813) (re:6901) (di:direct) D90729 D90729 g1651436 Escherichia coli 562 -11533221



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828819	8149	30305	570	190

Description

6500729364 sola:b1059 hypothetical protein:putative sarcosine oxidase  
(gtcfc:5.3:14.1) (ec:1.5.3.1) (keggfc:5.3) (rileyfc:5.7.0)  
(db:gtc-escherichia coli) b1059 b1059 Escherichia coli 562 -11533222 120435  
sola (ec:1.5.3.1) (de:putative sarcosine oxidase,) (db:swissprot) SAOX\_ECOLI  
P40874 ESCHERICHIA COLI 562 -11533222 7000686554 sola probable sarcosine  
oxidase (cl:sarcosine oxidase) (ec:1.5.3.-) (db:pir2.dat) JC5371 JC5371  
Escherichia coli 562 -11533222 7500891300 sola sola:a sarcosine  
oxidase-like protein (sr:escherichia coli (strain:k-12, sub\_strain:w3110)  
dna) (db:genpept-bct1) (de:escherichia coli dini and sola genes for dini and  
sola, completecds.) (le:1768) (re:2886) (di:direct) ECODINI D31709 g1236737  
Escherichia coli 562 -11533222 234153 sola sarcosine oxidase-like protein  
(fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli  
k-12 mg1655 section 97 of 400 of the completegenome.) (nt:f372; this 372 aa  
orf is 43 pct identical (10 gaps)) (le:2804) (re:3922) (di:complement)  
AE000207 AE000207 g1787298 Escherichia coli 562 -11533222 5000691977 soxa  
sarcosine oxidase ec 1.5.3.1 . (sr:escherichia coli(strain:k12) dna,  
clone:kohara clone #232) (db:genpept) (de:escherichia coli genomic dna.  
(23.8 - 24.2 min).) (nt:orf\_id:o233#7; similar to swissprot accession)  
(le:16088) (re:17206) (di:complement) D90742 D90742 g4062632 Escherichia  
coli 562 -11533222 7502851899 soxa sarcosine oxidase ec 1.5.3.1 .  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #233) (db:genpept)  
(de:escherichia coli genomic dna. (24.1 - 24.5 min).) (nt:orf\_id:o233#7;  
similar to swissprot accession) (le:5834) (re:6952) (di:complement) D90743  
D90743 g4062640 Escherichia coli 562 -11533222

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828832	8150	30306	183	60

Description

6500729365 thrs:b1719 threonyl-trna synthetase:threonine--trna ligase:thrrs (gtcfc:10.6:5.3) (ec:6.1.1.3) (keggfc:5.3:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli) b1719 b1719 Escherichia coli 562 -11533223 100202 thrs (ec:6.1.1.3) (de:(thrrs)) (db:swissprot) SYT\_ECOLI P00955 ESCHERICHIA COLI 562 -11533223 7000686731 thrs threonine--trna ligase::threonyl-trna synthetase (cl:threonine--trna ligase) (ec:6.1.1.3) (db:pir1.dat) (mp:38 min) SYECTT G64930 Escherichia coli 562 -11533223 224177 thrs threonine--trna ligase ec 6.1.1.3 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #323(38.6-39.0 min.)) (nt:orf\_id:o324#1; similar to (pir accession number) (le:10227) (re:12155) (di:complement) D90814 D90814 g1742811 Escherichia coli 562 -11533223 224183 thrs threonine--trna ligase ec 6.1.1.3 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #324(38.8-39.1 min.)) (nt:orf\_id:o324#1; similar to (pir accession number) (le:172) (re:2100) (di:complement) D90815 D90815 g1742818 Escherichia coli 562 -11533223 300836 thrs threonine trna synthetase (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:6.1.1.3) (de:escherichia coli k-12 mg1655 section 157 of 400 of the completegenome.) (nt:f642; 99 pct identical to syt\_ecoli sw: p00955; cg) (le:625) (re:2553) (di:complement) AE000267 AE000267 g1788013 Escherichia coli 562 -11533223 5000690434 (de:(ecoli\_1676) (pn:threonine trna synthetase) (gn:thrs) (gtcfc:5.3:10.6) (ec:6.1.1.3) (syt\_ecoli) (keggfc:5.3:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli)) ECOLI\_1676 ECOLI\_1676 Escherichia coli 562 10119790

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828837	8151	30307	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828838	8152	30308	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828841	8153	30309	411	136

Description

6500729366 sdaa:b1814 l-serine dehydratase 1:l-serine deaminase 1:sdh  
1:l-sd1 (gtcfc:5.3:5.5:6.6) (ec:4.2.1.13) (keggfc:5.3:5.5) (rileyfc:1.1.2)  
(db:gtc-escherichia coli) b1814 b1814 Escherichia coli 562 -11533224 98264  
sdaa (ec:4.2.1.13) (de:(l-sd1)) (db:swissprot) SDHL\_ECOLI P16095 ESCHERICHIA  
COLI 562 -11533224 7000686576 sdaa l-serine dehydratase:1:l-serine  
deaminase 1 (cl:microbial l-serine dehydratase) (ec:4.2.1.13) (db:pir1.dat)  
DWECL F64942 Escherichia coli 562 -11533224 224302 sdaa l-serine  
dehydratase 1 ec 4.2.1.13 l-serine (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #334(40.6-41.0 min.)) (nt:orf\_id:o334#6; similar to (swissprot  
accession) (le:9638) (re:11002) (di:direct) D90825 D90825 g1736451  
Escherichia coli 562 -11533224 300944 sdaa l-serine deaminase (sr:e.coli  
k12 dna, clone pmes22) (db:genpept-bct1) (de:e.coli l-serine deaminase  
(sdaa) gene, complete cds.) (nt:gtg start) (le:645) (re:2009) (di:direct)  
ECOSDAA M28695 g290464 Escherichia coli 562 -11533224 235955 sdaa l-serine  
deaminase (fn:enzyme; degradation of small molecules: amino)  
(db:genpept-bct2) (ec:4.2.1.13) (de:escherichia coli k-12 mg1655 section 165  
of 400 of the completegenome.) (nt:o454; 100 pct identical to sdhl\_ecoli sw:  
p16095;) (le:8936) (re:10300) (di:direct) AE000275 AE000275 g1788116  
Escherichia coli 562 -11533224 5000690435 (de:(ecoli\_1771) (pn:l-serine  
deaminase) (gn:sdaa) (gtcfc:5.3:5.5) (ec:4.2.1.13) (sdhl\_ecoli)  
(keggfc:5.3:5.5) (rileyfc:1.1.2) (db:gtc-escherichia coli)) ECOLI\_1771  
ECOLI\_1771 Escherichia coli 562 10040143

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828842	8154	30310	477	158

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828851	8155	30311	834	278

Description

6500729367 dsda:b2366 d-serine dehydratase:d-serine deaminase  
 (gtcfc:5.3:6.6) (ec:4.2.1.14) (keggfc:5.3) (rileyfc:1.1.2)  
 (db:gtc-escherichia coli) b2366 b2366 Escherichia coli 562 -11533225 98263  
 dsda (ec:4.2.1.14) (de:d-serine dehydratase, (d-serine deaminase))  
 (db:swissprot) SDHD\_ECOLI P00926 ESCHERICHIA COLI 562 -11533225 7000686575  
 dsda d-serine dehydratase (cl:d-serine dehydratase) (ec:4.2.1.14)  
 (db:pir1.dat) (mp:51 min) DWECS C65010 Escherichia coli 562 -11533225  
 224916 dsda d-serine dehydratase ec 4.2.1.14 (sr:escherichia coli  
 (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
 (de:e.coli genomic dna, kohara clone #411(53.2-53.6 min.)) (nt:similar to  
 (pir accession number a31784)) (le:12211) (re:13539) (di:direct) D90866  
 D90866 g1799768 Escherichia coli 562 -11533225 224924 dsda d-serine  
 dehydratase ec 4.2.1.14 (sr:escherichia coli (strain:k12) dna,  
 clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
 kohara clone #412(53.4-53.8 min.)) (nt:similar to (pir accession number  
 a31784)) (le:2970) (re:4298) (di:direct) D90867 D90867 g1799777 Escherichia  
 coli 562 -11533225 7500891421 dsda d-serine dehydratase deaminase  
 (fn:enzyme; degradation of small molecules: amino) (db:genpept-bct2)  
 (ec:4.2.1.14) (de:escherichia coli k-12 mg1655 section 214 of 400 of the  
 completengenome.) (nt:o442; 99 pct identical to sdhd\_ecoli sw: p00926)  
 (le:8621) (re:9949) (di:direct) AE000324 AE000324 g1788708 Escherichia coli  
 562 -11533225 5000690436 (de:(ecoli\_2314) (pn:d-serine deaminase) (gn:dsda)  
 (gtcfc:5.3) (ec:4.2.1.14) (sdhd\_ecoli) (keggfc:5.3) (rileyfc:1.1.2)  
 (db:gtc-escherichia coli)) ECOLI\_2314 ECOLI\_2314 Escherichia coli 562  
 10120149

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828878	8156	30312	1815	605

#### Description

6500729368 pssa:pss:b2585 cdp-diacylglycerol-serine  
o-phosphatidyltransferase:cdp-diacylglycerol--serine  
o-phosphatidyltransferase:phosphatidylserine synthase (gtcfc:5.3:8.1)  
(ec:2.7.8.8) (keggfc:5.3:8.1) (rileyfc:3.1.11) (db:gtc-escherichia coli)  
b2585 b2585 Escherichia coli 562 -11533226 7000689110 pssa:pss  
cdpdiacylglycerol--serine o-phosphatidyltransferase::phosphatidylserine  
synthase (cl:escherichia coli cdpdiacylglycerol--serine  
o-phosphatidyltransferase) (ec:2.7.8.8) (db:pir2.dat) H65036 H65036  
Escherichia coli 562 -11533226 7500954174 pssa phosphatidylserine  
synthase:phospholipid (fn:enzyme; macromolecule synthesis, modification:)  
(db:genpept-bct2) (ec:2.7.8.8) (de:escherichia coli k-12 mg1655 section 235  
of 400 of the completegenome.) (nt:o452; 98 pct identical to pss\_ecoli sw:  
p23830) (le:86) (re:1444) (di:direct) AE000345 AE000345 g1788940 Escherichia  
coli 562 -11533226 5000690437 (de:(ecoli\_2525) (pn:phosphatidylserine  
synthase; phospholipid synthesis) (gn:pssa) (gtcfc:5.3:8.1) (ec:2.7.8.8)  
(pss\_ecoli) (keggfc:5.3:8.1) (rileyfc:3.1.11) (db:gtc-escherichia coli))  
ECOLI\_2525 ECOLI\_2525 Escherichia coli 562 10123740

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828886	8157	30313	819	272

#### Description

6500729369 sdab:b2797 l-serine dehydratase 2:l-serine deaminase 2:sdh  
2:l-sd2 (gtcfc:5.3:5.5:6.6) (ec:4.2.1.13) (keggfc:5.3:5.5) (rileyfc:1.1.2)  
(db:gtc-escherichia coli) b2797 b2797 Escherichia coli 562 -11533227 98268  
sdab (ec:4.2.1.13) (de:(l-sd2)) (db:swissprot) SDHM\_ECOLI P30744 ESCHERICHIA  
COLI 562 -11533227 7000686578 sdab l-serine dehydratase:2:l-serine  
deaminase 2 (cl:microbial l-serine dehydratase) (ec:4.2.1.13) (db:pir2.dat)  
A65062 A65062 Escherichia coli 562 -11533227 7500891424 sdab l-serine  
dehydratase 2 l-serine deaminase 2 (db:genpept-bct1) (ec:4.2.1.13)  
(de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:cg  
site no. 33324; orf\_o455) (le:11131) (re:12498) (di:direct) ECU29581 U29581  
g882692 Escherichia coli 562 -11533227 239371 sdab l-serine dehydratase  
deaminase:l-sd2 (fn:enzyme; degradation of small molecules: amino)  
(db:genpept-bct2) (ec:4.2.1.13) (de:escherichia coli k-12 mg1655 section 253  
of 400 of the completegenome.) (nt:o455; 97 pct identical to sdhm\_ecoli sw:  
p30744; cg) (le:7289) (re:8656) (di:direct) AE000363 AE000363 g1789161  
Escherichia coli 562 -11533227 5000690438 (de:(ecoli\_2728) (pn:l-serine  
deaminase, l-sd2) (gn:sdab) (gtcfc:5.3:5.5) (ec:4.2.1.13) (sdhm\_ecoli)  
(keggfc:5.3:5.5) (rileyfc:1.1.2) (db:gtc-escherichia coli)) ECOLI\_2728  
ECOLI\_2728 Escherichia coli 562 10123839

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501828894	8158	30314	564	188

Description

6500729370 sera:b2913 d-3-phosphoglycerate dehydrogenase:pgdh (gtcfc:5.3) (ec:1.1.1.95) (keggfc:5.3) (rileyfc:1.4.3) (db:gtc-escherichia coli) b2913 b2913 Escherichia coli 562 -11533228 122569 sera phosphoglycerate dehydrogenase (cl:phosphoglycerate dehydrogenase) (ec:1.1.1.95) (db:pir1.dat) (mp:63 min) DEECPG A25200 Escherichia coli 562 -11533228 244276 sera d-3-phosphoglycerate dehydrogenase (db:genpept-bct1) (ec:1.1.1.95) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:cg site no. 173) (le:11569) (re:12801) (di:complement) ECU28377 U28377 g882442 Escherichia coli 562 -11533228 325822 sera phosphoglycerate dehydrogenase (sr:e.coli k12 genomic dna, clone pgt17) (db:genpept-bct1) (ec:1.1.1.95) (de:escherichia coli d-3-phosphoglycerate dehydrogenase (sera) gene,complete cds, clone pgt17.) (le:1) (re:1233) (di:direct) L29397 L29397 g459755 Escherichia coli 562 -11533228 4000709997 sera d-3-phosphoglycerate dehydrogenase (fn:enzyme; amino acid biosynthesis: serine) (db:genpept-bct2) (ec:1.1.1.95) (de:escherichia coli k-12 mg1655 section 264 of 400 of the completegenome.) (nt:f410; 100 pct identical to sera\_ecoli sw: p08328;) (le:8108) (re:9340) (di:complement) AE000374 AE000374 g1789279 Escherichia coli 562 -11533228 5000690440 sera (db:genpept-pat) (de:e. coli sera gene.) (le:1) (re:1233) (di:direct) A25268 A25268 g1247677 Escherichia coli 562 -11533228 7502851900 sera d-3-phosphoglyceratdehydrogenase (db:genpept-pat) (ec:1.1.1.95) (de:sequence 13 from patent wo9408031.) (le:1) (re:1232) (di:direct) A37877 A37877 g2294548 Escherichia coli 562 -11533228 239126 sera d-3-phosphoglycerate dehydrogenase (db:genpept-bct1) (ec:1.1.1.95) (de:escherichia coli k-12 mg1655 section 264 of 400 of the completegenome.) (nt:f410; 100 pct identical to sera\_ecoli sw: p08328;) (le:8108) (re:9340) (di:complement) ECAE000374 AE000374 g1789279 Escherichia coli 562 -11533228

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828911	8159	30315	654	217

#### Description

6500729371 yhap:b3111 putative l-serine dehydratase part 2:l-serine deaminase:sdh (gtcfc:5.3:5.5:14.3) (ec:4.2.1.13) (keggfc:5.3:5.5) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3111 b3111 Escherichia coli 562 -11533229 98270 yhap (ec:4.2.1.13) (de:deaminase) (sdh)) (db:swissprot) SDHY\_ECOLI P42629 ESCHERICHIA COLI 562 -11533229 7000686580 yhap hypothetical l-serine dehydratase carboxyl-terminal homolog (db:pir2.dat) D65100 D65100 Escherichia coli 562 -11533229 7500891426 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf\_f275) (le:39041) (re:39868) (di:complement) ECOUW67 U18997 g606052 Escherichia coli 562 -11533229 236351 yhap putative l-serine dehydratase (fn:putative enzyme; not classified) (db:genpept-bct2) (ec:4.2.1.13) (de:escherichia coli k-12 mg1655 section 282 of 400 of the completegenome.) (nt:f275; 100 pct identical amino acid sequence and) (le:9430) (re:10257) (di:complement) AE000392 AE000392 g1789498 Escherichia coli 562 -11533229 5000690441 (de:(ecoli\_3036) (pn:putative l-serine dehydratase part 2:l-serine deaminase:sdh) (gn:yhap) (gtcfc:5.3:5.5) (ec:4.2.1.13) (sdhy\_ecoli) (keggfc:5.3:5.5) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_3036 ECOLI\_3036 Escherichia coli 562 10040149

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828913	8160	30316	1254	417

#### Description

6500729372 yhaq:b3112 putative l-serine dehydratase part 1:l-serine deaminase:sdh (gtcfc:5.3:5.5:14.3) (ec:4.2.1.13) (keggfc:5.3:5.5) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3112 b3112 Escherichia coli 562 -11533230 98269 yhaq (ec:4.2.1.13) (de:deaminase) (sdh)) (db:swissprot) SDHX\_ECOLI P42630 ESCHERICHIA COLI 562 -11533230 7000686579 yhaq hypothetical l-serine dehydratase amino-terminal homolog (db:pir2.dat) E65100 E65100 Escherichia coli 562 -11533230 7500891425 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf\_f140) (le:39988) (re:40410) (di:complement) ECOUW67 U18997 g606053 Escherichia coli 562 -11533230 236352 yhaq putative l-serine dehydratase (fn:putative enzyme; not classified) (db:genpept-bct2) (ec:4.2.1.13) (de:escherichia coli k-12 mg1655 section 283 of 400 of the completegenome.) (nt:f140; 100 pct identical amino acid sequence and) (le:90) (re:512) (di:complement) AE000393 AE000393 g1789500 Escherichia coli 562 -11533230 5000690442 (de:(ecoli\_3037) (pn:putative l-serine dehydratase part 1:l-serine deaminase:sdh) (gn:yhaq) (gtcfc:5.3:5.5) (ec:4.2.1.13) (sdhx\_ecoli) (keggfc:5.3:5.5) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_3037 ECOLI\_3037 Escherichia coli 562 10040148

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828919	8161	30317	465	154

Description

6500729373 tdc b3117 catabolic threonine dehydratase:threonine dehydratase catabolic:threonine deaminase (gtcfc:5.3:6.6) (ec:4.2.1.16) (keggfc:5.3) (rileyfc:1.1.2) (db:gtc-escherichia coli) b3117 b3117 Escherichia coli 562 -11533231 7500893019 tdc b (ec:4.2.1.16) (de:threonine dehydratase catabolic, (threonine deaminase)) (db:swissprot) THD2\_ECOLI P05792 ESCHERICHIA COLI 562 -11533231 125647 tdc::tdc threonine dehydratase::biodegradative:threonine deaminase (cl:threonine dehydratase) (ec:4.2.1.16) (db:pir1.dat) (mp:67 min) DWECTD A26367 Escherichia coli 562 -11533231 236357 (sr:e.coli (strain kl227) dna, clones pec(6,61)) (db:genpept-bct1) (de:e.coli tdc locus with two genes encoding threonine dehydratase(tdc), complete cds.) (nt:threonine dehydratase 2 (ec 4.2.1.16)) (le:1197) (re:2186) (di:direct) ECOTDC M21312 g147923 Escherichia coli 562 -11533231 238331 tdc b catabolic threonine dehydratase (db:genpept-bct1) (ec:4.2.1.16) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 17587) (le:45793) (re:46782) (di:complement) ECOUW67 U18997 g606058 Escherichia coli 562 -11533231 5000690443 (db:genpept-bct1) (de:e. coli tdc operon for threonine dehydratase (ec 4.2.1.16).) (nt:tdc b gene product (aa 1 - 329)) (le:2941) (re:3930) (di:direct) ECTDCRAB X14430 g43043 Escherichia coli 562 -11533231 236070 tdc b threonine dehydratase:catabolic (fn:enzyme; degradation of small molecules: amino) (db:genpept-bct2) (ec:4.2.1.16) (de:escherichia coli k-12 mg1655 section 283 of 400 of the completegenome.) (nt:f329; cg site no. 17587; 100 pct identical) (le:5895) (re:6884) (di:complement) AE000393 AE000393 g1789505 Escherichia coli 562 -11533231 7502851901 (db:genpept) (de:e. coli tdc operon for threonine dehydratase (ec 4.2.1.16).) (nt:tdc b gene product (aa 1 - 329)) (le:2941) (re:3930) (di:direct) ECTDCRAB X14430 g43043 Escherichia coli 562 -11533231 101281 tdc b (ec:4.2.1.16) (de:threonine dehydratase catabolic, (threonine deaminase)) (db:swissprot) THD2\_ECOLI P05792 ESCHERICHIA COLI 562 -11533231



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828932	8162	30318	759	253

Description

6500729374 glysb:glysb:b3559 glycine-trna synthetase:beta subunit:glycyl-trna synthetase beta chain:glycine--trna ligase beta chain:glyrs (gtcfc:10.6:5.3) (ec:6.1.1.14) (keggfc:5.3:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli) b3559 b3559 Escherichia coli 562 -11533232 125917 glysb:glysb:b3559 glycine-trna ligase:beta chain:glycyl-trna synthetase beta chain (cl:glycine--trna ligase beta chain) (ec:6.1.1.14) (db:pir1.dat) (mp:80 min) SYECGB S47780 Escherichia coli 562 -11533232 7500953367 glysb:glysb:b3559 glycine-trna synthetase:beta subunit (sr:escherichia coli (sub\_strain mgl655, strain k-12) (library: lambda) (db:genpept-bct1) (ec:6.1.1.14) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:alternate gene name glysb; cg site no. 674) (le:136579) (re:138648) (di:complement) ECOUW76 U00039 g466697 Escherichia coli 562 -11533232 236796 glysb:glysb:b3559 glycine-trna synthetase:beta subunit (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:6.1.1.14) (de:escherichia coli k-12 mgl655 section 323 of 400 of the completegenome.) (nt:f689; 100 pct identical to sygb\_ecoli sw: p00961;) (le:3027) (re:5096) (di:complement) AE000433 AE000433 g1789982 Escherichia coli 562 -11533232 5000690445 (de:(ecoli\_3479) (pn:glycine trna synthetase, beta subunit) (gn:glysb) (gtcfc:5.3:10.6) (ec:6.1.1.14) (sygb\_ecoli) (keggfc:5.3:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli)) ECOLI\_3479 ECOLI\_3479 Escherichia coli 562 10066482

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828947	8163	30319	288	95

Description

GTC ORF with score 235 to: (sr:fission yeast strain=972) (db:genpept-pln1) (de:schizosaccharomyces pombe ars binding protein 1 (abp1) gene,complete cds.) (nt:abp1; abp1 has some similarity to human and mouse) (le:1036) (re:2604) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501828948	8164	30320	681	226

#### Description

6500729375 glyq:glysa:b3560 glycine-trna synthetase:alpha subunit:glycyl-trna synthetase alpha chain:glycine--trna ligase alpha chain:glyrs (gtcfc:10.6:5.3) (ec:6.1.1.14) (keggfc:5.3:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli) b3560 b3560 Escherichia coli 562 -11533233 100045 glyq:glys::a (ec:6.1.1.14) (de:alpha chain) (glyrs)) (db:swissprot) SYGA\_ECOLI P00960 ESCHERICHIA COLI 562 -11533233 7000686715 glyq:glys::a glycine--trna ligase:alpha chain:glycyl-trna synthetase alpha chain (cl:glycine--trna ligase alpha chain) (ec:6.1.1.14) (db:pir1.dat) (mp:80 min) SYECGA B65155 Escherichia coli 562 -11533233 7500892404 glyq glycine-trna synthetase:alpha subunit (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:alternate gene name glysa) (le:138658) (re:139569) (di:complement) ECOUW76 U00039 g466698 Escherichia coli 562 -11533233 236797 glyq glycine trna synthetase:alpha subunit (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:6.1.1.14) (de:escherichia coli k-12 mg1655 section 323 of 400 of the completegenome.) (nt:f303; 100 pct identical to syga\_ecoli sw: p00960;) (le:5106) (re:6017) (di:complement) AE000433 AE000433 g1789983 Escherichia coli 562 -11533233 5000690446 (de:(ecoli\_3480) (pn:glycine trna synthetase, alpha subunit) (gn:glyq) (gtcfc:5.3:10.6) (ec:6.1.1.14) (syga\_ecoli) (keggfc:5.3:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli)) ECOLI\_3480 ECOLI\_3480 Escherichia coli 562 10041899

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501828956	8165	30321	1605	534

#### Description

GTC ORF with score 567 to: (fn:required for disulfide bond formation in the) (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome ii cosmid c4f6.) (nt:spbc4f6.16c, len:467, similarity:saccharomyces) (le:35787) (re:37190) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501828966	8166	30322	1125	374

#### Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501828981	8167	30323	210	69

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828988	8168	30324	810	269
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828989	8169	30325	957	319
<u>Description</u>				

6500729376 tdh:b3616 threonine 3-dehydrogenase (gtcfc:5.3:6.6)  
(ec:1.1.1.103) (keggfc:5.3) (rileyfc:1.1.2) (db:gtc-escherichia coli) b3616  
b3616 Escherichia coli 562 -11533234 236853 tdh (ec:1.1.1.103)  
(de:threonine 3-dehydrogenase,) (db:swissprot) TDH\_ECOLI P07913 ESCHERICHIA  
COLI 562 -11533234 122481 tdh 1-threonine 3-dehydrogenase (cl:alcohol  
dehydrogenase:long-chain alcohol dehydrogenase homology) (ec:1.1.1.103)  
(db:pir1.dat) (mp:1 min) DEECTH A33276 Escherichia coli 562 -11533234  
5000690447 (db:genpept-bct1) (de:e. coli genes tdh and kbl.) (nt:tdh gene)  
(le:1704) (re:2729) (di:direct) ECKBLTDH X06690 g41864 Escherichia coli 562  
-11533234 7500892864 tdh threonine dehydrogenase (sr:escherichia coli  
(sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1)  
(ec:1.1.1.103) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.)  
(nt:cg site no. 17584) (le:204570) (re:205595) (di:complement) ECOUW76  
U00039 g466754 Escherichia coli 562 -11533234 233267 tdh threonine  
dehydrogenase (fn:enzyme; degradation of small molecules: amino)  
(db:genpept-bct2) (ec:1.1.1.103) (de:escherichia coli k-12 mg1655 section  
329 of 400 of the completegenome.) (nt:f341; 100 pct identical to tdh\_ecoli  
sw: p07913; cg) (le:7748) (re:8773) (di:complement) AE000439 AE000439  
gl790045 Escherichia coli 562 -11533234 100941 tdh (ec:1.1.1.103)  
(de:threonine 3-dehydrogenase,) (db:swissprot) TDH\_ECOLI P07913 ESCHERICHIA  
COLI 562 -11533234

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501828993	8170	30326	249	82
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501828998	8171	30327	342	113

Description

6500729377 ilva:b3772 threonine dehydratase biosynthetic:threonine deaminase (gtcfc:5.3:5.7) (ec:4.2.1.16) (keggfc:5.3) (rileyfc:1.4.7) (db:gtc-escherichia coli) b3772 b3772 Escherichia coli 562 -11533235 234854 ilva (ec:4.2.1.16) (de:deaminase)) (db:swissprot) THD1\_ECOLI P04968 ESCHERICHIA COLI 562 -11533235 125645 ilva threonine dehydratase::biosynthetic:l-serine dehydratase:serine deaminase:threonine deaminase (cl:threonine dehydratase) (ec:4.2.1.16) (db:pir1.dat) (mp:85 min) DWECTS B27310 Escherichia coli 562 -11533235 5000690449 ilva (db:genpept-bct1) (de:e.coli ilvgmeda operon.) (nt:threonine deaminase) (le:5504) (re:7048) (di:direct) ECILVGMED X04890 g288533 Escherichia coli 562 -11533235 7500893017 ilva threonine deaminase (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (ec:4.2.1.16) (de:e.coli ilv gene cluster encoding ilvd and ilva peptides,acetohydroxy acid synthase ii, and branched-chain amino acidaminotransferase, complete cds.) (le:5134) (re:6678) (di:dir... ECOILVGE M10313 g146462 Escherichia coli 562 -11533235 233203 ilva threonine deaminase dehydratase (fn:enzyme; amino acid biosynthesis: isoleucine,) (db:genpept-bct2) (ec:4.2.1.16) (de:escherichia coli k-12 mg1655 section 343 of 400 of the completegenome.) (nt:o514; 99 pct identical amino acid sequence and) (le:11689) (re:13233) (di:direct) AE000453 AE000453 g1790207 Escherichia coli 562 -11533235 101274 ilva (ec:4.2.1.16) (de:deaminase)) (db:swissprot) THD1\_ECOLI P04968 ESCHERICHIA COLI 562 -11533235

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829002	8172	30328	576	191

Description

6500729378 psd:b4160 phosphatidylserine decarboxylase proenzyme  
 (gtcfc:5.3:8.1) (ec:4.1.1.65) (keggfc:5.3:8.1) (rileyfc:3.1.11)  
 (db:gtc-escherichia coli) b4160 b4160 Escherichia coli 562 -11533236 69248  
 psd (ec:4.1.1.65) (de:phosphatidylserine decarboxylase proenzyme,)  
 (db:swissprot) DPSD\_ECOLI P10740 ESCHERICHIA COLI 562 -11533236 164295 psd  
 phosphatidylserine decarboxylase:precursor (ec:4.1.1.65) (db:pir2.dat)  
 (mp:95 min) A29234 A29234 Escherichia coli 562 -11533236 237368  
 phosphatidylserine decarboxylase (sr:escherichia coli (sub\_strain cs520,  
 strain k-12) (clone: plc8-47.) (db:genpept-bct1) (de:e.coli psd gene  
 encoding phosphatidylserine decarboxylase, completecds.) (nt:precursor)  
 (le:280) (re:1248) (di:direct) ECOPSD J03916 g551827 Escherichia coli 562  
 -11533236 7500880608 psd phosphatidylserine decarboxylase (db:genpept-bct1)  
 (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.)  
 (nt:cg site no. 356; ttg start codon) (le:80220) (re:81188) (di:complement)  
 ECOUW93 U14003 g537004 Escherichia coli 562 -11533236 235583 psd  
 phosphatidylserine decarboxylase:phospholipid (fn:enzyme; macromolecule  
 synthesis, modification:) (db:genpept-bct2) (ec:4.1.1.65) (de:escherichia  
 coli k-12 mg1655 section 378 of 400 of the completegenome.) (nt:f322; 100  
 pct identical to dpsd\_ecoli sw: p10740;) (le:7051) (re:8019) (di:complement)  
 AE000488 AE000488 g1790604 Escherichia coli 562 -11533236 5000690452  
 (de:(ecoli\_4046) (pn:phosphatidylserine decarboxylase; phospholipid  
 synthesis) (gn:psd) (gtcfc:5.3:8.1) (ec:4.1.1.65) (dpsd\_ecoli)  
 (keggfc:5.3:8.1) (rileyfc:3.1.11) (db:gtc-escherichia coli)) ECOLI\_4046  
 ECOLI\_4046 Escherichia coli 562 10011831

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829007	8173	30329	852	283

Description

6500729379 serb:b4388 phosphoserine phosphatase:psp:o-phosphoserine phosphohydrolase (gtcfc:5.3) (ec:3.1.3.3) (keggfc:5.3) (rileyfc:1.4.3) (db:gtc-escherichia coli) b4388 b4388 Escherichia coli 562 -11533237 7500891553 serb (ec:3.1.3.3) (de:phosphohydrolase)) (db:swissprot) SERB\_ECOLI P06862 ESCHERICHIA COLI 562 -11533237 124274 serb phosphoserine phosphatase::o-phosphoserine phosphohydrolase (cl:phosphoserine phosphatase) (ec:3.1.3.3) (db:pir1.dat) (mp:100 min) PAECS A24271 Escherichia coli 562 -11533237 238274 serb phosphoserine phosphatase (db:genpept-bct1) (ec:3.1.3.3) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 172) (le:315727) (re:316695) (di:direct) ECOUW93 U14003 g537228 Escherichia coli 562 -11533237 5000690453 serb phosphoserine phosphatase ec 3.1.3.3 (db:genpept-bct1) (ec:3.1.3.3) (de:e.coli phosphoserine phosphatase (serb) and smp protein genes,complete cds., and orf, 5' end.) (le:61) (re:1029) (di:complement) ECSMP X03046 g42948 Escherichia coli 562 -11533237 237593 serb 3-phosphoserine phosphatase (fn:enzyme; amino acid biosynthesis: serine) (db:genpept-bct2) (ec:3.1.3.3) (de:escherichia coli k-12 mg1655 section 399 of 400 of the completegenome.) (nt:o322; 100 pct identical to serb\_ecoli sw: p06862;) (le:83) (re:1051) (di:direct) AE000509 AE000509 g1790849 Escherichia coli 562 -11533237 98417 serb (ec:3.1.3.3) (de:phosphohydrolase)) (db:swissprot) SERB\_ECOLI P06862 ESCHERICHIA COLI 562 -11533237

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501829023	8174	30330	1626	541

# Description

6500729380 cysb:b1275 cys regulon transcriptional activator (gtcfc:5.3:10.2) (keggfc:14.2) (rileyfc:1.4.3) (db:gtc-escherichia coli) b1275 b1275 Escherichia coli 562 -11533238 67637 cysb (de:cys regulon transcriptional activator) (db:swissprot) CYSB\_ECOLI P06613 ESCHERICHIA COLI 562 -11533238 131502 cysb regulatory protein cysb (cl:regulatory protein lysr) (db:pir1.dat) (mp:28 min) RGECCB A26695 Escherichia coli 562 -11533238 223501 cysb regulatory protein cysb (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #254(28.4-28.9 min.)) (nt:orf\_id:o254#1; similar to (pir accession number) (le:13981) (re:14955) (di:direct) D90765 D90765 g1742086 Escherichia coli 562 -11533238 234099 cysb (sr:e.coli (k12 strain ja199) dna, clone pjohi) (db:genpept-bct1) (de:e.coli cysb gene encoding cysb regulatory protein, complete cds.) (nt:cysb regulatory protein) (le:718) (re:1692) (di:direct) ECOCYSB M15041 g145665 Escherichia coli 562 -11533238 300304 (sr:e.coli (mutant strain cb64) dna, clone plb1) (db:genpept-bct1) (de:e.coli cysteine regulatory protein (cysb) gene, complete cds.) (nt:cysteine regulatory protein (cysb)) (le:349) (re:1323) (di:direct) ECOCYSBA M34332 g145667 Escherichia coli 562 -11533238 234098 cysb positive transcriptional regulator for cysteine (fn:transport; amino acid biosynthesis: cysteine) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 115 of 400 of the completegenome.) (nt:o324; 100 pct identical to cysb\_ecoli sw: p06613;) (le:7139) (re:8113) (di:direct) AE000225 AE000225 g1787530 Escherichia coli 562 -11533238 5000690492 (de:(ecoli\_1235) (pn:positive regulator for cysteine regulon) (gn:cysb) (gtcfc:6.10) (ec:) (cysb\_ecoli) (keggfc:11.2) (rileyfc:1.4.3) (db:gtc-escherichia coli)) ECOLI\_1235 ECOLI\_1235 Escherichia coli 562 10010235

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829046	8175	30331	780	260
<u>Description</u>				
6500729381 metg:b2114 methionyl-trna synthetase:methionine--trna ligase:metrs (gtcfc:10.6:5.4) (ec:6.1.1.10) (keggfc:5.4:6.4:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli) b2114 b2114 Escherichia coli 562 -11533239 125912 metg methionine--trna ligase::methionyl-trna synthetase (cl:methionine--trna ligase) (ec:6.1.1.10) (db:pir1.dat) (mp:46 min) SYECMT S14427 Escherichia coli 562 -11533239 235126 metg methionine-trna ligase (db:genpept-bct1) (ec:6.1.1.10) (de:e. coli metg gene for methionyl-trna synthetase (ec 6.1.1.10).) (nt:methionyl-trna synthetase) (le:1385) (re:3418) (di:direct) ECMRPMET X55791 g42016 Escherichia coli 562 -11533239 7500953366 metg (sr:e.coli (k12; merodiploid strain em20031) episome f32 dna, clon) (db:genpept-bct1) (de:e.coli metg gene coding for methionyl-trna synthetase, completecds.) (nt:methionyl-trna synthetase (metg)) (le:291) (re:2324) (di:direct) ECOMETG K02671 g146829 Escherichia coli 562 -11533239 233406 metg methionine trna synthetase (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:6.1.1.10) (de:escherichia coli k-12 mg1655 section 190 of 400 of the completegenome.) (nt:o677; 100 pct identical to sym_ecoli sw: p00959; cg) (le:6991) (re:9024) (di:direct) AE000300 AE000300 g1788432 Escherichia coli 562 -11533239 5000690454 (de:(ecoli_2062) (pn:methionine trna synthetase) (gn:metg) (gtcfc:5.4:6.4:10.6) (ec:6.1.1.10) (sym_ecoli) (keggfc:5.4:6.4:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli)) ECOLI_2062 ECOLI_2062 Escherichia coli 562 10066480				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829047	8176	30332	378	125
<u>Description</u>				
6500729382 fmt:b3288 methionyl-trna formyltransferase (gtcfc:10.6:5.4) (ec:2.1.2.9) (keggfc:5.4:9.8:10.1) (rileyfc:3.1.5) (db:gtc-escherichia coli) b3288 b3288 Escherichia coli 562 -11533240 164063 fmt methionyl-trna formyltransferase (cl:methionyl-trna formyltransferase:phosphoribosylglycinamide formyltransferase homology) (ec:2.1.2.9) (db:pir2.dat) S23108 S23108 Escherichia coli 562 -11533240 232902 fmt methionyl-trna formyltransferase (db:genpept-bct1) (ec:2.1.2.9) (de:e.coli fmt gene for l-methionyl-trnametf n-formyltransferase.) (le:578) (re:1525) (di:direct) ECFMT X63666 g581088 Escherichia coli 562 -11533240 304568 fmt methionyl-trna formyltransferase (db:genpept-bct1) (ec:2.1.2.9) (de:e.coli fms, fmt, fmu, fmv, smf, smg and trka genes.) (nt:methionyl-trnametf formyltransferase) (le:1950) (re:2897) (di:direct) ECFMUV X77091 g581089 Escherichia coli 562 -11533240 232895 fmt 10-formyltetrahydrofolate:l-methionyl-trna fmet (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:2.1.2.9) (de:escherichia coli k-12 mg1655 section 297 of 400 of the completegenome.) (nt:o315; 99 pct identical amino acid sequence and) (le:2284) (re:3231) (di:direct) AE000407 AE000407 g1789683 Escherichia coli 562 -11533240 5000690456 (de:(ecoli_3206) (pn:10-formyltetrahydrofolate:l-methionyl-trna:10-formyltetrahydrofolate, l-methionyl-trna:fmet n- formyltransferase) (gn:fmt) (gtcfc:5.4:9.6:10.6) (ec:2.1.2.9) (fmt_ecoli) (keggfc:5.4:9.8:10.1) (rileyfc:3.1.5)) ECOLI_3206 ECOLI_3206 Escherichia coli 562 10087150				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829059	8177	30333	234	77
<u>Description</u>				
Hypothetical protein				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829060	8178	30334	1719	572

Description

6500729383 cyss:b0526 cysteinyl-trna synthetase:cysteine--trna ligase:cysrs (gtcfc:10.6:5.5) (ec:6.1.1.16) (keggfc:5.5:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli) b0526 b0526 Escherichia coli 562 -11533241 234115 cyss (ec:6.1.1.16) (de:(cysrs)) (db:swissprot) SYC\_ECOLI P21888 ESCHERICHIA COLI 562 -11533241 125919 cyss cysteine--trna ligase::cysteinyl-trna synthetase (cl:cysteine--trna ligase) (ec:6.1.1.16) (db:pir1.dat) (mp:12 min) YYEC A37868 Escherichia coli 562 -11533241 5000690459 cyss cysteinyl-trna synthetase (db:genpept-bct1) (ec:6.1.1.16) (de:escherichia coli cyss gene for cysteinyl-trna synthetase.) (le:378) (re:1763) (di:direct) ECCYSSGEN X59293 g41206 Escherichia coli 562 -11533241 240300 cyss transfer rna-cys synthetase (sr:e.coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli cysteine trna synthetase (cyss) gene, complete cds.) (le:18) (re:1403) (di:direct) ECOCYSS M59381 g145692 Escherichia coli 562 -11533241 7500892336 syc cysteinyl-trna synthetase (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:134060) (re:135445) (di:direct) ECU82664 U82664 g1773207 Escherichia coli 562 -11533241 232628 cyss cysteine trna synthetase (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:6.1.1.16) (de:escherichia coli k-12 mg1655 section 48 of 400 of the completegenome.) (nt:o461; 100 pct identical to syc\_ecoli sw: p21888) (le:8119) (re:9504) (di:direct) AE000158 AE000158 g1786737 Escherichia coli 562 -11533241 99996 cyss (ec:6.1.1.16) (de:(cysrs)) (db:swissprot) SYC\_ECOLI P21888 ESCHERICHIA COLI 562 -11533241

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829071	8179	30335	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829087	8180	30336	489	162

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829094	8181	30337	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829095	8182	30338	273	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829100	8183	30339	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829120	8184	30340	1173	390

Description

6500729384 ilve:b3770 branched-chain amino-acid  
aminotransferase:branched-chain amino acid aminotransferase:transaminase  
b:bcac (gtcfc:5.6:5.7:9.5) (ec:2.6.1.42) (keggfc:5.6:5.7:9.5)  
(rileyfc:1.4.7) (db:gtc-escherichia coli) b3770 Escherichia coli 562  
-11533242 7000688862 ilve branched-chain-amino-acid  
transaminase::branched-chain-amino-acid aminotransferase:transaminase b  
(cl:branched-chain-amino-acid aminotransferase) (ec:2.6.1.42) (db:pir1.dat)  
(mp:85 min) XNECV E65180 Escherichia coli 562 -11533242 7500953244  
ilve::cgsc no. 605 branched-chain amino-acid aminotransferase  
(db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to  
86.5 minutes.) (le:5620) (re:6549) (di:direct) ECOUW85 M87049 g148177  
Escherichia coli 562 -11533242 237001 ilve branched-chain amino-acid  
aminotransferase (fn:enzyme; amino acid biosynthesis: isoleucine,)  
(db:genpept-bct2) (ec:2.6.1.42) (de:escherichia coli k-12 mg1655 section 343  
of 400 of the completegenome.) (nt:o309; 99 pct identical amino acid  
sequence and) (le:8844) (re:9773) (di:direct) AE000453 AE000453 g1790205  
Escherichia coli 562 -11533242 5000690460 (de:(ecoli\_3682)  
(pn:branched-chain amino-acid aminotransferase) (gn:ilve) (gtcfc:5.6:5.7)  
(ec:2.6.1.42) (ilve\_ecoli) (keggfc:5.6:5.7) (rileyfc:1.4.7)  
(db:gtc-escherichia coli)) ECOLI\_3682 ECOLI\_3682 Escherichia coli 562  
10124090

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829128	8185	30341	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829138	8186	30342	594	198

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829160	8187	30343	1794	598

Description

6500729385 iles:ilvs:b0026 isoleucyl-trna synthetase:isoleucine--trna  
ligase:ilers (gtcfc:10.6:5.7) (ec:6.1.1.5) (keggfc:5.7:10.1:10.2)  
(rileyfc:3.1.5) (db:gtc-escherichia coli) b0026 b0026 Escherichia coli 562  
-11533243 7000688907 iles isoleucine--trna ligase::isoleucyl-trna  
synthetase (cl:isoleucine--trna ligase) (ec:6.1.1.5) (db:pir1.dat) (mp:1  
min) SYECIT B64723 Escherichia coli 562 -11533243 7500953360 iles  
isoleucine trna synthetase (fn:enzyme; aminoacyl trna synthetases, trna)  
(db:genpept-bct2) (ec:6.1.1.5) (de:escherichia coli k-12 mg1655 section 3 of  
400 of the completegenome.) (nt:o938; 100 pct identical to syi\_ecoli sw:  
p00956;) (le:1732) (re:4548) (di:direct) AE000113 AE000113 g2367096  
Escherichia coli 562 -11533243

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829166	8188	30344	336	111

Description

6500729386 leud:b0071 3-isopropylmalate dehydratase:3-isopropylmalate  
dehydratase small subunit:isopropylmalate isomerase:alpha-ipm isomerase  
(gtcfc:5.7) (ec:4.2.1.33) (keggfc:5.7) (rileyfc:1.4.7) (db:gtc-escherichia  
coli) b0071 b0071 Escherichia coli 562 -11533244 81960 leud (ec:4.2.1.33)  
(de:(isopropylmalate isomerase) (alpha-ipm isomerase)) (db:swissprot)  
LEUD\_ECOLI P30126 ESCHERICHIA COLI 562 -11533244 163387 leud  
3-isopropylmalate dehydratase:small chain (cl:3-isopropylmalate dehydratase  
small chain) (ec:4.2.1.33) (db:pir2.dat) S40585 S40585 Escherichia coli 562  
-11533244 7500884957 orf (sr:escherichia coli (strain:k-12) dna)  
(db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (nt:leud protein  
homolog(pir:s07306)) (le:78505) (re:79110) (di:complement) ECO110K D10483  
g216489 Escherichia coli 562 -11533244 233599 leud isopropylmalate  
isomerase subunit (fn:enzyme; amino acid biosynthesis: leucine)  
(db:genpept-bct2) (ec:4.2.1.33) (de:escherichia coli k-12 mg1655 section 7  
of 400 of the completegenome.) (nt:f201; 100 pct identical to leud\_ecoli sw:  
p30126) (le:8661) (re:9266) (di:complement) AE000117 AE000117 g1786258  
Escherichia coli 562 -11533244 5000690462 (de:(ecoli\_71)  
(pn:isopropylmalate isomerase subunit) (gn:leud) (gtcfc:5.7) (ec:4.2.1.33)  
(leud\_ecoli) (keggfc:5.7) (rileyfc:1.4.7) (db:gtc-escherichia coli))  
ECOLI\_71 ECOLI\_71 Escherichia coli 562 10024194

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829167	8189	30345	396	131

Description

6500729387 leuc:b0072 3-isopropylmalate dehydratase:isopropylmalate isomerase:alpha-ipm isomerase:ipmi (gtcfc:5.7) (ec:4.2.1.33) (keggfc:5.7) (rileyfc:1.4.7) (db:gtc-escherichia coli) b0072 b0072 Escherichia coli 562 -11533245 7000690839 leuc 3-isopropylmalate dehydratase:alpha chain (ec:4.2.1.33) (db:pir2.dat) H64728 H64728 Escherichia coli 562 -11533245 7500959665 leuc 3-isopropylmalate isomerase dehydratase (fn:enzyme; amino acid biosynthesis: leucine) (db:genpept-bct2) (ec:4.2.1.33) (de:escherichia coli k-12 mg1655 section 7 of 400 of the completegenome.) (nt:f466; 98 pct identical (4 gaps) to leu2\_ecoli) (le:9277) (re:10677) (di:complement) AE000117 AE000117 g1786259 Escherichia coli 562 -11533245 5000690463 (de:(ecoli\_72) (pn:isopropylmalate isomerase subunit) (gn:leuc) (gtcfc:5.7) (ec:4.2.1.33) (leu2\_ecoli) (keggfc:5.7) (rileyfc:1.4.7) (db:gtc-escherichia coli)) ECOLI\_72 ECOLI\_72 Escherichia coli 562 10122645

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829171	8190	30346	204	67

Description

GTC ORF with score 97 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829175	8191	30347	621	206

Description

GTC ORF with score 195 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829176	8192	30348	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829178	8193	30349	300	99

Description

GTC ORF with score 104 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completedcds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829189	8194	30350	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829195	8195	30351	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829215	8196	30352	243	80

Description

6500729388 leub:b0073 3-isopropylmalate dehydrogenase:beta-ipm dehydrogenase:imd3:3-ipm-dh (gtcfc:5.7) (ec:1.1.1.85) (keggfc:5.7) (rileyfc:1.4.7) (db:gtc-escherichia coli) b0073 b0073 Escherichia coli 562 -11533246 7000689028 leub 3-isopropylmalate dehydrogenase (cl:3-isopropylmalate dehydrogenase) (ec:1.1.1.85) (db:pir2.dat) A64729 A64729 Escherichia coli 562 -11533246 7500953807 leub 3-isopropylmalate dehydrogenase (fn:enzyme; amino acid biosynthesis: leucine) (db:genpept-bct2) (ec:1.1.1.85) (de:escherichia coli k-12 mg1655 section 7 of 400 of the completegenome.) (nt:f364; 100 pct identical to leu3\_ecoli sw: p30125) (le:10680) (re:11774) (di:complement) AE000117 AE000117 g1786260 Escherichia coli 562 -11533246 5000690464 (de:(ecoli\_73) (pn:3-isopropylmalate dehydrogenase) (gn:leub) (gtcfc:5.7) (ec:1.1.1.85) (leu3\_ecoli) (keggfc:5.7) (rileyfc:1.4.7) (db:gtc-escherichia coli)) ECOLI\_73 ECOLI\_73 Escherichia coli 562 10122646

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829221	8197	30353	1437	479

Description

6500729389 leus:b0642 leucyl-trna synthetase:leucine--trna ligase:leurs  
 (gtcfc:10.6:5.7) (ec:6.1.1.4) (keggfc:5.7:10.1:10.2) (rileyfc:3.1.5)  
 (db:gtc-escherichia coli) b0642 b0642 Escherichia coli 562 -11533247 100114  
 leus (ec:6.1.1.4) (de:leucyl-trna synthetase, (leucine--trna ligase)  
 (leurs)) (db:swissprot) SYL\_ECOLI P07813 ESCHERICHIA COLI 562 -11533247  
 7000686722 leus leucine--trna ligase::leucyl-trna synthetase  
 (cl:leucine--trna ligase) (ec:6.1.1.4) (db:pir1.dat) (mp:15 min) SYECL  
 H64798 Escherichia coli 562 -11533247 223128 leus leucine-trna ligase  
 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #169)  
 (db:genpept-bct1) (de:escherichia coli genomic dna. (14.3 - 14.7 min).)  
 (le:8449) (re:11031) (di:complement) D90704 D90704 g1651269 Escherichia coli  
 562 -11533247 7500892494 leus leucine trna synthetase (fn:enzyme; aminoacyl  
 trna synthetases, trna) (db:genpept-bct2) (ec:6.1.1.4) (de:escherichia coli  
 k-12 mg1655 section 58 of 400 of the completegenome.) (nt:f860; 99 pct  
 identical to syl\_ecoli sw: p07813) (le:9936) (re:12518) (di:complement)  
 AE000168 AE000168 g1786861 Escherichia coli 562 -11533247 5000690465 leus  
 leucine-trna ligase ec 6.1.1.4 . (sr:escherichia coli(strain:k12) dna,  
 clone:kohara clone #169) (db:genpept) (de:escherichia coli genomic dna.  
 (14.3 - 14.7 min).) (nt:orf\_id:o169#10; similar to pir accession number)  
 (le:8449) (re:11031) (di:complement) D90704 D90704 g1651269 Escherichia coli  
 562 -11533247

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829231	8198	30354	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829245	8199	30355	1728	575

Description

6500729390 ilvd:b3771 dihydroxyacid dehydratase:dihydroxy-acid dehydratase:dad (gtcfc:5.7:9.5) (ec:4.2.1.9) (keggfc:5.7:9.5) (rileyfc:1.4.7) (db:gtc-escherichia coli) b3771 b3771 Escherichia coli 562 -11533248 79253 ilvd (ec:4.2.1.9) (de:dihydroxy-acid dehydratase, (dad)) (db:swissprot) ILVD\_ECOLI P05791 ESCHERICHIA COLI 562 -11533248 7500884044 ilvd dihydroxyacid dehydratase (fn:enzyme; amino acid biosynthesis: isoleucine,) (db:genpept-bct2) (ec:4.2.1.9) (de:escherichia coli k-12 mg1655 section 343 of 400 of the completegenome.) (nt:o605; 99 pct identical amino acid sequence and) (le:9869) (re:11686) (di:direct) AE000453 AE000453 g1790206 Escherichia coli 562 -11533248 5000690467 (de:(ecoli\_3683) (pn:dihydroxyacid dehydratase) (gn:ilvd) (gtcfc:5.7:9.5) (ec:4.2.1.9) (ilvd\_ecoli) (keggfc:5.7:9.5) (rileyfc:1.4.7) (db:gtc-escherichia coli)) ECOLI\_3683 ECOLI\_3683 Escherichia coli 562 10021581

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829249	8200	30356	315	105

Description

GTC ORF with score 109 to: (sr:s. cerevisiae (strain dc-5) genomic dna, clone pl33) (db:genpept-pln1) (de:s. cerevisiae gene for yml33, mitochondrial ribosomal proteins oflarge subunit.) (nt:yml33) (le:608) (re:907) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829282	8201	30357	2190	729

Description

GTC ORF with score 1333 to: (sr:norway rat) (db:genpept-rod) (de:rattus norvegicus plasma membrane ca2+-atpase isoform 4 mrna, complete cds and alternatively spliced variations.) (nt:pmca4, alternatively spliced c) (le:168:3652) (re:3476:3954) ...



ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501829298	8202	30358	726	241

#### Description

6500729391 ilvc:b3774 ketol-acid reductoisomerase:acetohydroxy-acid isomeroreductase:alpha-keto-beta-hydroxylacil reductoisomerase (gtcfc:5.7:9.5) (ec:1.1.1.86) (keggfc:5.7:9.5) (rileyfc:1.4.7) (db:gtc-escherichia coli) b3774 b3774 Escherichia coli 562 -11533249  
7000688843 ilvc ketol-acid reductoisomerase::acetohydroxy acid isomeroreductase:dihydroxyisovalerate dehydrogenase (cl:escherichia coli ketol-acid reductoisomerase:ketol-acid reductoisomerase homology) (ec:1.1.1.86) (db:pir1.dat) (mp:85 min) ISECKR A65181 Escherichia coli 562 -11533249 7500953176 ilvc::cgsc no. 607 ketol-acid reductoisomerase (db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (nt:protein spot sequence confirms start) (le:11104) (re:12579) (di:direct) ECOUW85 M87049 g148181 Escherichia coli 562 -11533249  
237005 ilvc ketol-acid reductoisomerase (fn:enzyme; amino acid biosynthesis: isoleucine,) (db:genpept-bct2) (ec:1.1.1.86) (de:escherichia coli k-12 mg1655 section 344 of 400 of the completegenome.) (nt:o491; 100 pct identical to ilvc\_ecoli sw: p05793) (le:61) (re:1536) (di:direct) AE000454 AE000454 g1790210 Escherichia coli 562 -11533249 5000690468 (de:(ecoli\_3686) (pn:ketol-acid reductoisomerase) (gn:ilvc) (gtcfc:5.7:9.5) (ec:1.1.1.86) (ilvc\_ecoli) (keggfc:5.7:9.5) (rileyfc:1.4.7) (db:gtc-escherichia coli)) ECOLI\_3686 ECOLI\_3686 Escherichia coli 562 10124091

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501829303	8203	30359	324	107

#### Description

6500729392 vals:b4258 valyl-trna synthetase:valine--trna ligase:valrs (gtcfc:10.6:5.7) (ec:6.1.1.9) (keggfc:5.7:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli) b4258 b4258 Escherichia coli 562 -11533250 100214 vals (ec:6.1.1.9) (de:valyl-trna synthetase, (valine--trna ligase) (valrs)) (db:swissprot) SYV\_ECOLI P07118 ESCHERICHIA COLI 562 -11533250 7000686734 vals valine--trna ligase::valyl-trna synthetase (cl:valine--trna ligase) (ec:6.1.1.9) (db:pir1.dat) (mp:97 min) SYECVT E65238 Escherichia coli 562 -11533250 7500892619 vals valine trna synthetase (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:6.1.1.9) (de:escherichia coli k-12 mg1655 section 386 of 400 of the completegenome.) (nt:f951; 99 pct identical amino acid sequence and) (le:6831) (re:9686) (di:complement) AE000496 AE000496 g1790708 Escherichia coli 562 -11533250 5000690469 (de:(ecoli\_4142) (pn:valine trna synthetase) (gn:vals) (gtcfc:5.7:10.6) (ec:6.1.1.9) (syv\_ecoli) (keggfc:5.7:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli)) ECOLI\_4142 ECOLI\_4142 Escherichia coli 562 10124161

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829308	8204	30360	339	112

Description

GTC ORF with score 137 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid t08b2.) (nt:similar to a human putative tumor suppressor (nid:) (le:10179:10325:10476:10643) (re:10277:10429:10593:10849) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829315	8205	30361	762	253

Description

6500729393 leul:leulp:b0075 leu operon leader peptide (gtcfc:5.7) (keggfc:14.2) (rileyfc:1.4.7) (db:gtc-escherichia coli) b0075 b0075 Escherichia coli 562 -11533251 227982 leul:leulp (de:leu operon leader peptide) (db:swissprot) LPL\_ECOLI P09149 ESCHERICHIA COLI 562 -11533251 131596 leul:leulp leu operon leader peptide (cl:leu leader peptide) (db:pir1.dat) (mp:2 min) LFECL A30376 Escherichia coli 562 -11533251 304519 leu operon leader peptide (db:genpept-bct1) (de:e. coli 2 minute region.) (le:156) (re:242) (di:complement) EC2MIN X55034 g40843 Escherichia coli 562 -11533251 7502851902 (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli leu operon, leader peptide gene and leua gene coding foralpha-isopropylmalate synthase, control region.) (nt:leu operon leader peptide) (le:65) (re:151) (di:direct) ECOLEUA J01642 g146602 Escherichia coli 562 -11533251 234965 leul leu operon leader peptide (fn:leader; amino acid biosynthesis: leucine) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 8 of 400 of the completegenome.) (nt:f28; 100 pct identical to lpl\_ecoli sw: p09149) (le:77) (re:163) (di:complement) AE000118 AE000118 g1786263 Escherichia coli 562 -11533251 82410 leul:leulp (de:leu operon leader peptide) (db:swissprot) LPL\_ECOLI P09149 ESCHERICHIA COLI 562 -11533251

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829318	8206	30362	384	127

Description

6500729394 leuo (gtcfc:5.7) (keggfc:14.2) (rileyfc:1.4.7) (db:gtc-escherichia coli) b0076 b0076 Escherichia coli 562 -11533252 7000689455 leuo probable activator protein leuo (cl:leuo protein) (db:pir2.dat) (mp:2 min) D64729 D64729 Escherichia coli 562 -11533252 7500955730 leuo probable transcriptional activator for leuabcd (fn:putative regulator; amino acid biosynthesis:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 8 of 400 of the completegenome.) (nt:o373; 100 pct identical to leuo\_ecoli sw:) (le:646) (re:1767) (di:direct) AE000118 AE000118 g1786264 Escherichia coli 562 -11533252

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829326	8207	30363	1890	630

Description

6500729395 ivbl:b3672 ilvbn operon leader peptide (gtcfc:5.7) (keggfc:14.2) (rileyfc:1.4.7) (db:gtc-escherichia coli) b3672 b3672 Escherichia coli 562 -11533253 234847 ivbl (de:ilvbn operon leader peptide) (db:swissprot) LPIV\_ECOLI P03061 ESCHERICHIA COLI 562 -11533253 131594 ilvbn operon leader peptide (cl:ilvb leader peptide) (db:pir1.dat) (mp:82 min) LFECIV A03597 Escherichia coli 562 -11533253 236909 (db:genpept-bct1) (de:e. coli ilvbn operon for ahas-i (acetohydroxy acid synthase).) (nt:put. leader peptide (aa 1-32)) (le:141) (re:239) (di:direct) ECILVBN X02541 g41784 Escherichia coli 562 -11533253 7500885125 ilvb (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli acetohydroxy acid synthase (ahas) i (ilvb) and acetolactatesynthase small subunit (ilvn) genes (from the ilv-leu operon), complete cds.) (nt:ilv operon leader peptide) (le:149) (re:247) (di:direct) ECOILVBPR J01633 g146454 Escherichia coli 562 -11533253 7502851903 f32 ilvbn operon leader peptide (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:42284) (re:42382) (di:complement) ECOUW82 L10328 g290521 Escherichia coli 562 -11533253 233190 ivbl ilvb operon leader peptide (fn:leader; amino acid biosynthesis: isoleucine,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 335 of 400 of the completgenome.) (nt:f32) (le:65) (re:163) (di:complement) AE000445 AE000445 g1790106 Escherichia coli 562 -11533253 82399 ivbl (de:ilvbn operon leader peptide) (db:swissprot) LPIV\_ECOLI P03061 ESCHERICHIA COLI 562 -11533253

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829344	8208	30364	672	223

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829345	8209	30365	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501829355	8210	30366	1554	517

# Description

6500729396 ilvl:b3766 ilvgmeda operon leader peptide:attenuator peptide (gtcfc:5.7) (keggfc:14.2) (rileyfc:1.4.7) (db:gtc-escherichia coli) b3766 b3766 Escherichia coli 562 -11533254 7500885124 ilvl (de:ilvgmeda operon leader peptide (attenuator peptide)) (db:swissprot) LPID\_ECOLI P03060 ESCHERICHIA COLI 562 -11533254 7502851904 ilvl (de:ilvgmeda operon leader peptide (attenuator peptide)) (db:swissprot) LPID\_ECOLI P03060 SERRATIA MARCESCENS 615 -11533254 7502851905 ilvl (de:ilvgmeda operon leader peptide (attenuator peptide)) (db:swissprot) LPID\_ECOLI P03060 SALMONELLA TYPHIMURIUM 602 -11533254 7502851906 ilvl (de:ilvgmeda operon leader peptide (attenuator peptide)) (db:swissprot) LPID\_ECOLI P03060 KLEBSIELLA AEROGENES 28451 -11533254 131592 ilvl ilvgmeda operon leader peptide (cl:ilvgeda leader peptide) (db:pir1.dat) LFECI A93841 Escherichia coli 562 -11533254 131593 ilvgeda leader peptide (cl:ilvgeda leader peptide) (db:pir1.dat) LFEBIT A04601 Salmonella typhimurium 602 -11533254 7500885123 (db:genpept-bct1) (de:e. coli ilvg gene.) (nt:reading frame (attenuator peptide)) (le:123) (re:221) (di:direct) ECILVG V00289 g41792 Escherichia coli 562 -11533254 264300 ilvl (db:genpept-bct1) (de:e. coli genes ilvl, ilvg and ilve'. ilvg is acetolactate synthetaseii (e.c.4.1.3.18) ilve is branched-chain-amino-acidaminotransferase (e.c.2.6.1.42).) (le:80) (re:178) (di:direct) ECILVX V00290 g41798 Escherichia coli 562 -11533254 233197 (sr:escherichia coli (strain b) dna; and escherichia coli (strain k-12) (db:genpept-bct1) (de:e.coli b ilvgeda operon leader peptide gene, complete cds. e.coliilvgeda operon, leader (attenuator) peptide gene (ilvl) and ilvgand ilve genes coding for ace... ECOILVGEB M11651 g146464 Escherichia coli 562 -11533254 233206 leader peptide (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli ilvgmeda operon encoding biosynthesis of isoleucine andvaline, complete cds.) (le:494) (re:592) (di:direct) ECOILVG MED M32253 g146466 Escherichia coli 562 -11533254 234855 ilvl ilvgmeda operon leader peptide (db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (le:3458) (re:3556) (di:direct) ECOUW85 M87049 g148174 Escherichia coli 562 -11533254 244028 (sr:k.aerogenes dna, clone ppul38) (db:genpept-bct1) (de:k.aerogenes ilvgeda operon leader peptide gene, complete cds.) (nt:ilvgeda leader peptide) (le:89) (re:187) (di:direct) KPNILVGED M11652 g149213 Klebsiella aerogenes 28451 -11533254 236998 (sr:s.typhimurium dna, clone prl103 (1); clone ppu46 (2)) (db:genpept-bct1) (de:s.typhimurium ilvgeda operon leader peptide gene, complete cds.) (nt:ilvgeda leader peptide) (le:120) (re:218) (di:direct) STYILVPA J01806 g154147 Salmonella typhimurium 602 -11533254 7500885122 ilvl ilvgeda operon leader peptide (fn:leader; amino acid biosynthesis: isoleucine,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 343 of 400 of the completegenome.) (nt:o32; 100 pct identical to lpid\_ecoli sw: p03060) (le:6682) (re:6780) (di:direct) AE000453 AE000453 g1790202 Escherichia coli 562 -11533254 82394 ilvl (de:ilvgmeda operon leader peptide (attenuator peptide)) (db:swissprot) LPID\_ECOLI P03060 ESCHERICHIA COLI 562 -11533254 7502851907 ilvl (de:ilvgmeda operon leader peptide (attenuator peptide)) (db:swissprot) LPID\_ECOLI P03060 SERRATIA MARCESCENS

(attenuator peptide)) (db:swissprot) LPID\_ECOLI P03060 SERRATIA MARCESCENS  
615 -11533254 7502851908 ilvL (de:ilvymeda operon leader peptide

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829359	8211	30367	198	65
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829371	8212	30368	921	306
<u>Description</u>				

6500729397 ilvy:b3773 transcriptional activator protein ilvy  
(gtcfc:5.7:10.2) (keggfc:14.2) (rileyfc:1.4.7) (db:gtc-escherichia coli)  
b3773 b3773 Escherichia coli 562 -11533255 79278 ilvy (de:transcriptional  
activator protein ilvy) (db:swissprot) ILVY\_ECOLI P05827 ESCHERICHIA COLI  
562 -11533255 131519 ilvy regulatory protein ilvy:ilvc activator ilvy  
(cl:regulatory protein ilvy) (db:pir1.dat) (mp:85 min) RGECIY B26287  
Escherichia coli 562 -11533255 237004 ilvy positive regulatory protein  
(fn:positive regulation of ilvc gene) (sr:escherichia coli (strain k-12)  
(library: clarke-carbon) dna) (db:genpept-bct1) (de:e.coli (clone  
prw(1y,1c)) threonine deaminase (ilva) gene, 3' end;acetoxy acid  
isomeroreductase (ilvc) and its positive co... ECOILVYC M11689 g146476  
Escherichia coli 562 -11533255 7500884065 ilvy::cgsc no. 598 (fn:positive  
activator of ilvc) (db:genpept-bct1) (de:e. coli genomic sequence of the  
region from 84.5 to 86.5 minutes.) (nt:other potential starts) (le:10061)  
(re:10954) (di:complement) ECOUW85 M87049 g148180 Escherichia coli 562  
-11533255 234864 ilvy positive regulator for ilvc (fn:regulator; amino acid  
biosynthesis: isoleucine,) (db:genpept-bct2) (de:escherichia coli k-12  
mg1655 section 343 of 400 of the completegenome.) (nt:f297; 100 pct  
identical amino acid sequence and) (le:13285) (re:14178) (di:complement)  
AE000453 AE000453 g1790208 Escherichia coli 562 -11533255

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829373	8213	30369	972	323

Description

6500729398 mure:b0085 meso-diaminopimelate-adding  
enzyme:udp-n-acetylmuramoylalanyl-d-glutamate--2:6-diaminopimelate  
ligase:udp-n-acetylmuramyl-tripeptide synthetase (gtcfc:11.4:5.8)  
(ec:6.3.2.13) (keggfc:5.8:7.3) (rileyfc:3.3.4) (db:gtc-escherichia coli)  
b0085 b0085 Escherichia coli 562 -11533256 164802 mure  
udp-n-acetylmuramoylalanyl-d-glutamate--2:6-diaminopimelate  
ligase::meso-diaminopimelate-adding enzyme:udp-murnac-tripeptide synthetase  
mure:udp-n-acetylmuramyl-tripeptide synthetase (ec:6.3.2.13) (db:pir2.dat)  
S14384 S14384 Escherichia coli 562 -11533256 227992 mure  
udp-murnac-tripeptide synthetase mure (db:genpept-bct1) (de:e. coli 2 minute  
region.) (le:9696) (re:11183) (di:direct) EC2MIN X55034 g581032 Escherichia  
coli 562 -11533256 304529 mure udp-murnac-tripeptide synthetase mure  
(sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12  
genome, 0-2.4min. region.) (le:92820) (re:94307) (di:direct) ECO110K D10483  
g285768 Escherichia coli 562 -11533256 233609 mure  
meso-diaminopimelate-adding enzyme (fn:enzyme; murein sacculus,  
peptidoglycan) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 8  
of 400 of the completegenome.) (nt:o495; 100 pct identical to mure\_ecoli sw:  
p22188) (le:9621) (re:11108) (di:direct) AE000118 AE000118 g1786273  
Escherichia coli 562 -11533256 5000690471 (de:(ecoli\_85)  
(pn:meso-diaminopimelate-adding enzyme) (gn:mure) (gtcfc:5.8:11.4)  
(ec:6.3.2.13) (mure\_ecoli) (keggfc:5.8:7.3) (rileyfc:3.3.4)  
(db:gtc-escherichia coli)) ECOLI\_85 ECOLI\_85 Escherichia coli 562 10087470

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829389	8214	30370	354	117

Description

6500729399 murf:mra:b0086 d-alanyl:d-alanine-adding  
enzyme:udp-n-acetylmuramoylalanyl-d-glutamyl-2:6-diaminopimelate--d-alanyl-d  
-alanyl ligase:udp-murnac-pentapeptide synthetase:d-alanyl-d-alanine-adding  
enzyme (gtcfc:11.4:5.8) (ec:6.3.2.15) (keggfc:5.8:7.3) (rileyfc:3.3.4)  
(db:gtc-escherichia coli) b0086 b0086 Escherichia coli 562 -11533257 84714  
murf:mra (ec:6.3.2.15) (de:(d-alanyl-d-alanine-adding enzyme))  
(db:swissprot) MURF\_ECOLI P11880 ESCHERICHIA COLI 562 -11533257 7000685888  
murf  
udp-n-acetylmuramoylalanyl-d-glutamyl-2:6-diaminopimelate--d-alanyl-d-alanin  
e ligase:precursor:udp-n-acetylmuramoyl-pentapeptide synthetase  
(ec:6.3.2.15) (db:pir2.dat) (mp:2 min) F64730 F64730 Escherichia coli 562  
-11533257 239761 murf d-alanine:d-alanine-adding enzyme (fn:enzyme; murein  
sacculus, peptidoglycan) (db:genpept-bct2) (de:escherichia coli k-12 mg1655  
section 8 of 400 of the completegenome.) (nt:o452; 99 pct identical to  
murf\_ecoli sw: p11880;) (le:11105) (re:12463) (di:direct) AE000118 AE000118  
g1786274 Escherichia coli 562 -11533257 7500886146 murf  
udp-murnac-tripeptide:d-ala-d-ala-adding enzyme (db:genpept-bct2)  
(de:escherichia coli udpmurnac-tripeptide:d-ala-d-ala-adding enzyme(murf)  
gene, complete cds.) (nt:murein synthesis gene) (le:309) (re:1667)  
(di:direct) ECU67891 U67891 g1743865 Escherichia coli 562 -11533257  
5000690472 (de:(ecoli\_86) (pn:d-alanine:d-alanine-adding enzyme:d-alanine,  
d-alanine-adding enzyme) (gn:murf) (gtcfc:5.8:11.4) (ec:6.3.2.15)  
(murf\_ecoli) (keggfc:5.8:7.3) (rileyfc:3.3.4) (db:gtc-escherichia coli))  
ECOLI\_86 ECOLI\_86 Escherichia coli 562 10122651

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501829394	8215	30371	1374	457

#### Description

6500729400 lyss:herc:asud:b2890 lysyl trna synthetase:lysrs:constitutive:lysyl-trna synthetase:lysine--trna ligase:lysrs (gtcfc:10.6:5.9) (ec:6.1.1.6) (keggfc:5.8:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli) b2890 b2890 Escherichia coli 562 -11533258 7000688908 lyss:herc lysine--trna ligase::lysyl-trna synthetase i (cl:lysine--trna ligase) (ec:6.1.1.6) (db:pir1.dat) (mp:62 min) SYECKT B65073 Escherichia coli 562 -11533258 239103 (sr:e.coli (strain k12, isolate c600) dna, clone pkk94(1,5)) (db:genpept-bct1) (de:e.coli peptide chain release factor 2 (prfb) gene, 3' end, and hercprotein gene, complete cds.) (nt:herc protein) (le:229) (re:1746) (di:direct) ECOHERC J03795 g146341 Escherichia coli 562 -11533258 7500953361 lyss lysyl trna synthetase lysrs:constitutive (db:genpept-bct1) (ec:6.1.1.6) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:cg site no. 17662; alternate gene names asud, herc) (le:43471) (re:44988) (di:complement) ECU28375 U28375 g887840 Escherichia coli 562 -11533258 234638 lyss lysine trna synthetase:constitutive:suppressor (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:6.1.1.6) (de:escherichia coli k-12 mg1655 section 262 of 400 of the completegenome.) (nt:f505; 100 pct identical to syk1\_ecoli sw: p13030;) (le:9446) (re:10963) (di:complement) AE000372 AE000372 g1789256 Escherichia coli 562 -11533258 5000690477 (de:(ecoli\_2814) (pn:lysine trna synthetase, constitutive; suppressor of cole1 mutation in primer rna) (gn:lyss) (gtcfc:5.8:10.6) (ec:6.1.1.6) (syk1\_ecoli) (keggfc:5.8:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli)) ECOLI\_2814 ECOLI\_2814 Escherichia coli 562 10123897

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501829402	8216	30372	474	157

#### Description

GTC ORF with score 107 to: (or:Boreogadus saida) (db:genpept-vrt) (de:boreogadus saida antifreeze glycopeptide afgp polyprotein precursorgene, complete cds.) (nt:cleavage of polyprotein at conserved spacers r or) (le:209:281) (re:211:1801) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501829406	8217	30373	765	254

#### Description

GTC ORF with score 594 to: (sr:aspergillus aculeatus (strain ksm 510) cdna to mrna) (db:genpept-pln1) (de:aspergillus aculeatus mannanase (man1) mrna, complete cds.) (nt:n-linked glycosylation sites at bp 105, bp 255, bp) (le:24) (re:1157) (di:direct)



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829409	8218	30374	276	91
<u>Description</u>				
6500729401 lysu:b4129 lysyl-trna synthetase:lysyl-trna synthetase:heat inducible:lysine--trna ligase:lysrs (gtcfc:10.6:5.9) (ec:6.1.1.6) (keggfc:5.8:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli) b4129 b4129 Escherichia coli 562 -11533259 142261 lysu lysine--trna ligase::thermoinducible:lysyl-trna synthetase ii:lysyl-trna synthetase:thermoinducible (cl:lysine--trna ligase) (ec:6.1.1.6) (db:pir1.dat) (mp:94 min) SYECKU S56358 Escherichia coli 562 -11533259 237338 (db:genpept-bct1) (de:escherichia coli lysu gene for lysyl-trna synthetase (ec 6.1.1.6).) (nt:lysyl-trna synthetase (aa 1-505)) (le:1) (re:1518) (di:direct) ECLYSUG X16542 g398703 Escherichia coli 562 -11533259 7500953362 lysu lysyl-trna synthetase (db:genpept-bct1) (ec:6.1.1.6) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 16693) (le:44028) (re:45545) (di:complement) ECOUW93 U14003 g536974 Escherichia coli 562 -11533259 233337 lysu lysine trna synthetase:inducible:heat shock (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:6.1.1.6) (de:escherichia coli k-12 mg1655 section 375 of 400 of the completegenome.) (nt:f505; 100 pct identical to syk2_ecoli sw: p14825;) (le:7611) (re:9128) (di:complement) AE000485 AE000485 g1790571 Escherichia coli 562 -11533259 5000690479 (de:(ecoli_4016) (pn:lysine trna synthetase, inducible; heat shock protein) (gn:lysu) (gtcfc:5.8:10.6) (ec:6.1.1.6) (syk2_ecoli) (keggfc:5.8:10.1:10.2) (rileyfc:3.1.5) (db:gtc-escherichia coli)) ECOLI_4016 ECOLI_4016 Escherichia coli 562 10072844				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829410	8219	30375	600	199
<u>Description</u>				
6500729402 yjea:b4155 lysyl-trna synthetase analog (gtcfc:10.6:5.9) (ec:6.1.1.6) (keggfc:5.8:10.1:10.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4155 b4155 Escherichia coli 562 -11533260 164018 yjea:genx lysine--trna ligase:genx:lysyl-trna synthetase:protein f-162 (ec:6.1.1.6) (db:pir2.dat) (mp:94 min) S56383 S56383 Escherichia coli 562 -11533260 7500960375 genx lysyl-trna synthetase analog (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:alternate gene name yjea) (le:73441) (re:74448) (di:direct) ECOUW93 U14003 g536999 Escherichia coli 562 -11533260 237363 yjea putative lysyl-trna synthetase (fn:putative enzyme; aminoacyl trna synthetases,) (db:genpept-bct2) (ec:6.1.1.6) (de:escherichia coli k-12 mg1655 section 378 of 400 of the completegenome.) (nt:o335; 100 pct identical to 325 amino acids) (le:272) (re:1279) (di:direct) AE000488 AE000488 g1790599 Escherichia coli 562 -11533260 5000690480 (de:(ecoli_4041) (pn:hypothetical lysyl-trna synthetase homolog:gx) (gn:yjea) (gtcfc:5.8:13.7:14.1) (ec:6.1.1.6) (syk3_ecoli) (keggfc:5.8:10.1:10.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4041 ECOLI_4041 Escherichia coli 562 10087132				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829411	8220	30376	552	183

Description

6500729403 ldcc:ldch:ldc:b0186 lysine decarboxylase:lysine  
decarboxylase:constitutive:ldc (gtcfc:5.9:14.3) (ec:4.1.1.18) (keggfc:5.9)  
(rileyfc:5.8.0) (db:gtc-escherichia coli) b0186 b0186 Escherichia coli 562  
-11533261 68022 ldcc:ldch:ldc (ec:4.1.1.18) (de:lysine decarboxylase,  
constitutive, (ldc)) (db:swissprot) DCLZ\_ECOLI P52095 ESCHERICHIA COLI 562  
-11533261 7000684990 ldcc:ldch lysine decarboxylase:ldcc (ec:4.1.1.18)  
(db:pir2.dat) B64743 B64743 Escherichia coli 562 -11533261 222544 ldcc  
ldcc:probably constitutive lysine (sr:escherichia coli (strain:k-12,  
isolate:w3110) dna) (db:genpept-bct1) (de:escherichia coli genes for dnae,  
acca, ldcc, yaer, yaen, yaeo,yaep, yaeq, yaej, nlpe, yaef complete cds and  
partial cds.) (le:1146) (re:3287) (di:direct) D49445 D49445 g1785842  
Escherichia coli 562 -11533261 239814 ldc lysine decarboxylase  
(sr:escherichia coli (strain:k-12, sub\_strain:w3110) dna) (db:genpept-bct1)  
(de:escherichia coli dna for aalpha subunit of acetyl-coa carboxylaseand  
lysine decarboxylase, partial and complete cds.) (nt:constitutive lysine  
decarboxylase:ldc) (le:571) (r... D87518 D87518 g2285883 Escherichia coli  
562 -11533261 7500880057 ldcc lysine decarboxylase (db:genpept-bct1)  
(de:escherichia coli chromosome minutes 4-6.) (le:40754) (re:42895)  
(di:direct) ECU70214 U70214 g1552763 Escherichia coli 562 -11533261  
4000714736 ldcc lysine decarboxylase 2:constitutive (fn:enzyme; energy  
metabolism, carbon: pyruvate) (db:genpept-bct2) (ec:4.1.1.18)  
(de:escherichia coli k-12 mg1655 section 18 of 400 of the completegenome.)  
(nt:o713; 98 pct identical (1 gap) to dclz\_ecoli) (le:80) (re:2221)  
(di:direct) AE000128 AE000128 g1786384 Escherichia coli 562 -11533261  
5000690482 (de:(ecoli\_186) (pn:lysine decarboxylase, constitutive:ldc)  
(gn:ldcc) (gtcfc:5.9) (ec:4.1.1.18) (dclz\_ecoli) (keggfc:5.9)  
(rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_186 ECOLI\_186 Escherichia  
coli 562 10118928

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829413	8221	30377	1026	341

Description

GTC ORF with score 804 to: (sr:aspergillus aculeatus (strain ksm 510) cdna  
to mrna) (db:genpept-pln1) (de:aspergillus aculeatus mannanase (man1) mrna,  
complete cds.) (nt:n-linked glycosylation sites at bp 105, bp 255, bp)  
(le:24) (re:1157) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829435	8222	30378	1155	384

Description

6500729404 ybct:b0556 bacteriophage lambda endopeptidase homolog:putative endopeptidase (gtcfc:5.9:14.3) (ec:3.4.-.-) (keggfc:5.9) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0556 b0556 Escherichia coli 562 -11533262 4000707644 ybct (ec:3.4.-.-) (de:putative endopeptidase,) (db:swissprot) ENPP\_ECOLI P75719 ESCHERICHIA COLI 562 -11533262 7000685162 ybct endopeptidase ybct (cl:phage pa2 endopeptidase) (ec:3.4.-.-) (db:pir2.dat) B64788 B64788 Escherichia coli 562 -11533262 7500881060 ybct bacteriophage lambda endopeptidase homolog (fn:is, phage, tn; phage-related functions and) (db:genpept-bct2) (ec:3.4.-.-) (de:escherichia coli k-12 mg1655 section 51 of 400 of the completegenome.) (nt:o153; 96 pct identical to enpp\_lambd sw: p00726) (le:996) (re:1457) (di:direct) AE000161 AE000161 g1786769 Escherichia coli 562 -11533262 5000690483 (de:(ecoli\_538) (pn:bacteriophage lambda endopeptidase homolog) (gtcfc:5.9) (ec:3.4.-.-) (keggfc:5.9) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_538 ECOLI\_538 Escherichia coli 562 10122894

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829437	8223	30379	717	238

Description

GTC ORF with score 106 to: (sr:streptomyces coriofaciens (library: isp 5485) dna) (db:genpept-bct1) (de:streptomyces coriofaciens beta-ketoacyl synthase homologue gene,partial cds.) (nt:homologous to saccharopolyspora erythraea) (le:<1) (re:1581) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829439	8224	30380	621	206

Description

6500729405 sohb:b1272 possible protease:possible protease sohb  
 (gtcfc:5.9:10.11) (ec:3.4.-.-) (keggfc:5.9) (rileyfc:3.2.3)  
 (db:gtc-escherichia coli) b1272 b1272 Escherichia coli 562 -11533263 98947  
 sohb (ec:3.4.-.-) (de:possible protease sohb,) (db:swissprot) SOHB\_ECOLI  
 P24213 ESCHERICHIA COLI 562 -11533263 7000686617 sohb probable serine  
 proteinase:sohb (ec:3.4.-.-) (db:pir2.dat) (mp:28 min) C64875 C64875  
 Escherichia coli 562 -11533263 223483 sohb probable microbial serine  
 proteinase ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda  
 minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
 #253(28.4-28.7 min.)) (nt:orf\_id:o253#12; similar to (pir accession number)  
 (le:11952) (re:13001) (di:direct) D90764 D90764 g1742067 Escherichia coli  
 562 -11533263 300301 sohb probable microbial serine proteinase ec  
 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
 (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #254(28.4-28.9  
 min.)) (nt:orf\_id:o253#12; similar to (pir accession number) (le:9458)  
 (re:10507) (di:direct) D90765 D90765 g1742083 Escherichia coli 562 -11533263  
 300286 sohb putative protease (fn:putative enzyme; not classified)  
 (db:genpept-bct2) (ec:3.4.-.-) (de:escherichia coli k-12 mg1655 section 115  
 of 400 of the completgenome.) (nt:o349; 99 pct identical to sohb\_ecoli sw:  
 p24213; cg) (le:2616) (re:3665) (di:direct) AE000225 AE000225 g1787527  
 Escherichia coli 562 -11533263 223498 sohb probable microbial serine  
 proteinase ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda  
 minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
 #254(28.4-28.9 min.)) (nt:orf\_id:o253#12; similar to (pir accession number)  
 (le:9458) (re:10507) (di:direct) D90765 D90765 g1742083 Escherichia coli 562  
 -11533263 5000690485 (de:(ecoli\_1232) (pn:putative protease) (gn:sohb)  
 (gtcfc:5.9) (ec:3.4.-.-) (sohb\_ecoli) (keggfc:5.9) (rileyfc:3.2.3)  
 (db:gtc-escherichia coli)) ECOLI\_1232 ECOLI\_1232 Escherichia coli 562  
 10119494

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829459	8225	30381	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829464	8226	30382	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829476	8227	30383	1344	447

Description

6500729406 sppa:b1766 protease iv:endopeptidase iv (gtcfc:5.9:10.11) (ec:3.4.-.-) (keggfc:5.9) (rileyfc:3.2.3) (db:gtc-escherichia coli) b1766 b1766 Escherichia coli 562 -11533264 7000688880 sppa proteinase iv (cl:proteinase iv) (ec:3.4.-.-) (db:pir1.dat) PRECT4 F64936 Escherichia coli 562 -11533264 224237 sppa proteinase iv ec 3.4.-.- (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #329(39.7-40.0 min.).) (nt:orf\_id:o329#3; similar to (pir accession number) (le:5694) (re:7550) (di:direct) D90820 D90820 g1742877 Escherichia coli 562 -11533264 300879 sppa protease iv:a signal peptide peptidase (fn:enzyme; degradation of proteins, peptides,) (db:genpept-bct2) (ec:3.4.-.-) (de:escherichia coli k-12 mg1655 section 161 of 400 of the completegenome.) (nt:o618; 99 pct identical to sppa\_ecoli sw: p08395; cg) (le:6614) (re:8470) (di:direct) AE000271 AE000271 g1788064 Escherichia coli 562 -11533264 5000690486 (de:(ecoli\_1723) (pn:protease iv, a signal peptide peptidase) (gn:sppa) (gtcfc:5.9) (ec:3.4.-.-) (sppa\_ecoli) (keggfc:5.9) (rileyfc:3.2.3) (db:gtc-escherichia coli)) ECOLI\_1723 ECOLI\_1723 Escherichia coli 562 10119819

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829479	8228	30384	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829486	8229	30385	351	117

Description

6500729407 yegq:b2081 hypothetical protein:putative protease in baer-ogr  
intergenic region (gtcfc:10.11:5.9:14.1) (ec:3.4.-.-) (keggfc:5.9)  
(rileyfc:5.7.0) (db:gtc-escherichia coli) b2081 b2081 Escherichia coli 562  
-11533265 5500686567 yegq (ec:3.4.-.-) (de:putative protease in baer-ogr  
intergenic region,) (db:swissprot) YEGQ\_ECOLI P76403 ESCHERICHIA COLI 562  
-11533265 7000687623 hypothetical protein b2081 (cl:collagenase prtc)  
(db:pir2.dat) H64974 H64974 Escherichia coli 562 -11533265 224619  
collagenase precursor ec 3.4.-.-. (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #357(46.5-46.8 min.)) (nt:orf\_id:o357#6; similar to (swissprot  
accession) (le:8420) (re:9781) (di:direct) D90846 D90846 g1736789  
Escherichia coli 562 -11533265 301270 collagenase precursor ec 3.4.-.-.  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #358(46.6-46.9  
min.)) (nt:orf\_id:o357#6; similar to (swissprot accession) (le:3065)  
(re:4426) (di:direct) D90847 D90847 g1736801 Escherichia coli 562 -11533265  
301259 yegq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 188 of 400 of the completegenome.)  
(nt:o453; this 453 aa orf is 80 pct identical (4 gaps)) (le:624) (re:1985)  
(di:direct) AE000298 AE000298 g1788397 Escherichia coli 562 -11533265  
224630 collagenase precursor ec 3.4.-.-. (sr:escherichia coli (strain:k12)  
dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic  
dna, kohara clone #358(46.6-46.9 min.)) (nt:orf\_id:o357#6; similar to  
(swissprot accession) (le:3065) (re:4426) (di:direct) D90847 D90847 g1736801  
Escherichia coli 562 -11533265 5000692686 (de:(ecoli\_2029) (pn:function not  
assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0)  
(db:gtc-escherichia coli)) ECOLI\_2029 ECOLI\_2029 Escherichia coli 562  
10119994

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829487	8230	30386	501	166

Description

6500729408 yhbu:b3158 putative protease in soha-mtr intergenic region:putative protease in soha-mtr intergenic region precursor (gtcfc:10.11:5.9:14.3) (ec:3.4.-.-) (keggfc:5.9) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3158 b3158 Escherichia coli 562 -11533266 112649 yhbu (ec:3.4.-.-) (de:(ec 3.4.-.-)) (db:swissprot) YHBU\_ECOLI P45527 ESCHERICHIA COLI 562 -11533266 7000687908 yhbu probable proteinase:soha-mtr intergenic region (ec:3.4.-.-) (db:pir2.dat) B65106 B65106 Escherichia coli 562 -11533266 7500936781 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf\_o331) (le:82237) (re:83232) (di:direct) ECOUW67 U18997 g606098 Escherichia coli 562 -11533266 236397 yhbu putative collagenase (fn:orf; not classified) (db:genpept-bct2) (ec:3.4.-.-) (de:escherichia coli k-12 mg1655 section 286 of 400 of the completgenome.) (nt:o331; 100 pct identical amino acid sequence and) (le:8148) (re:9143) (di:direct) AE000396 AE000396 g1789548 Escherichia coli 562 -11533266 5000690487 (de:(ecoli\_3082) (pn:putative protease in soha-mtr intergenic region:o331) (gn:yhbu) (gtcfc:5.9) (ec:3.4.-.-) (yhbu ecoli) (keggfc:5.9) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_3082 ECOLI\_3082 Escherichia coli 562 10054377

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829495	8231	30387	852	284

Description

6500729409 pepe:b4021 peptidase e:alpha-aspartyl dipeptidase (gtcfc:5.9:10.11) (ec:3.4.-.-) (keggfc:5.9) (rileyfc:3.2.3) (db:gtc-escherichia coli) b4021 b4021 Escherichia coli 562 -11533267 89016 pepe (ec:3.4.-.-) (de:peptidase e, (alpha-aspartyl dipeptidase)) (db:swissprot) PEPE\_ECOLI P32666 ESCHERICHIA COLI 562 -11533267 7000686111 pepe peptidase e (cl:alpha-aspartyl dipeptidase) (db:pir2.dat) D65209 D65209 Escherichia coli 562 -11533267 237227 pepe peptidase e:a dipeptidase where amino-terminal (fn:enzyme; degradation of proteins, peptides,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 365 of 400 of the completgenome.) (nt:f229a) (le:6809) (re:7498) (di:complement) AE000475 AE000475 g1790452 Escherichia coli 562 -11533267 7500887815 pepe peptidase e (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:94695) (re:95384) (di:complement) ECOUW89 U00006 g396356 Escherichia coli 562 -11533267 5000690488 (de:(ecoli\_3907) (pn:peptidase e, a dipeptidase where amino-terminal residue is aspartate) (gn:pepe) (gtcfc:5.9) (ec:3.4.-.-) (pepe\_ecoli) (keggfc:5.9) (rileyfc:3.2.3) (db:gtc-escherichia coli)) ECOLI\_3907 ECOLI\_3907 Escherichia coli 562 10031142



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829498	8232	30388	270	89
<u>Description</u>				
6500729410 cada:b4131 lysine decarboxylase:lysine decarboxylase:inducible:ldc (gtcfc:5.9:6.6) (ec:4.1.1.18) (keggfc:5.9) (rileyfc:1.1.2) (db:gtc-escherichia coli) b4131 b4131 Escherichia coli 562 -11533268 68020 cada (ec:4.1.1.18) (de:lysine decarboxylase, inducible, (ldc)) (db:swissprot) DCLY_ECOLI P23892 ESCHERICHIA COLI 562 -11533268 164014 cada lysine decarboxylase:cada (ec:4.1.1.18) (db:pir2.dat) (mp:94 min) B41842 B41842 Escherichia coli 562 -11533268 237340 cada (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli cada gene, 5' cds and cadb and cadc genes, complete cds.) (le:1913) (re:4060) (di:direct) ECOCADABC M76411 g145458 Escherichia coli 562 -11533268 7500880056 cada lysine decarboxylase (db:genpept-bct1) (ec:4.1.1.18) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 943) (le:47298) (re:49445) (di:complement) ECOUW93 U14003 g536976 Escherichia coli 562 -11533268 233933 cada lysine decarboxylase 1 (fn:enzyme; degradation of small molecules: amino) (db:genpept-bct2) (ec:4.1.1.18) (de:escherichia coli k-12 mg1655 section 375 of 400 of the completegenome.) (nt:f715; 100 pct identical to dcly_ecoli sw: p23892;) (le:10881) (re:13028) (di:complement) AE000485 AE000485 g1790573 Escherichia coli 562 -11533268 5000690489 (de:(ecoli_4018) (pn:lysine decarboxylase) (gn:cada) (gtcfc:5.9) (ec:4.1.1.18) (dcly_ecoli) (keggfc:5.9) (rileyfc:1.1.2) (db:gtc-escherichia coli)) ECOLI_4018 ECOLI_4018 Escherichia coli 562 10010613				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829508	8233	30389	459	152

Description

6500729411 ampc:ampa:b4150 beta-lactamase precursor:cephalosporinase  
 (gtcfc:5.9:13.3) (ec:3.5.2.6) (keggfc:5.9) (rileyfc:5.4.0)  
 (db:gtc-escherichia coli) b4150 b4150 Escherichia coli 562 -11533269 59354  
 ampc:ampa (ec:3.5.2.6) (de:beta-lactamase precursor, (cephalosporinase))  
 (db:swissprot) AMPC\_ECOLI P00811 ESCHERICHIA COLI 562 -11533269 125050 ampc  
 beta-lactamase:precursor:cephalosporinase (cl:escherichia coli  
 beta-lactamase) (ec:3.5.2.6) (db:pir1.dat) (mp:93.8 min) QKEC A01007  
 Escherichia coli 562 -11533269 237358 ampc (sr:escherichia coli (strain  
 k-12) dna) (db:genpept-bct1) (de:e.coli frd operon, fumarate reductase  
 (flavoprotein subunit frdaand iron/sulfur subunit frdb), and beta-lactamase  
 (ampc) genes,complete cds.) (nt:beta-lactamase) (le:4156) (re:5289)  
 (di:direct) ECOAMPCFR J01611 g145267 Escherichia coli 562 -11533269  
 7500876832 ampc beta-lactamase (db:genpept-bct1) (de:escherichia coli k-12  
 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 1033)  
 (le:68639) (re:69772) (di:complement) ECOUW93 U14003 g536994 Escherichia  
 coli 562 -11533269 233783 ampc beta-lactamase:penicillin resistance  
 (fn:enzyme; drug/analog sensitivity) (db:genpept-bct2) (ec:3.5.2.6)  
 (de:escherichia coli k-12 mg1655 section 377 of 400 of the completegenome.)  
 (nt:f377; 100 pct identical to ampc\_ecoli sw: p00811;) (le:9301) (re:10434)  
 (di:complement) AE000487 AE000487 g1790593 Escherichia coli 562 -11533269  
 5000690490 (de:(ecoli\_4036) (pn:beta-lactamase; penicillin resistance)  
 (gn:ampc) (gtcfc:5.9) (ec:3.5.2.6) (ampc\_ecoli) (keggfc:5.9) (rileyfc:5.4.0)  
 (db:gtc-escherichia coli)) ECOLI\_4036 ECOLI\_4036 Escherichia coli 562  
 10002092

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829511	8234	30390	702	234

Description

6500729412 hflc:hfla:b4175 hflc protein (gtcfc:5.9:10.11) (ec:3.4.-.-)  
(keggfc:5.9) (rileyfc:3.2.3) (db:gtc-escherichia coli) b4175 b4175  
Escherichia coli 562 -11533270 76908 hflc:hfla (ec:3.4.-.-) (de:hflc  
protein,) (db:swissprot) HFLC\_ECOLI P25661 ESCHERICHIA COLI 562 -11533270  
164386 hflc probable integral membrane proteinase:hflc (ec:3.4.-.-)  
(db:pir2.dat) C43653 C43653 Escherichia coli 562 -11533270 237380 hflc  
(db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to  
00.1 minutes.) (nt:cg site no. 17520; alternate gene name hfla;) (le:94128)  
(re:95132) (di:direct) ECOUW93 U14003 g537016 Escherichia coli 562 -11533270  
234643 hflc protease specific for phage lambda cii (fn:enzyme; degradation  
of proteins, peptides,) (db:genpept-bct2) (ec:3.4.-.-) (de:escherichia coli  
k-12 mg1655 section 379 of 400 of the completegenome.) (nt:o334; 100 pct  
identical to hflc\_ecoli sw: p25661;) (le:11014) (re:12018) (di:direct)  
AE000489 AE000489 g1790617 Escherichia coli 562 -11533270 7500883236 hflc  
(sr:escherichia coli k12) (db:genpept-bct2) (de:e. coli hfla locus encoding  
the hflx, hflk and hflc genes, hfggene, complete cds; miaa gene, partial  
cds.) (nt:putative integral membrane protease required for) (le:3750)  
(re:4754) (di:direct) ECOHFLA U00005 g436158 Escherichia coli 562 -11533270  
5000690491 (de:(ecoli\_4058) (pn:protease specific for phage lambda cii  
repressor) (gn:hflc) (gtcfc:5.9) (ec:3.4.-.-) (hflc\_ecoli) (keggfc:5.9)  
(rileyfc:3.2.3) (db:gtc-escherichia coli)) ECOLI\_4058 ECOLI\_4058 Escherichia  
coli 562 10019270

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829515	8235	30391	222	73

Description

6500729413 panc:b0133 pantoate:beta-alanine ligase:pantoate--beta-alanine  
ligase:pantothenate synthetase:pantoate activating enzyme (gtcfc:6.1:9.5)  
(ec:6.3.2.1) (keggfc:6.1:9.5) (rileyfc:1.7.5) (db:gtc-escherichia coli)  
b0133 b0133 Escherichia coli 562 -11533271 88575 panc (ec:6.3.2.1)  
(de:(pantoate activating enzyme)) (db:swissprot) PANC\_ECOLI P31663  
ESCHERICHIA COLI 562 -11533271 7000686080 panc pantoate--beta-alanine  
ligase (cl:pantoate--beta-alanine ligase) (ec:6.3.2.1) (db:pir2.dat) E64736  
E64736 Escherichia coli 562 -11533271 7500887645 panc pantothenate  
synthetase (fn:pantoate + beta-alanine + atp -- pantothenate)  
(sr:escherichia coli (sub\_strain w3110, strain k-12) dna) (db:genpept-bct1)  
(de:e. coli alpha-ketopantoate hydroxymethyl transferase (panb),pantothenate  
synthetase (panc), aspartate-1-decarboxylase (pa... ECOPANBCD L17086 g304928  
Escherichia coli 562 -11533271 235330 panc pantothenate synthetase  
(fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2)  
(ec:6.3.2.1) (de:escherichia coli k-12 mg1655 section 12 of 400 of the  
completegenome.) (nt:f283; 100 pct identical to panc\_ecoli sw: p31663)  
(le:9240) (re:10091) (di:complement) AE000122 AE000122 g1786325 Escherichia  
coli 562 -11533271 5000690493 (de:(ecoli\_133) (pn:pantothenate synthetase)  
(gn:panc) (gtcfc:6.1:9.5) (ec:6.3.2.1) (panc\_ecoli) (keggfc:6.1:9.5)  
(rileyfc:1.7.5) (db:gtc-escherichia coli)) ECOLI\_133 ECOLI\_133 Escherichia  
coli 562 10030702

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829516	8236	30392	294	97

Description

6500729414 ddlb:ddl:b0092 d-alanine:d-alanine ligase b:d-alanine--d-alanine ligase b:d-alanylalanine synthetase (gtcfc:11.4:6.15:8.1) (ec:6.3.2.4) (keggfc:6.8:7.3:8.1) (rileyfc:3.3.4) (db:gtc-escherichia coli) b0092 b0092 Escherichia coli 562 -11533272 126000 ddlb:ddl d-alanine--d-alanine ligase:b:alanylalanine synthetase (cl:d-alanine--d-alanine ligase) (ec:6.3.2.4) (db:pir1.dat) (mp:2 min) CEECDL A30289 Escherichia coli 562 -11533272 227999 ddl d-ala:d-ala ligase ddl (db:genpept-bct1) (de:e. coli 2 minute region.) (le:18763) (re:19683) (di:direct) EC2MIN X55034 g40860 Escherichia coli 562 -11533272 234134 ddl d-alanine-d-alanine ligase (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (ec:6.3.2.4) (de:e.coli k12 genome, 0-2.4min. region.) (le:101887) (re:102807) (di:direct) ECO110K D10483 g216506 Escherichia coli 562 -11533272 234408 ddl (sr:e.coli dna) (db:genpept-bct1) (de:e.coli ddl gene complete cds and ftsq' gene, partial cds.) (nt:ddl cell wall enzyme) (le:146) (re:1066) (di:direct) ECODDLFTS M14029 g145724 Escherichia coli 562 -11533272 304536 ddl (sr:e.coli dna, clone lambda-16-2) (db:genpept-bct1) (de:e. coli ddl gene encoding d-alanine:d-alanine ligase and ftsq andfts genes, complete cds, and ftsz gene, 5' end.) (nt:d-alanine:d-alanine ligase) (le:146) (re:1066) (di:direct) ECOFTSQA K02668 g146030 Escherichia coli 562 -11533272 233616 ddlb d-alanine-d-alanine ligase b:affects cell (fn:enzyme; murein sacculus, peptidoglycan) (db:genpept-bct2) (ec:6.3.2.4) (de:escherichia coli k-12 mg1655 section 8 of 400 of the completegenome.) (nt:o306; 100 pct identical to ddlb\_ecoli sw: p07862) (le:18688) (re:19608) (di:direct) AE000118 AE000118 g1786280 Escherichia coli 562 -11533272 5000690494 (de:(ecoli\_92) (pn:d-alanine-d-alanine ligase b) (gn:ddlb) (gtcfc:6.15:11.4) (ec:6.3.2.4) (ddlb\_ecoli) (keggfc:6.8:7.3) (rileyfc:3.3.4) (db:gtc-escherichia coli)) ECOLI\_92 ECOLI\_92 Escherichia coli 562 10066509

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829518	8237	30393	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829526	8238	30394	1992	664

Description

6500729415 ddla:b0381 d-alanine:d-alanine ligase a:d-alanine--d-alanine  
ligase a:d-alanylalanine synthetase (gtcfc:11.4:6.15:8.1) (ec:6.3.2.4)  
(keggfc:6.8:7.3:8.1) (rileyfc:3.3.4) (db:gtc-escherichia coli) b0381 b0381  
Escherichia coli 562 -11533273 68157 ddla (ec:6.3.2.4) (de:synthetase))  
(db:swissprot) DDLA\_ECOLI P23844 ESCHERICHIA COLI 562 -11533273 126001 ddla  
d-alanine--d-alanine ligase:a:d-alanylalanine synthetase a  
(cl:d-alanine--d-alanine ligase) (ec:6.3.2.4) (db:pir1.dat) CEECD A39182  
Escherichia coli 562 -11533273 239997 ddla d-alanine:d-alanine ligase a  
(sr:e.coli (strain w3110) dna) (db:genpept-bct1) (ec:6.3.2.4) (de:e.coli  
d-alanine:d-alanine ligase a (ddla) gene, complete cds.) (le:431) (re:1525)  
(di:direct) ECODDLA M58467 g145722 Escherichia coli 562 -11533273  
7500880107 ddla d-alanine--d-alanine ligase a (db:genpept-bct1)  
(ec:6.3.2.4) (de:escherichia coli chromosome minutes 6-8.) (le:107419)  
(re:108513) (di:complement) ECU73857 U73857 g1657576 Escherichia coli 562  
-11533273 234133 ddla d-alanine-d-alanine ligase a (fn:enzyme; murein  
sacculus, peptidoglycan) (db:genpept-bct2) (ec:6.3.2.4) (de:escherichia coli  
k-12 mg1655 section 34 of 400 of the completegenome.) (nt:f364; 100 pct  
identical to ddla\_ecoli sw: p23844) (le:9651) (re:10745) (di:complement)  
AE000144 AE000144 g1786579 Escherichia coli 562 -11533273 5000690495  
(de:(ecoli\_365) (pn:d-alanine-d-alanine ligase a) (gn:ddla)  
(gtcfc:6.15:11.4) (ec:6.3.2.4) (ddla\_ecoli) (keggfc:6.8:7.3) (rileyfc:3.3.4)  
(db:gtc-escherichia coli)) ECOLI\_365 ECOLI\_365 Escherichia coli 562 10010750

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829536	8239	30395	285	94

Description

6500729416 gst:b1635 glutathione s-transferase (gtcfc:6.16:14.3)  
(ec:2.5.1.18) (keggfc:6.9) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1635  
b1635 Escherichia coli 562 -11533274 74971 gst (ec:2.5.1.18)  
(de:glutathione s-transferase,) (db:swissprot) GT\_ECOLI P39100 ESCHERICHIA  
COLI 562 -11533274 163132 gst glutathione transferase (cl:glutathione  
transferase) (ec:2.5.1.18) (db:pir2.dat) A55495 A55495 Escherichia coli 562  
-11533274 224074 gst glutathione s-transferase ec 2.5.1.18 .  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #316(36.7-37.1  
min.)) (nt:orf\_id:o316#14; similar to (swissprot accession) (le:11983)  
(re:12588) (di:direct) D90807 D90807 g1742701 Escherichia coli 562 -11533274  
300757 glutathione transferase (sr:escherichia coli (strain k12, sub\_strain  
w3110) (library: kohara') (db:genpept-bct1) (ec:2.5.1.18) (de:escherichia  
coli gene for glutathione transferase, complete cds.) (le:140) (re:745)  
(di:direct) ECOGST D38497 g1213565 Escherichia coli 562 -11533274 234584  
gst glutathionine s-transferase (fn:enzyme; biosynthesis of cofactors,  
carriers:) (db:genpept-bct2) (ec:2.5.1.18) (de:escherichia coli k-12 mg1655  
section 149 of 400 of the completengenome.) (nt:o201; 100 pct identical to  
gt\_ecoli sw: p39100) (le:1984) (re:2589) (di:direct) AE000259 AE000259  
g1787923 Escherichia coli 562 -11533274 5000690496 (de:(ecoli\_1594)  
(pn:glutathionine s-transferase) (gn:gst) (gtcfc:6.16) (ec:2.5.1.18)  
(gt\_ecoli) (keggfc:6.9) (rileyfc:5.7.0) (db:gtc-escherichia coli))  
ECOLI\_1594 ECOLI\_1594 Escherichia coli 562 10017483

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829537	8240	30396	234	77

# Description

6500729417 ggt:b3447  
gamma-glutamyltranspeptidase:gamma-glutamyltranspeptidase precursor  
(gtcfc:6.16:6.4:6.5:8.2:9.2) (ec:2.3.2.2) (keggfc:6.4:6.5:6.9:8.6)  
(rileyfc:1.7.9) (db:gtc-escherichia coli) (gtcfc:metabolism of other amino  
acids-glutathione metabolism:metabolism of other amino acids-selenoamino  
acid metabolism:metabolism of other a... b3447 b3447 Escherichia coli 562  
-11533275 73583 ggt (ec:2.3.2.2) (de:gamma-glutamyltranspeptidase  
precursor,) (db:swissprot) GGT\_ECOLI P18956 ESCHERICHIA COLI 562 -11533275  
123409 ggt gamma-glutamyltransferase:precursor:ggt protein:glutamyl  
transpeptidase (cl:gamma-glutamyltransferase) (ec:2.3.2.2) (db:pir1.dat)  
(mp:76 min) EKECEX JV0028 Escherichia coli 562 -11533275 236681 ggt  
gamma-glutamyltranspeptidase (sr:escherichia coli (strain k-12) dna)  
(db:genpept-bct1) (ec:2.3.2.2) (de:escherichia coli  
gamma-glutamyltranspeptidase (ggt) gene, completecds.) (le:137) (re:1879)  
(di:direct) ECOGGT M28722 g146133 Escherichia coli 562 -11533275 7500882327  
ggt gamma-glutamyltranspeptidase (db:genpept-bct1) (ec:2.3.2.2)  
(de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.)  
(nt:cg site no. 18280) (le:365818) (re:367560) (di:complement) ECOUW67  
U18997 g606382 Escherichia coli 562 -11533275 234479 ggt  
gamma-glutamyltranspeptidase (fn:enzyme; biosynthesis of cofactors,  
carriers:) (db:genpept-bct2) (ec:2.3.2.2) (de:escherichia coli k-12 mg1655  
section 311 of 400 of the completegenome.) (nt:f580; 100 pct identical amino  
acid sequence and) (le:634) (re:2376) (di:complement) AE000421 AE000421  
g1789856 Escherichia coli 562 -11533275 5000690497 (de:(ecoli\_3365)  
(pn:gamma-glutamyltranspeptidase) (gn:ggt) (gtcfc:6.16:6.4:6.5) (ec:2.3.2.2)  
(ggt\_ecoli) (keggfc:6.4:6.5:6.9) (rileyfc:1.7.9) (db:gtc-escherichia coli))  
ECOLI\_3365 ECOLI\_3365 Escherichia coli 562 10016117



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829538	8241	30397	273	90

Description

6500729418 seld:fdhb:b1764 selenophosphate synthase:selenide:water  
dikinase:selenophosphate synthetase:selenium donor protein (gtcfc:6.4:10.6)  
(ec:2.7.9.3) (keggfc:6.4) (rileyfc:3.1.5) (db:gtc-escherichia coli) b1764  
b1764 Escherichia coli 562 -11533276 98385 seld:fdhb (ec:2.7.9.3)  
(de:(selenium donor protein)) (db:swissprot) SELD\_ECOLI P16456 ESCHERICHIA  
COLI 562 -11533276 164596 seld selenophosphate synthase (db:pir2.dat)  
JW0033 JW0033 Escherichia coli 562 -11533276 224235 seld:fdhb  
selenide:water dikinase ec 2.7.9.3 (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #329(39.7-40.0 min.)) (nt:orf\_id:o329#1; similar to (swissprot  
accession) (le:3822) (re:4865) (di:complement) D90820 D90820 g1742875  
Escherichia coli 562 -11533276 300877 seld selenium metabolism protein  
(sr:escherichia coli (strain mc4100) (clone: pmn302) dna) (db:genpept-bct1)  
(de:e.coli selenium metabolism protein (seld) gene, complete cds.) (le:38)  
(re:1081) (di:direct) ECOSEL D M30184 g147806 Escherichia coli 562 -11533276  
235968 seld selenophosphate synthase:h 2 se added to (fn:enzyme; aminoacyl  
trna synthetases, trna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655  
section 161 of 400 of the completegenome.) (nt:f347; 100 pct identical to  
seld\_ecoli sw: p16456;) (le:4742) (re:5785) (di:complement) AE000271  
AE000271 g1788062 Escherichia coli 562 -11533276 5000690511  
(de:(ecoli\_1721) (pn:selenophosphate synthase, h:2se added to acrylyl-trna)  
(gn:seld) (gtcfc:6.4) (ec:2.7.9.3) (seld\_ecoli) (keggfc:6.4) (rileyfc:3.1.5)  
(db:gtc-escherichia coli)) ECOLI\_1721 ECOLI\_1721 Escherichia coli 562  
10040262

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829539	8242	30398	219	72

Description

6500729419 sela:fdha:b3591 l-seryl-trna:cysteiny-trna:ser selenium  
transferase:selenocysteine synthase:selenocysteiny-trna:ser synthase  
(gtcfc:10.6:5.5) (ec:2.9.1.1) (keggfc:6.4) (rileyfc:3.1.5)  
(db:gtc-escherichia coli) b3591 b3591 Escherichia coli 562 -11533277  
7000691856 sela seryl-trna ser selenium transferase::cysteiny-trna ser  
selenium transferase:selenocysteine synthase:selenocysteiny-trna ser  
synthase (ec:2.9.1.1) (db:pir2.dat) A65159 A65159 Escherichia coli 562  
-11533277 7500960456 sela selenocysteine synthase:l-seryl-trna ser  
(fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:2.9.1.1)  
(de:escherichia coli k-12 mg1655 section 326 of 400 of the completegenome.)  
(nt:f463; 99 pct identical amino acid sequence and) (le:8931) (re:10322)  
(di:complement) AE000436 AE000436 g2367248 Escherichia coli 562 -11533277

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829540	8243	30399	222	73

Description

6500729420 dsdc:b2364 d-serine deaminase activator (gtcfc:6.6) (keggfc:14.2) (rileyfc:1.1.2) (db:gtc-escherichia coli) b2364 b2364 Escherichia coli 562 -11533278 69319 dsdc (de:d-serine deaminase activator) (db:swissprot) DSDC\_ECOLI P46068 ESCHERICHIA COLI 562 -11533278 7000685103 dsdc d-serine deaminase activator (cl:regulatory protein ampr) (db:pir2.dat) A65010 A65010 Escherichia coli 562 -11533278 224911 dsdc d-serine deaminase activator. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #411(53.2-53.6 min.)) (nt:similar to (swissprot accession number p46068)) (le:9703) (re:10638) (di:complement) D90866 D90866 g1799763 Escherichia coli 562 -11533278 224919 dsdc d-serine deaminase activator. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #412(53.4-53.8 min.)) (nt:similar to (swissprot accession number p46068)) (le:462) (re:1397) (di:complement) D90867 D90867 g1799772 Escherichia coli 562 -11533278 7500880674 dsdc d-serine dehydratase deaminase transcriptional (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 214 of 400 of the completegenome.) (nt:f311; 99 pct identical to dsdc\_ecoli sw: p46068) (le:6113) (re:7048) (di:complement) AE000324 AE000324 g1788706 Escherichia coli 562 -11533278 5000690513 (de:(ecoli\_2312) (pn:activator of sdhd) (gn:dsdc) (gtcfc:6.6) (ec:) (dsdc\_ecoli) (keggfc:11.2) (rileyfc:1.1.2) (db:gtc-escherichia coli)) ECOLI\_2312 ECOLI\_2312 Escherichia coli 562 10120145

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829544	8244	30400	504	167

Description

6500729421 tdca:b3118 bc operon transcriptional activator (gtcfc:6.6:10.2) (keggfc:14.2) (rileyfc:1.1.2) (db:gtc-escherichia coli) b3118 b3118  
Escherichia coli 562 -11533279 7500892860 tdca (de:tdc operon transcriptional activator) (db:swissprot) TDCA\_ECOLI P11036 ESCHERICHIA COLI 562 -11533279 154802 tdca tdca protein:tdcabc operon transcriptional activator (cl:regulatory protein ilvy) (db:pir1.dat) (mp:67 min) QQECRG S46415 Escherichia coli 562 -11533279 238330 tdca tdcabc operon transcriptional activator (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 29702) (le:46881) (re:47819) (di:complement) ECOUW67 U18997 g606059 Escherichia coli 562 -11533279 5000690514 (db:genpept-bct1) (de:e. coli tdc operon for threonine dehydratase (ec 4.2.1.16).) (nt:tdca gene product (aa 1 - 312)) (le:1904) (re:2842) (di:direct) ECTDCRAB X14430 g43042 Escherichia coli 562 -11533279 236358 tdca transcriptional activator of tdc operon (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 283 of 400 of the completegenome.) (nt:f312; cg site no. 29702; 100 pct identical) (le:6983) (re:7921) (di:complement) AE000393 AE000393 g1789506 Escherichia coli 562 -11533279 7502851913 (db:genpept) (de:e. coli tdc operon for threonine dehydratase (ec 4.2.1.16).) (nt:tdca gene product (aa 1 - 312)) (le:1904) (re:2842) (di:direct) ECTDCRAB X14430 g43042 Escherichia coli 562 -11533279 100938 tdca (de:tdc operon transcriptional activator) (db:swissprot) TDCA\_ECOLI P11036 ESCHERICHIA COLI 562 -11533279

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829547	8245	30401	843	281

Description

6500729422 tdcrc:b3119 tdcabc operon transcriptional activator  
(gtcfc:6.6:10.2) (keggfc:14.2) (rileyfc:1.1.2) (db:gtc-escherichia coli)  
b3119 b3119 Escherichia coli 562 -11533280 7000688985 tdcrc tdcabc operon  
transcription activator (cl:tdcabc operon transcription activator)  
(db:pir1.dat) (mp:67 min) BVCTD D65101 Escherichia coli 562 -11533280  
7500953659 tdcrc tdcabc operon transcriptional activator (db:genpept-bct1)  
(de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.)  
(nt:cg site no. 29692; differences from database) (le:48008) (re:48352)  
(di:direct) ECOUW67 U18997 g606060 Escherichia coli 562 -11533280 236359  
tdcrc threonine dehydratase operon activator protein (fn:regulator;  
degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12  
mg1655 section 283 of 400 of the completegenome.) (nt:ol14; 100 pct  
identical to tdcrc\_ecoli sw: p11866) (le:8110) (re:8454) (di:direct) AE000393  
AE000393 g1789507 Escherichia coli 562 -11533280 5000690515  
(de:(ecoli\_3044) (pn:threonine dehydratase operon activator protein)  
(gn:tdcrc) (gtcfc:6.6) (ec:) (tdcrc\_ecoli) (keggfc:11.2) (rileyfc:1.1.2)  
(db:gtc-escherichia coli)) ECOLI\_3044 ECOLI\_3044 Escherichia coli 562  
10123979

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829557	8246	30402	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829567	8247	30403	498	166

Description

GTC ORF with score 398 to: (sr:t.reesei (strain vtt-d-80133) dna, clone w12;  
and cdna to mrna) (db:genpept-pln1) (de:trichoderma reesei endoglucanase i  
gene, complete cds.) (nt:endoglucanase i precursor) (le:11:851:1498)  
(re:780:1440:1517) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829577	8248	30404	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829591	8249	30405	228	75

Description

6500729423 tnal:tnac:b3707 tna operon leader peptide:tryptophanase leader peptide (gtcfc:6.6) (keggfc:14.2) (rileyfc:1.1.2) (db:gtc-escherichia coli) b3707 b3707 Escherichia coli 562 -11533281 82433 tnal:tnac (de:tryptophanase leader peptide) (db:swissprot) LPTN\_ECOLI P09408 ESCHERICHIA COLI 562 -11533281 164689 tnal tnac protein:tna operon leader peptide (cl:unassigned leader peptides) (db:pir2.dat) I54862 I54862 Escherichia coli 562 -11533281 236943 (sr:e.coli k-12 dna from plasmid pmd4) (db:genpept-bct1) (de:e.coli tnaa gene, encoding tryptophanase, promoter region.) (nt:tnac) (le:264) (re:338) (di:direct) ECOTNAAA M11990 g148000 Escherichia coli 562 -11533281 7500885134 tnac tna operon leader peptide (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:77832) (re:77906) (di:direct) ECOUW82 L10328 g290555 Escherichia coli 562 -11533281 236109 tnal tryptophanase leader peptide (fn:leader; degradation of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 338 of 400 of the completegenome.) (nt:o24; 100 pct identical amino acid sequence and) (le:152) (re:226) (di:direct) AE000448 AE000448 g1790143 Escherichia coli 562 -11533281 5000690516 (de:(ecoli\_3625) (pn:tryptophanase leader peptide) (gn:tnal) (gtcfc:6.6) (ec:) (lptn\_ecoli) (keggfc:11.2) (rileyfc:1.1.2) (db:gtc-escherichia coli)) ECOLI\_3625 ECOLI\_3625 Escherichia coli 562 10024657

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829592	8250	30406	351	116

Description

GTC ORF with score 153 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f41e6.) (nt:coded for by c. elegans cdna yk9a5.5; coded for by) (le:19297:20061:20687:20987) (re:19568:20637:20941:21895) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829593	8251	30407	216	72

Description

GTC ORF with score 180 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1040.) (nt:unnamed protein product) (le:<1) (re:631) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829609	8252	30408	1470	489
<u>Description</u>				
6500729424 adiy:b4116 putative regulatory protein adiy (gtcfc:6.6) (keggfc:14.2) (rileyfc:1.1.2) (db:gtc-escherichia coli) b4116 b4116 Escherichia coli 562 -11533282 58784 adiy (de:putative regulatory protein adiy) (db:swissprot) ADIY_ECOLI P33234 ESCHERICHIA COLI 562 -11533282 164397 adiy probable transcription regulator adiy (db:pir2.dat) S56345 S56345 Escherichia coli 562 -11533282 228046 adiy putative regulatory protein (db:genpept-bct1) (de:escherichia coli k12 arginine decarboxylase (adi) gene, 3' regionand putative regulatory protein (adiy) gene, complete cds.) (le:299) (re:1060) (di:direct) ECADIY U02384 g407284 Escherichia coli 562 -11533282 7500876598 adiy (fn:putative regulatory protein) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:27996) (re:28757) (di:complement) ECOUW93 U14003 g536961 Escherichia coli 562 -11533282 237325 adiy putative arac-type regulatory protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 374 of 400 of the completegenome.) (nt:f253; 100 pct identical amino acid sequence and) (le:1541) (re:2302) (di:complement) AE000484 AE000484 g1790557 Escherichia coli 562 -11533282 5000690517 (de:(ecoli_4003) (pn:putative regulatory protein adiy) (gn:adiy) (gtcfc:6.6) (ec:) (adiy_ecoli) (keggfc:11.2) (rileyfc:1.1.2) (db:gtc-escherichia coli)) ECOLI_4003 ECOLI_4003 Escherichia coli 562 10001529				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829619	8253	30409	465	154
<u>Description</u>				
6500729425 cadc:b4133 transcriptional activator:transcriptional activator cadc (gtcfc:6.6:10.2) (keggfc:14.2) (rileyfc:1.1.2) (db:gtc-escherichia coli) b4133 b4133 Escherichia coli 562 -11533283 62421 cadc (de:transcriptional activator cadc) (db:swissprot) CADC_ECOLI P23890 ESCHERICHIA COLI 562 -11533283 164732 cadc transcription activator cadc (db:pir2.dat) C41968 C41968 Escherichia coli 562 -11533283 237342 cadc transcriptional activator (fn:required for pcad induction, is similar to phob) (sr:e.coli k-12 dna, clones lambda-(5g7, 21h11)) (db:genpept-bct1) (de:escherichia coli lysine decarboxylase (cadb, and cadc, completecds, and cada, 5' end) genes.) (le:872) (re:2410) (di:direct) ECOCADAB M67452 g145452 Escherichia coli 562 -11533283 7500878080 cadc (fn:transcriptional activator) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:51224) (re:52762) (di:complement) ECOUW93 U14003 g536978 Escherichia coli 562 -11533283 233928 cadc transcriptional activator of cad operon (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 376 of 400 of the completegenome.) (nt:f512; 100 pct identical to cadc_ecoli sw: p23890) (le:1769) (re:3307) (di:complement) AE000486 AE000486 g1790576 Escherichia coli 562 -11533283 5000690518 (de:(ecoli_4020) (pn:transcriptional activator of cad operon) (gn:cadc) (gtcfc:6.6) (ec:) (cadc_ecoli) (keggfc:11.2) (rileyfc:1.1.2) (db:gtc-escherichia coli)) ECOLI_4020 ECOLI_4020 Escherichia coli 562 10005119				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829628	8254	30410	513	170

Description

6500729426 murd:b0088 udp-n-acetylmuramoyl-l-alanine:d-glutamate  
ligase:udp-n-acetylmuramoylalanine--d-glutamate  
ligase:udp-n-acetylmuranoyl-l-alanyl-d-glutamate synthetase (gtcfc:11.4:6.7)  
(ec:6.3.2.9) (keggfc:6.6:7.3) (rileyfc:3.3.4) (db:gtc-escherichia coli)  
b0088 b0088 Escherichia coli 562 -11533284 126009 murd  
udp-n-acetylmuramoylalanine--d-glutamate  
ligase::udp-n-acetylmuramoyl-l-alanyl-d-glutamate synthetase  
(cl:udp-n-acetylmuramate--alanine ligase) (ec:6.3.2.9) (db:pir1.dat) (mp:2  
min) CEECME S08396 Escherichia coli 562 -11533284 227995 murd  
udp-murnac-l-ala-d-glu murd aa 1-438 (db:genpept-bct1) (de:e. coli 2 minute  
region.) (le:13617) (re:14933) (di:direct) EC2MIN X55034 g40856 Escherichia  
coli 562 -11533284 233612 (db:genpept-bct1) (de:escherichia coli murd gene  
and orf-y (ec 6.3.2.9).) (nt:murd gene product (aa 1-438)) (le:1196)  
(re:2512) (di:direct) ECMUROY X51584 g42060 Escherichia coli 562 -11533284  
304532 murd udp-n-acetylmuramoylalanine-d-glutamate ligase (sr:escherichia  
coli (strain:k-12) dna) (db:genpept-bct1) (ec:6.3.2.9) (de:e.coli k12  
genome, 0-2.4min. region.) (le:96741) (re:98057) (di:direct) ECO110K D10483  
g216502 Escherichia coli 562 -11533284 233432 murd  
udp-n-acetylmuramoylalanine-d-glutamate ligase (fn:enzyme; murein sacculus,  
peptidoglycan) (db:genpept-bct2) (ec:6.3.2.9) (de:escherichia coli k-12  
mg1655 section 8 of 400 of the completegenome.) (nt:o438; 100 pct identical  
to murd\_ecoli sw: p14900) (le:13542) (re:14858) (di:direct) AE000118  
AE000118 g1786276 Escherichia coli 562 -11533284 5000690519 (de:(ecoli\_88)  
(pn:udp-n-acetylmuramoylalanine-d-glutamate ligase) (gn:murd)  
(gtcfc:6.7:11.4) (ec:6.3.2.9) (murd\_ecoli) (keggfc:6.6:7.3) (rileyfc:3.3.4)  
(db:gtc-escherichia coli)) ECOLI\_88 ECOLI\_88 Escherichia coli 562 10066512



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829631	8255	30411	408	135

Description

6500729427 murc:b0091 udp-n-acetylmuramate:alanine  
ligase:udp-n-acetylmuramate--alanine ligase:udp-n-acetylmuranoyl-l-alanine  
synthetase (gtcfc:11.4:6.7:5.2) (ec:6.3.2.8) (keggfc:6.6:7.3)  
(rileyfc:3.3.4) (db:gtc-escherichia coli) b0091 b0091 Escherichia coli 562  
-11533285 233615 murc (ec:6.3.2.8) (de:acetylmuranoyl-l-alanine  
synthetase)) (db:swissprot) MURC\_ECOLI P17952 ESCHERICHIA COLI 562 -11533285  
126008 murc udp-n-acetylmuramate--alanine  
ligase::udp-n-acetylmuramoyl-l-alanine synthetase  
(cl:udp-n-acetylmuramate--alanine ligase) (ec:6.3.2.8) (db:pir1.dat) (mp:2  
min) CEECAM JQ0545 Escherichia coli 562 -11533285 227998 murc  
udp-n-acetylmuramate--alanine ligase (db:genpept-bct1) (ec:6.3.2.8) (de:e.  
coli 2 minute region.) (le:17295) (re:18770) (di:direct) EC2MIN X55034  
g40859 Escherichia coli 562 -11533285 5000690520 murc  
udp-n-acetylmuramate:l-alanine ligase aa (db:genpept-bct1) (de:escherichia  
coli murg and murc genes for an unidentified readingframe and  
udp-n-acetylmuramate:l-alanine ligase (ec 6.3.2.8)respectively.) (le:1203)  
(re:2678) (di:direct) ECMURGC X52644 g42056 Escherichia coli 562 -11533285  
304535 murc udp-n-acetylmuramate-alanine ligase (sr:escherichia coli  
(strain:k-12) dna) (db:genpept-bct1) (ec:6.3.2.8) (de:e.coli k12 genome,  
0-2.4min. region.) (le:100419) (re:101894) (di:direct) ECO110K D10483  
g216505 Escherichia coli 562 -11533285 233429 murc l-alanine adding enzyme  
(fn:enzyme; murein sacculus, peptidoglycan) (db:genpept-bct2) (ec:6.3.2.8)  
(de:escherichia coli k-12 mg1655 section 8 of 400 of the completegenome.)  
(nt:o491; 100 pct identical to murc\_ecoli sw: p17952) (le:17220) (re:18695)  
(di:direct) AE000118 AE000118 g1786279 Escherichia coli 562 -11533285 84706  
murc (ec:6.3.2.8) (de:acetylmuranoyl-l-alanine synthetase)) (db:swissprot)  
MURC\_ECOLI P17952 ESCHERICHIA COLI 562 -11533285

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829642	8256	30412	465	154

Description

6500729428 lpxa:b0181 udp-n-acetylglucosamine  
o-acyltransferase:acyl-acyl-carrier-protein--udp-n-acetylglucosamine  
o-acyltransferase:udp-n-acetylglucosamine acyltransferase  
(gtcfc:11.2:7.1:11.4) (ec:2.3.1.129) (keggfc:4.4) (rileyfc:3.3.2)  
(db:gtc-escherichia coli) b0181 b0181 Escherichia coli 562 -11533286 82452  
lpxa (ec:2.3.1.129) (de:(ec 2.3.1.129) (udp-n-acetylglucosamine  
acyltransferase)) (db:swissprot) LPXA\_ECOLI P10440 ESCHERICHIA COLI 562  
-11533286 7000685764 lpxa acyl-acyl-carrier-protein  
--udp-n-acetylglucosamine o-acyltransferase,:lpxa protein)  
(cl:udp-n-acetylglucosamine acyltransferase) (ec:2.3.1.129) (db:pir1.dat)  
(mp:4 min) XUECDP E64742 Escherichia coli 562 -11533286 7500885142 lpxa  
acyl-acyl carrier (db:genpept-bct1) (de:escherichia coli chromosome minutes  
4-6.) (le:33635) (re:34423) (di:direct) ECU70214 U70214 g1552758 Escherichia  
coli 562 -11533286 239809 lpxa udp-n-acetylglucosamine  
acetyltransferase:lipid (fn:enzyme; surface polysaccharides and antigens)  
(db:genpept-bct2) (ec:2.3.1.129) (de:escherichia coli k-12 mg1655 section 17  
of 400 of the completegenome.) (nt:o262; 98 pct identical to lpxa\_ecoli sw:  
p10440) (le:7780) (re:8568) (di:direct) AE000127 AE000127 g1786378  
Escherichia coli 562 -11533286 5000690527 (de:(ecoli\_181)  
(pn:udp-n-acetylglucosamine acetyltransferase; lipid a biosynthesis)  
(gn:lpxa) (gtcfc:7.1) (ec:2.3.1.129) (lpxa\_ecoli) (keggfc:4.4)  
(rileyfc:3.3.2) (db:gtc-escherichia coli)) ECOLI\_181 ECOLI\_181 Escherichia  
coli 562 10122696

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829659	8257	30413	1296	431

#### Description

6500729429 lpxb:pgsb:b0182 lipid-a-disaccharide synthase (gtcfc:7.1:11.2) (ec:2.4.1.182) (keggfc:4.4) (rileyfc:3.3.2) (db:gtc-escherichia coli) b0182 b0182 Escherichia coli 562 -11533287 7000688986 lpxb lipid-a-disaccharide synthase (cl:lipid a disaccharide synthase) (ec:2.4.1.182) (db:pir1.dat) (mp:4 min) SYECLA F64742 Escherichia coli 562 -11533287 7500953660 lpxb lipid a disaccharide synthase (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:34423) (re:35571) (di:direct) ECU70214 U70214 g1552759 Escherichia coli 562 -11533287 239810 lpxb tetraacyldisaccharide-1-p:lipid a biosynthesis (fn:enzyme; macromolecule metabolism:) (db:genpept-bct2) (ec:2.4.1.182) (de:escherichia coli k-12 mg1655 section 17 of 400 of the completegenome.) (nt:o382; 99 pct identical to lpxb\_ecoli sw: p10441) (le:8568) (re:9716) (di:direct) AE000127 AE000127 g1786379 Escherichia coli 562 -11533287 5000690528 (de:(ecoli\_182) (pn:tetraacyldisaccharide-1-po4; lipid a biosynthesis, penultimate step) (gn:lpxb) (gtcfc:7.1) (ec:2.4.1.182) (lpxb\_ecoli) (keggfc:4.4) (rileyfc:3.3.2) (db:gtc-escherichia coli)) ECOLI\_182 ECOLI\_182 Escherichia coli 562 10122697

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829666	8258	30414	384	127

#### Description

6500729430 prpb:b0331 hypothetical protein:putative carboxyphosphoenolpyruvate phosphonmutase:cpep phosphonmutase (gtcfc:7.1:8.3:14.1) (ec:2.7.8.-) (keggfc:4.4:8.3) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0331 b0331 Escherichia coli 562 -11533288 1500687020 prpb (ec:2.7.8.-) (de:(cpep phosphonmutase)) (db:swissprot) CPPM\_ECOLI P77541 ESCHERICHIA COLI 562 -11533288 7000684902 prpb probable carboxyphosphoenolpyruvate phosphonmutase:prpb (cl:carboxyphosphoenolpyruvate phosphonmutase) (ec:5.4.2.-) (db:pir2.dat) C64760 C64760 Escherichia coli 562 -11533288 7500879343 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:similar to prpb of s. typhimurium) (le:56477) (re:57367) (di:direct) ECU73857 U73857 g1657527 Escherichia coli 562 -11533288 239948 prpb putative phosphonmutase 2 (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 30 of 400 of the completegenome.) (nt:o296; 37 pct identical (5 gaps) to 293 residues of) (le:3530) (re:4420) (di:direct) AE000140 AE000140 g1786525 Escherichia coli 562 -11533288 5000691519 (de:(ecoli\_315) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_315 ECOLI\_315 Escherichia coli 562 10063368

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829670	8259	30415	558	185

Description

6500729431 naga:b0677 n-acetylglucosamine-6-phosphate deacetylase (gtcfc:7.1) (ec:3.5.1.25) (keggfc:4.4) (rileyfc:1.3.4) (db:gtc-escherichia coli) b0677 b0677 Escherichia coli 562 -11533289 7500886257 naga (ec:3.5.1.25) (de:deacetylase)) (db:swissprot) NAGA\_ECOLI P15300 ESCHERICHIA COLI 562 -11533289 164114 naga n-acetylglucosamine-6-phosphate deacetylase (ec:3.5.1.25) (db:pir2.dat) (mp:15 min) A37018 A37018 Escherichia coli 562 -11533289 223137 naga n-acetylglucosamine-6-phosphate deacetylase (db:genpept-bct1) (de:escherichia coli n-acetylglucosamine-6-phosphate isomerase (nagb),n-acetylglucosamine-6-phosphate deacetylase (naga),n-acetylglucosamine repressor (nagc), and nagd (nagd) genes,complete cds.) (le:1194) (re:2342) (di:direct) AF052007 AF052007 g3005595 Escherichia coli 562 -11533289 223142 naga n-acetylglucosamine-6-phosphate deacetylase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #171) (db:genpept-bct1) (de:escherichia coli genomic dna. (14.8 - 15.2 min).) (le:14581) (re:15729) (di:complement) D90706 D90706 g1651280 Escherichia coli 562 -11533289 233447 naga n-acetylglucosamine-6-phosphate deacetylase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #172) (db:genpept-bct1) (de:escherichia coli genomic dna. (15.0 - 15.4 min).) (le:1431) (re:2579) (di:complement) D90707 D90707 g1651286 Escherichia coli 562 -11533289 5000690529 (db:genpept-bct1) (de:escherichia coli naga, nagc and nagd genes forn-acetylglucosamine-6-phosphate deacetylase.) (nt:naga gene product (aa 1-382)) (le:55) (re:1203) (di:direct) ECNAGACD X14135 g42079 Escherichia coli 562 -11533289 7000685906 naga n-acetylglucosamine-6-phosphate deacetylase (fn:enzyme; central intermediary metabolism: amino) (db:genpept-bct2) (ec:3.5.1.25) (de:escherichia coli k-12 mg1655 section 61 of 400 of the completegenome.) (nt:f382; 100 pct identical to naga\_ecoli sw: p15300) (le:4310) (re:5458) (di:complement) AE000171 AE000171 g1786892 Escherichia coli 562 -11533289 7502851914 naga n-acetylglucosamine-6-phosphate deacetylase ec (sr:escherichia coli(strain:k12) dna, clone:kohara clone #171) (db:genpept) (de:escherichia coli genomic dna. (14.8 - 15.2 min).) (nt:orf\_id:o172#2; similar to pir accession number) (le:14396) (re:15544) (di:complement) D90706 D90706 g1651280 Escherichia coli 562 -11533289 7502851915 naga n-acetylglucosamine-6-phosphate deacetylase ec (sr:escherichia coli(strain:k12) dna, clone:kohara clone #172) (db:genpept) (de:escherichia coli genomic dna. (15.1 - 15.5 min).) (nt:orf\_id:o172#2; similar to pir accession number) (le:1431) (re:2579) (di:complement) D90707 D90707 g1651286 Escherichia coli 562 -11533289 85157 naga (ec:3.5.1.25) (de:deacetylase)) (db:swissprot) NAGA\_ECOLI P15300 ESCHERICHIA COLI 562 -11533289

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829672	8260	30416	618	205
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829673	8261	30417	270	89
<u>Description</u>				

6500729432 nagb:glmd:b0678 glucosamine-6-phosphate isomerase:glucosamine-6-phosphate deaminase (gtcfc:7.1) (ec:5.3.1.10) (keggfc:4.4) (rileyfc:1.3.4) (db:gtc-escherichia coli) b0678 b0678 Escherichia coli 562 -11533290 85160 nagb:glmd (ec:5.3.1.10) (de:phosphate deaminase) (gnpda)) (db:swissprot) NAGB\_ECOLI P09375 ESCHERICHIA COLI 562 -11533290 125808 nagb glucosamine-6-phosphate isomerase (cl:glucosamine-6-phosphate isomerase) (ec:5.3.1.10) (db:pirl.dat) (mp:16 min) MUECNG A29895 Escherichia coli 562 -11533290 223138 nagb glucosamine-6-phosphate isomerase glucosamine- (sr:escherichia coli(strain:k12) dna, clone:kohara clone #171) (db:genpept-bct1) (de:escherichia coli genomic dna. (14.8 - 15.2 min).) (le:15789) (re:16589) (di:complement) D90706 D90706 g1651281 Escherichia coli 562 -11533290 223143 nagb glucosamine-6-phosphate isomerase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #172) (db:genpept-bct1) (de:escherichia coli genomic dna. (15.0 - 15.4 min).) (le:2639) (re:3439) (di:complement) D90707 D90707 g1651287 Escherichia coli 562 -11533290 7500886272 nagb (sr:e.coli dna, (library of l.clarke and j.carbon) (1), clone ppy10) (db:genpept-bct1) (de:e.coli n-acetylglucosamine transport protein (nage), andglucosamine-6-phosphate deaminase (nagb) genes, complete cds.) (nt:glucosamine-6-phosphate deaminase prot... ECONAGBE M19284 g455176 Escherichia coli 562 -11533290 235211 nagb glucosamine-6-phosphate deaminase (fn:enzyme; central intermediary metabolism: amino) (db:genpept-bct2) (ec:5.3.1.10) (de:escherichia coli k-12 mg1655 section 61 of 400 of the completegenome.) (nt:f266; 100 pct identical to nagb\_ecoli sw: p09375) (le:5518) (re:6318) (di:complement) AE000171 AE000171 g1786893 Escherichia coli 562 -11533290 5000690530 glmd glucosamine-6-phosphate isomerase ec 5.3.1.10 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #171) (db:genpept) (de:escherichia coli genomic dna. (14.8 - 15.2 min).) (nt:orf\_id:o172#3; similar to swissprot accession) (le:15604) (re:16404) (di:complement) D90706 D90706 g1651281 Escherichia coli 562 -11533290 7502851916 glmd glucosamine-6-phosphate isomerase ec 5.3.1.10 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #172) (db:genpept) (de:escherichia coli genomic dna. (15.1 - 15.5 min).) (nt:orf\_id:o172#3; similar to swissprot accession) (le:2639) (re:3439) (di:complement) D90707 D90707 g1651287 Escherichia coli 562 -11533290

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829684	8262	30418	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829687	8263	30419	477	158

Description

6500729433 rne:ams:hmp1:b1084 ribonuclease e:rnase e (gtcfc:7.1:10.9) (ec:3.1.4.-) (keggfc:4.4) (rileyfc:3.2.1) (db:gtc-escherichia coli) b1084 b1084 Escherichia coli 562 -11533291 7000688876 rne:ams:hmp1 ribonuclease e::cell shape-determining protein:message stability-altering protein:rnase e (cl:ribonuclease e) (ec:3.1.4.-) (db:pir1.dat) (mp:24 min) S27311 A64852 Escherichia coli 562 -11533291 223352 rne ribonuclease e (sr:escherichia coli(strain:k12) dna, clone:kohara clone #234) (db:genpept-bct1) (de:escherichia coli genomic dna. (24.4 - 24.7 min).) (le:8136) (re:11321) (di:complement) D90744 D90744 g1651530 Escherichia coli 562 -11533291 7500953295 rne rnase e:membrane attachment:mrna turnover (fn:enzyme; degradation of rna) (db:genpept-bct2) (ec:3.1.4.-) (de:escherichia coli k-12 mg1655 section 99 of 400 of the completegenome.) (nt:f1061; 99 pct identical to rne\_ecoli sw: p21513) (le:2867) (re:6052) (di:complement) AE000209 AE000209 g1787325 Escherichia coli 562 -11533291 5000690531 ams ribonuclease e ec 3.1.4.- rnase e . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #234) (db:genpept) (de:escherichia coli genomic dna. (24.5 - 24.8 min).) (nt:orf\_id:o235#3; similar to swissprot accession) (le:8136) (re:11321) (di:complement) D90744 D90744 g1651530 Escherichia coli 562 -11533291

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829693	8264	30420	261	86

# Description

6500729434 cls:nov:b1249 cardiolipin synthetase (gtcfc:7.1:8.1:8.3) (ec:2.7.8.-) (keggfc:4.4:8.3) (rileyfc:3.1.11) (db:gtc-escherichia coli) b1249 b1249 Escherichia coli 562 -11533292 64850 cls:nov (ec:2.7.8.-) (de:cardiolipin synthetase,) (db:swissprot) CLS\_ECOLI P31071 ESCHERICHIA COLI 562 -11533292 164170 cls:nov cardiolipin synthetase::novobiocin resistance-related protein nov (ec:2.7.8.-) (db:pir2.dat) A56145 A56145 Escherichia coli 562 -11533292 223455 cls:nov cardiolipin synthetase ec 2.7.8.-. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #252(28.1-28.4 min.)) (nt:orf\_id:o252#6; similar to (swissprot accession) (le:5506) (re:6966) (di:complement) D90763 D90763 g1742038 Escherichia coli 562 -11533292 234916 cls cardiolipin synthase (fn:condensation of two molecules of) (sr:escherichia coli (strain:k-12, sub\_strain:c600) dna) (db:genpept-bct1) (de:escherichia coli cls gene for cardiolipin synthase, complete cds.) (nt:exactly same as 'ycij' in ecokch (l12044) as) (le:545) (re:2005)... ECOCLS D38779 g565276 Escherichia coli 562 -11533292 238447 ycij (sr:escherichia coli (sub\_strain w3110, strain k-12) dna) (db:genpept-bct1) (de:escherichia coli potassium channel homologue, complete cds.) (nt:(orf2 in genbank accession x55704 and swiss-prot) (le:2345) (re:3805) (di:direct) ECOKCH L12044 g511300 Escherichia coli 562 -11533292 238718 nov nov (fn:affects resistance to gyrase inhibitor) (db:genpept-bct1) (de:escherichia coli nov (nov) gene, complete cds.) (le:547) (re:2007) (di:direct) ECU01911 U01911 g558417 Escherichia coli 562 -11533292 238857 cls cardiolipin synthase (db:genpept-bct1) (de:escherichia coli cardiolipin synthase (cls) gene, complete cds.) (le:139) (re:1599) (di:direct) ECU15986 U15986 g562114 Escherichia coli 562 -11533292 238865 cls cardiolipin synthase (db:genpept-bct1) (de:escherichia coli ecor 1 (ycid) gene, partial cds, and (ycic),(ycib),(ycia), membrane protein (tonb), (ycii), putative potassiumchannel (kch), and cardiolipin synthase (cls) genes, complete cds.) (le:5895) (re:7355) (di:direct) ECU24195 U24195 g902386 Escherichia coli 562 -11533292 238881 cls cardiolipin synthase (db:genpept-bct1) (de:escherichia coli ecor 4 (ycid) gene, partial cds, and (ycic),(ycib),(ycia), membrane protein (tonb), (ycii), putative potassiumchannel (kch), and cardiolipin synthase (cls) genes, complete cds.) (le:5895) (re:7355) (di:direct) ECU24196 U24196 g902395 Escherichia coli 562 -11533292 238889 cls cardiolipin synthase (db:genpept-bct1) (de:escherichia coli ecor 28 (ycid) gene, partial cds, and (ycic),(ycib),(ycia), membrane protein (tonb), (ycii), putative potassiumchannel (kch), and cardiolipin synthase (cls) genes, complete cds.) (le:5894) (re:7354) (di:direct) ECU24198 U24198 g902413 Escherichia coli 562 -11533292 238897 cls cardiolipin synthase (db:genpept-bct1) (de:escherichia coli ecor 31 (ycid) gene, partial cds, and (ycic),(ycib),(ycia), membrane protein (tonb), (ycii), putative potassiumchannel (kch), and cardiolipin synthase (cls) genes, complete cds.) (le:5895) (re:7355) (di:direct) ECU24199 U24199 g902422 Escherichia coli 562 -11533292 238921 cls cardiolipin synthase (db:genpept-bct1) (de:escherichia coli ecor 37 (ycid) gene, partial cds, and

(db:genpept-bct1) (de:escherichia coli ecor 37 (ycid) gene, partial cds, and (ycic), (ycib), (ycia), membrane protein (tonb), (ycii), putative

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501829697	8265	30421	618	205

Description

6500729435 mura:murz:b3189 udp-n-acetylglucosamine  
 1-carboxyvinyltransferase:udp-n-acetylglucosamine  
 1-carboxyvinyltransferase:enoylpyruvate transferase:udp-n-acetylglucosamine  
 enolpyruvyl transferase:ept (gtcfc:11.3:13.11:1.8) (ec:2.5.1.7) (keggfc:4.4) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3189 b3189 Escherichia coli 562 -11533293 84695 mura:murz (ec:2.5.1.7) (de:transferase) (ept))  
 (db:swissprot) MURA\_ECOLI P28909 ESCHERICHIA COLI 562 -11533293 164801 mura  
 udp-n-acetylglucosamine 1-carboxyvinyltransferase:murz  
 (cl:udp-n-acetylglucosamine 1-carboxyvinyltransferase murz) (ec:2.5.1.7)  
 (db:pir2.dat) A44917 A44917 Escherichia coli 562 -11533293 236426 murz  
 udp-n-acetylglucosamine enolpyruvyl transferase (sr:escherichia coli (strain ab 1157) dna) (db:genpept-bct1) (de:escherichia coli udp-n-acetylglucosamine enolpyruvyl transferase(murz) gene, complete cds.) (le:564) (re:1823)  
 (di:direct) ECOMURZ M92358 g146902 Escherichia coli 562 -11533293  
 7500886091 murz udp-n-acetylglucosamine enolpyruvyl transferase  
 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (le:115987) (re:117246) (di:complement) ECOUW67 U18997  
 g606127 Escherichia coli 562 -11533293 235202 mura first step in murein  
 (fn:enzyme; murein sacculus, peptidoglycan) (db:genpept-bct2) (ec:2.5.1.7) (de:escherichia coli k-12 mg1655 section 289 of 400 of the completegenome.) (nt:f419; 100 pct identical amino acid sequence and) (le:6508) (re:7767) (di:complement) AE000399 AE000399 g1789580 Escherichia coli 562 -11533293  
 5000690534 (de:(ecoli\_3111) (pn:first step in murein biosynthesis;udp-n-glucosamine 1- carboxyvinyltransferase) (gn:mura) (gtcfc:7.1) (ec:2.5.1.7) (mura\_ecoli) (keggfc:4.4) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_3111 ECOLI\_3111 Escherichia coli 562 10026886



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829699	8266	30422	630	209

Description

6500729436 nana:npl:b3225 n-acetylneuraminate lyase:n-acetylneuraminate lyase subunit:n-acetylneuraminic acid aldolase:n-acetylneuraminate pyruvate lyase:nalase (gtcfc:11.2:7.1) (ec:4.1.3.3) (keggfc:4.4) (rileyfc:3.3.2) (db:gtc-escherichia coli) b3225 b3225 Escherichia coli 562 -11533294 125531 nana:npl n-acetylneuraminate lyase::n-acetylneuraminate aldolase (cl:n-acetylneuraminate lyase) (ec:4.1.3.3) (db:pir1.dat) (mp:69 min) WZECN JP0002 Escherichia coli 562 -11533294 235213 nana n-acetylneuraminate lyase (sr:escherichia coli (strain:je1011) dna) (db:genpept-bct1) (de:escherichia coli nana gene for n-acetylneuraminate lyase, completecds.) (le:93) (re:986) (di:direct) ECONANA D00067 g216589 Escherichia coli 562 -11533294 236463 nana n-acetylneuraminate lyase (db:genpept-bct1) (ec:4.1.3.3) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 17647) (le:153428) (re:154321) (di:complement) ECOUW67 U18997 g606164 Escherichia coli 562 -11533294 222499 nana n-acetylneuraminate lyase aldolase:catabolism (fn:enzyme; surface polysaccharides and antigens) (db:genpept-bct2) (ec:4.1.3.3) (de:escherichia coli k-12 mg1655 section 292 of 400 of the completegenome.) (nt:f297; cg site no. 17647; 100 pct identical) (le:70) (re:963) (di:complement) AE000402 AE000402 g1789620 Escherichia coli 562 -11533294 5000690535 (de:(ecoli\_3148) (pn:n-acetylneuraminate lyase:aldolase) (gn:nana) (gtcfc:7.1) (ec:4.1.3.3) (npl\_ecoli) (keggfc:4.4) (rileyfc:3.3.2) (db:gtc-escherichia coli)) ECOLI\_3148 ECOLI\_3148 Escherichia coli 562 10066352

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829708	8267	30423	741	246

Description

6500729437 rffe:b3786 (gtcfc:7.1:11.2) (ec:5.1.3.14) (keggfc:4.4) (rileyfc:3.3.2) (db:gtc-escherichia coli) b3786 b3786 Escherichia coli 562 -11533295 7000691905 rffe:nfrc bacteriophage n4 adsorption protein:hypothetical protein o389 (db:pir2.dat) E65182 E65182 Escherichia coli 562 -11533295 7500959679 webc udp-n-acetyl glucosamine -2-epimerase:synthesis (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 345 of 400 of the completegenome.) (nt:o389; formerly designated rffe) (le:11) (re:1180) (di:direct) AE000455 AE000455 g2367283 Escherichia coli 562 -11533295

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829716	8268	30424	669	222

Description

6500729438 murb:b3972 udp-n-acetylenolpyruvoylglucosamine reductase:udp-n-acetylmuramate dehydrogenase (gtcfc:11.4:13.11:1.8) (ec:1.1.1.158) (keggfc:4.4) (rileyfc:3.3.4) (db:gtc-escherichia coli) b3972 b3972 Escherichia coli 562 -11533296 84701 murb (ec:1.1.1.158) (de:acetylmuramate dehydrogenase)) (db:swissprot) MURB\_ECOLI P08373 ESCHERICHIA COLI 562 -11533296 135215 murb udp-n-acetylmuramate dehydrogenase (cl:udp-n-acetylmuramate dehydrogenase) (ec:1.1.1.158) (db:pir1.dat) (mp:89 min) QQECB8 A24029 Escherichia coli 562 -11533296 237186 (sr:e.coli dna, clone pba11) (db:genpept-bct1) (de:e.coli bira gene coding for bira, a bifunctional protein with biotin operon-repressor and biotin-operon-synthetase activity.) (nt:unidentified reading frame ii) (le:301) (re:1329) (di:direct) ECOBIRA M10123 g145431 Escherichia coli 562 -11533296 233916 murb udp-n-acetylenolpyruvoylglucosamine reductase (fn:enzyme; murein sacculus, peptidoglycan) (db:genpept-bct2) (ec:1.1.1.158) (de:escherichia coli k-12 mg1655 section 361 of 400 of the complete genome.) (nt:o342; 100 pct identical to murb\_ecoli sw: p08373) (le:8642) (re:9670) (di:direct) AE000471 AE000471 g1790407 Escherichia coli 562 -11533296 7500886097 murb udp-n-acetylenolpyruvoylglucosamine reductase (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (ec:1.1.1.158) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:37299) (re:38327) (di:direct) ECOUW89 U00006 g396315 Escherichia coli 562 -11533296 5000690538 (de:(ecoli\_3866) (pn:udp-n-acetylenolpyruvoylglucosamine reductase) (gn:murb) (gtcfc:7.1) (ec:1.1.1.158) (murb\_ecoli) (keggfc:4.4) (rileyfc:3.3.4) (db:gtc-escherichia coli)) ECOLI\_3866 ECOLI\_3866 Escherichia coli 562 10026892

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829726	8269	30425	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829727	8270	30426	360	119

#### Description

6500729439 dsbc:xpra:b2893 disulfide interchange  
protein:precursor:thiol:disulfide interchange protein dsbc precursor  
(gtcfc:7.1:11.3) (ec:5.3.4.1) (keggfc:7.2) (rileyfc:3.3.3)  
(db:gtc-escherichia coli) b2893 b2893 Escherichia coli 562 -11533297 69309  
dsbc:xpra (de:thiol:disulfide interchange protein dsbc precursor)  
(db:swissprot) DSBC\_ECOLI P21892 ESCHERICHIA COLI 562 -11533297 7000685100  
dsbc:xpra protein disulfide-isomerase:dsbc precursor:thiol:disulfide  
interchange protein:xpra protein (cl:protein disulfide-isomerase dsbc)  
(ec:5.3.4.1) (db:pir2.dat) E65073 E65073 Escherichia coli 562 -11533297  
7500880670 dsbc thiol:disulfide interchange protein:precursor (fn:required  
for disulfide bond formation in some) (db:genpept-bct1) (de:escherichia coli  
k-12 genome; approximately 64 to 65 minutes.) (nt:cg site no. 33355;  
alternate gene name xpra) (le:47926) (re:48636) (di:complement) ECU28375  
U28375 g887843 Escherichia coli 562 -11533297 239106 dsbc protein disulfide  
isomerase ii (fn:enzyme; surface structures) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 263 of 400 of the completegenome.)  
(nt:f236; 100 pct identical to dsbc\_ecoli sw: p21892;) (le:1815) (re:2525)  
(di:complement) AE000373 AE000373 gl789260 Escherichia coli 562 -11533297

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829736	8271	30427	1701	566

#### Description

6500729440 ispb:cel:b3187 octaprenyl pyro:octaprenyl-diphosphate  
synthase:octaprenyl pyrophosphate synthetase (gtcfc:7.1:9.12:11.3)  
(ec:2.5.1.-) (keggfc:7.2:9.13) (rileyfc:1.7.11) (db:gtc-escherichia coli)  
b3187 b3187 Escherichia coli 562 -11533298 79994 ispb:cel (ec:2.5.1.-)  
(de:synthetase)) (db:swissprot) ISPB\_ECOLI P19641 ESCHERICHIA COLI 562  
-11533298 7000685651 ispb octaprenyl-diphosphate synthase (cl:prenyl  
transferase a) (ec:2.5.1.-) (db:pir2.dat) (mp:69 min) E65109 E65109  
Escherichia coli 562 -11533298 7500884298 (db:genpept-bct1) (de:escherichia  
coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf\_o323)  
(le:114462) (re:115433) (di:direct) ECOUW67 U18997 g606125 Escherichia coli  
562 -11533298 236424 ispb octaprenyl diphosphate synthase (fn:enzyme;  
biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:2.5.1.-)  
(de:escherichia coli k-12 mg1655 section 289 of 400 of the completegenome.)  
(nt:o323; 100 pct identical amino acid sequence and) (le:4983) (re:5954)  
(di:direct) AE000399 AE000399 gl789578 Escherichia coli 562 -11533298  
5000690624 (de:(ecoli\_3109) (pn:octaprenyl diphosphate synthase) (gn:ispb)  
(gtcfc:9.12) (ec:2.5.1.-) (ispb\_ecoli) (keggfc:7.2:9.13) (rileyfc:1.7.11)  
(db:gtc-escherichia coli)) ECOLI\_3109 ECOLI\_3109 Escherichia coli 562  
10022244

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829741	8272	30428	207	68

Description

Hypothetical protein

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829779	8273	30429	600	199

Description

Hypothetical protein

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829780	8274	30430	495	164

Description

6500729441 ubia:cyr:b4040 4-hydroxybenzoate-octaprenyl transferase:4-hydroxybenzoate octaprenyltransferase:4-hb polyprenyltransferase (gtcfc:7.1:9.12:11.3) (ec:2.5.1.-) (keggfc:7.2:9.13) (rileyfc:1.7.11) (db:gtc-escherichia coli) b4040 b4040 Escherichia coli 562 -11533299 7500893665 ubia:cyr (ec:2.5.1.-) (de:polyprenyltransferase)) (db:swissprot) UBIA\_ECOLI P26601 ESCHERICHIA COLI 562 -11533299 162624 ubia:cyr 4-hydroxybenzoate octaprenyltransferase (ec:2.5.1.-) (db:pir2.dat) (mp:92 min) JC2316 JC2316 Escherichia coli 562 -11533299 236243 cyr (db:genpept-bct1) (de:e.coli cyr gene.) (le:134) (re:1006) (di:direct) ECCY X69522 g41181 Escherichia coli 562 -11533299 236248 ubia 4-hydroxybenzoate-octaprenyl transferase (fn:enzymatic - 3-octaprenyl-4-hydroxybenzoate) (sr:escherichia coli (sub\_strain w3110, strain k-12) (library: kohar) (db:genpept-bct1) (de:escherichia coli chorismate lyase (ubic), 4-hydroxybenzoateoctaprenyl transferase (ubia) genes, complete cds, an... ECOUBICA M93136 g148101 Escherichia coli 562 -11533299 240319 ubia 4-hydroxybenzoate-octaprenyl transferase (fn:enzymatic - 3-octaprenyl-4-hydroxybenzoate) (sr:escherichia coli (sub\_strain w3110, strain k-12) (library: kohar) (db:genpept-bct1) (de:escherichia coli 4-hydroxybenzoate octaprenyl transferase (ubia)gene complete cds, chorismate lyase (ubic) gene ... ECOUBIPLS M93413 g148108 Escherichia coli 562 -11533299 240321 ubia 4-hydroxybenzoate-octaprenyl transferase (db:genpept-bct1) (de:e.coli genes ubic and ubia.) (le:1080) (re:1952) (di:direct) ECUBI X66619 g43232 Escherichia coli 562 -11533299 5000690625 ubia 4-hydroxybenzoate octaprenyltransferase (db:genpept-bct1) (de:e.coli ubic and ubia genes for chorismate lyase and4-hydroxybenzoate octaprenyltransferase.) (le:912) (re:1784) (di:direct) ECUBIAC X57434 g43235 Escherichia coli 562 -11533299 232607 ubia 4-hydroxybenzoate-octaprenyltransferase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:2.5.1.-) (de:escherichia coli k-12 mg1655 section 367 of 400 of the completegenome.) (nt:o290b; 99 pct identical amino acid sequence and) (le:5111) (re:5983) (di:direct) AE000477 AE000477 g1790473 Escherichia coli 562 -11533299 103070 ubia:cyr (ec:2.5.1.-) (de:polyprenyltransferase)) (db:swissprot) UBIA\_ECOLI P26601 ESCHERICHIA COLI 562 -11533299

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829783	8275	30431	276	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829806	8276	30432	627	208
<u>Description</u>				
6500729442 nagd:b0675 nagd protein (gtcfc:7.1) (keggfc:14.2) (rileyfc:1.3.4) (db:gtc-escherichia coli) b0675 b0675 Escherichia coli 562 -11533300				
7500886275 nagd (de:nagd protein) (db:swissprot) NAGD_ECOLI P15302				
ESCHERICHIA COLI 562 -11533300 7000685909 nagd nagd protein (cl:nagd protein) (db:pir2.dat) (mp:15 min) B64802 B64802 Escherichia coli 562 -11533300 223135 nagd nagd protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #171) (db:genpept-bct1) (de:escherichia coli genomic dna. (14.8 - 15.2 min).) (le:12552) (re:13304) (di:complement) D90706 D90706 g1651278 Escherichia coli 562 -11533300 5000690540 (db:genpept-bct1) (de:escherichia coli naga, nagc and nagd genes				
forn-acetylglucosamine-6-phosphate deacetylase.) (nt:nagd gene product (aa 1-250)) (le:2480) (re:3232) (di:direct) ECNAGACD X14135 g42081 Escherichia coli 562 -11533300 233449 nagd n-acetylglucosamine metabolism (fn:enzyme; central intermediary metabolism: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 61 of 400 of the completegenome.) (nt:f250; 99 pct identical to nagd_ecoli sw: p15302) (le:2281) (re:3033) (di:complement) AE000171 AE000171 g1786890 Escherichia coli 562 -11533300 7502851917 nagd nagd protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #171) (db:genpept) (de:escherichia coli genomic dna. (14.8 - 15.2 min).) (nt:orf_id:o171#8; similar to pir accession number) (le:12367) (re:13119) (di:complement) D90706 D90706 g1651278 Escherichia coli 562 -11533300 85168 nagd (de:nagd protein) (db:swissprot) NAGD_ECOLI P15302 ESCHERICHIA COLI 562 -11533300				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829807	8277	30433	303	100

# Description

6500729443 nagc:nagr:b0676 n-acetylglucosamine repressor (gtcfc:7.1) (keggfc:14.2) (rileyfc:1.3.4) (db:gtc-escherichia coli) b0676 b0676 Escherichia coli 562 -11533301 85162 nagc:nagr (de:n-acetylglucosamine repressor) (db:swissprot) NAGC\_ECOLI P15301 ESCHERICHIA COLI 562 -11533301 7000685907 nagc n-acetylglucosamine repressor (cl:n-acetylglucosamine repressor:glucose kinase homology) (db:pir2.dat) (mp:15 min) C64802 C64802 Escherichia coli 562 -11533301 223136 nagc n-acetylglucosamine repressor (db:genpept-bct1) (de:escherichia coli n-acetylglucosamine-6-phosphate isomerase (nagb),n-acetylglucosamine-6-phosphate deacetylase (naga),n-acetylglucosamine repressor (nagc), and nagd (nagd) genes,complete cds.) (le:2351) (re:3571) (di:direct) AF052007 AF052007 g3005596 Escherichia coli 562 -11533301 223141 nagc nagc protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #171) (db:genpept-bct1) (de:escherichia coli genomic dna. (14.8 - 15.2 min).) (le:13352) (re:14572) (di:complement) D90706 D90706 g1651279 Escherichia coli 562 -11533301 7000685908 nagc nagc protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #172) (db:genpept-bct1) (de:escherichia coli genomic dna. (15.0 - 15.4 min).) (le:202) (re:1422) (di:complement) D90707 D90707 g1651285 Escherichia coli 562 -11533301 7500886274 nagc transcriptional repressor of nag (fn:regulator; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 61 of 400 of the completgenome.) (nt:f406; 99 pct identical to nagc\_ecoli sw: p15301) (le:3081) (re:4301) (di:complement) AE000171 AE000171 g1786891 Escherichia coli 562 -11533301 5000690541 nagc n-acetylglucosamine repressor. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #171) (db:genpept) (de:escherichia coli genomic dna. (14.8 - 15.2 min).) (nt:orf\_id:o172#1; similar to swissprot accession) (le:13167) (re:14387) (di:complement) D90706 D90706 g1651279 Escherichia coli 562 -11533301 7502851918 nagc n-acetylglucosamine repressor. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #172) (db:genpept) (de:escherichia coli genomic dna. (15.1 - 15.5 min).) (nt:orf\_id:o172#1; similar to swissprot accession) (le:202) (re:1422) (di:complement) D90707 D90707 g1651285 Escherichia coli 562 -11533301

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829812	8278	30434	258	86
<u>Description</u>				
6500729444 trea:osma:b1197 periplasmic trehalase precursor:alpha:alpha-trehalase:alpha:alpha-trehalose glucohydrolase (gtcfc:7.1:12.11) (ec:3.2.1.28) (keggfc:7.1) (rileyfc:4.6.0) (db:gtc-escherichia coli) b1197 b1197 Escherichia coli 562 -11533302 7500893371 trea:osma (ec:3.2.1.28) (de:(alpha,alpha-trehalose glucohydrolase)) (db:swissprot) TREA_ECOLI P13482 ESCHERICHIA COLI 562 -11533302 162707 trea:osma alpha:alpha-trehalase:precursor:periplasmic (sr:strain k12, , strain k12) (sr:strain k12, ) (ec:3.2.1.28) (db:pir2.dat) (mp:26 min) S04782 S04782 Escherichia coli 562 -11533302 223408 trea periplasmic trehalase precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #245) (db:genpept-bct1) (de:escherichia coli genomic dna. (26.6-27.0 min).) (le:6577) (re:8274) (di:complement) D90754 D90754 g1651595 Escherichia coli 562 -11533302 5000690542 (db:genpept-bct1) (de:e.coli trea gene encoding periplasmic trehalase (ec 3.2.1.28).) (nt:precursor peptide (aa -30 to 535)) (le:496) (re:2193) (di:direct) ECTREA X15868 g43131 Escherichia coli 562 -11533302 238397 trea trehalase:periplasmic (fn:enzyme; osmotic adaptation) (db:genpept-bct2) (ec:3.2.1.28) (de:escherichia coli k-12 mg1655 section 108 of 400 of the completegenome.) (nt:f565; 99 pct identical to trea_ecoli sw: p13482) (le:1082) (re:2779) (di:complement) AE000218 AE000218 g1787447 Escherichia coli 562 -11533302 7502851919 osma periplasmic trehalase precursor ec 3.2.1.28 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #245) (db:genpept) (de:escherichia coli genomic dna. (26.8 - 27.1 min).) (nt:orf_id:o245#6; similar to swissprot accession) (le:6577) (re:8274) (di:complement) D90754 D90754 g1651595 Escherichia coli 562 -11533302 102158 trea:osma (ec:3.2.1.28) (de:(alpha,alpha-trehalose glucohydrolase)) (db:swissprot) TREA_ECOLI P13482 ESCHERICHIA COLI 562 -11533302				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829834	8279	30435	300	99

Description

6500729445 otsa:b1896 alpha trehalose phosphate synthase:alpha:alpha-trehalose-phosphate synthase:udp-forming:trehalose-6-phosphate synthase:udp-glucose-glucosephosphate glucosyltransferase (gtcfc:11.3:7.1:13.10) (ec:2.4.1.15) (keggfc:7.1) (rileyfc:4.6.0) (db:gtc-escherichia coli) b1896 b1896 Escherichia coli 562 -11533303 164765 otsa alpha:alpha-trehalose-phosphate synthase udp-forming (ec:2.4.1.15) (db:pir2.dat) I83402 I83402 Escherichia coli 562 -11533303 7500959673 otsa trehalose-6-phosphate synthase (db:genpept-bct1) (de:e.coli genes otsb and otsa.) (le:1450) (re:2874) (di:direct) ECOTSAB X69160 g603543 Escherichia coli 562 -11533303 236160 otsa trehalose-6-phosphate synthase (fn:enzyme; osmotic adaptation) (db:genpept-bct2) (ec:2.4.1.15) (de:escherichia coli k-12 mg1655 section 173 of 400 of the completegenome.) (nt:f474; 100 pct identical to otsa\_ecoli sw: p31677) (le:3016) (re:4440) (di:complement) AE000283 AE000283 g1788206 Escherichia coli 562 -11533303 5000690544 (de:(ecoli\_1853) (pn:trehalose-6-phosphate synthase) (gn:otsa) (gtcfc:7.2) (ec:2.4.1.15) (otsa\_ecoli) (keggfc:7.1) (rileyfc:4.6.0) (db:gtc-escherichia coli)) ECOLI\_1853 ECOLI\_1853 Escherichia coli 562 10087456

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829835	8280	30436	288	95

Description

6500729446 otsb:b1897 trehalose phosphatase:trehalose-phosphatase:trehalose 6-phosphate phosphatase:tpp (gtcfc:7.2:12.11) (ec:3.1.3.12) (keggfc:7.1) (rileyfc:4.6.0) (db:gtc-escherichia coli) b1897 b1897 Escherichia coli 562 -11533304 301041 otsb (ec:3.1.3.12) (de:phosphatase) (tpp)) (db:swissprot) OTSB\_ECOLI P31678 ESCHERICHIA COLI 562 -11533304 164766 otsb trehalose-phosphatase (ec:3.1.3.12) (db:pir2.dat) I83401 I83401 Escherichia coli 562 -11533304 224401 otsb trehalose-phosphatase ec 3.1.3.12 trehalose (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #339(42.4-42.8 min.)) (nt:orf\_id:o339#12; similar to (swissprot accession) (le:13327) (re:14127) (di:complement) D90831 D90831 g1736556 Escherichia coli 562 -11533304 5000690545 otsb trehalose-6-phosphate phosphatase (db:genpept-bct1) (de:e.coli genes otsb and otsa.) (nt:start codon gtg) (le:675) (re:1475) (di:direct) ECOTSAB X69160 g577561 Escherichia coli 562 -11533304 236159 otsb trehalose-6-phosphate phosphatase:biosynthetic (fn:enzyme; osmotic adaptation) (db:genpept-bct2) (ec:3.1.3.12) (de:escherichia coli k-12 mg1655 section 173 of 400 of the completegenome.) (nt:f266; 100 pct identical to otsb\_ecoli sw: p31678;) (le:4415) (re:5215) (di:complement) AE000283 AE000283 g1788207 Escherichia coli 562 -11533304 87982 otsb (ec:3.1.3.12) (de:phosphatase) (tpp)) (db:swissprot) OTSB\_ECOLI P31678 ESCHERICHIA COLI 562 -11533304

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829840	8281	30437	558	186

Description

6500729447 amya:b1927 cytoplasmic alpha-amylase:1:4-alpha-d-glucan glucanohydrolase (gtcfc:7.2) (ec:3.2.1.1) (keggfc:7.1) (rileyfc:3.2.4) (db:gtc-escherichia coli) b1927 b1927 Escherichia coli 562 -11533305 59440 amya (ec:3.2.1.1) (de:glucanohydrolase)) (db:swissprot) AMY2\_ECOLI P26612 ESCHERICHIA COLI 562 -11533305 7000684578 amya alpha-amylase::cytosolic:1:4-alpha-d-glucan glucanohydrolase (cl:alpha-amylase, amyloliquefaciens type:alpha-amylase core homology) (ec:3.2.1.1) (db:pir1.dat) A45738 D64956 Escherichia coli 562 -11533305 224438 amya alpha-amylase ec 3.2.1.1:cytoplasmic (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #342(43.0-43.4 min.).) (nt:orf\_id:o342#6; similar to (pir accession number) (le:7899) (re:9386) (di:direct) D90833 D90833 g1736595 Escherichia coli 562 -11533305 301078 amya cytoplasmic alpha-amylase (fn:enzyme; degradation of polysaccharides) (db:genpept-bct2) (ec:3.2.1.1) (de:escherichia coli k-12 mg1655 section 175 of 400 of the completegenome.) (nt:o495; cg site no. 30745; alternate name orf1) (le:5757) (re:7244) (di:direct) AE000285 AE000285 g1788236 Escherichia coli 562 -11533305 5000690546 (de:(ecoli\_1881) (pn:cytoplasmic alpha-amylase) (gn:amya) (gtcfc:7.2) (ec:3.2.1.1) (amy2\_ecoli) (keggfc:7.1) (rileyfc:3.2.4) (db:gtc-escherichia coli)) ECOLI\_1881 ECOLI\_1881 Escherichia coli 562 10119916

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829841	8282	30438	294	97

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829842	8283	30439	426	141

Description

6500729448 malq:mala:b3416  
 4-alpha-glucanotransferase:amylomaltase:disproportionating enzyme:d-enzyme  
 (gtcfc:7.2) (ec:2.4.1.25) (keggfc:7.1) (rileyfc:3.2.4) (db:gtc-escherichia  
 coli) b3416 b3416 Escherichia coli 562 -11533306 82908 malq:mala  
 (ec:2.4.1.25) (de:(disproportionating enzyme) (d-enzyme)) (db:swissprot)  
 MALQ\_ECOLI P15977 ESCHERICHIA COLI 562 -11533306 7000685783 malq  
 4-alpha-glucanotransferase::amylomaltase (cl:4-alpha-glucanotransferase)  
 (ec:2.4.1.25) (db:pir2.dat) (mp:75 min) C65137 C65137 Escherichia coli 562  
 -11533306 7500885274 malq amylomaltase (db:genpept-bct1) (ec:2.4.1.25)  
 (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.)  
 (nt:cg site no. 527; alternate name mala) (le:328725) (re:330809)  
 (di:complement) ECOUW67 U18997 g606351 Escherichia coli 562 -11533306  
 236650 malq 4-alpha-glucanotransferase amylomaltase (fn:enzyme; degradation  
 of polysaccharides) (db:genpept-bct2) (ec:2.4.1.25) (de:escherichia coli  
 k-12 mg1655 section 307 of 400 of the completegenome.) (nt:f694; cg site no.  
 527; alternate name mala; 100 pct) (le:4948) (re:7032) (di:complement)  
 AE000417 AE000417 g1789821 Escherichia coli 562 -11533306 5000690526  
 (de:(ecoli\_3334) (pn:4-alpha-glucanotransferase:amylomaltase) (gn:malq)  
 (gtcfc:7.1:7.2) (ec:2.4.1.25) (malq\_ecoli) (keggfc:11.1) (rileyfc:3.2.4)  
 (db:gtc-escherichia coli)) ECOLI\_3334 ECOLI\_3334 Escherichia coli 562  
 10025128

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829844	8284	30440	471	157

Description

6500729449 glgp:glgy:b3428 alpha-glucan phosphorylase:glycogen phosphorylase  
 (gtcfc:7.2) (ec:2.4.1.1) (keggfc:7.1) (rileyfc:3.1.10) (db:gtc-escherichia  
 coli) b3428 b3428 Escherichia coli 562 -11533307 7500888076 glgp:glgy  
 (ec:2.4.1.1) (de:glycogen phosphorylase,) (db:swissprot) PHSG\_ECOLI P13031  
 ESCHERICHIA COLI 562 -11533307 7000688858 glgp:glgy glycogen  
 phosphorylase::alpha-glucan phosphorylase (cl:phosphorylase) (ec:2.4.1.1)  
 (db:pir1.dat) (mp:75 min) PHECGG G65138 Escherichia coli 562 -11533307  
 7500888078 glgp glycogen phosphorylase (fn:enzyme; macromolecule synthesis,  
 modification:) (db:genpept-bct2) (ec:2.4.1.1) (de:escherichia coli k-12  
 mg1655 section 309 of 400 of the completegenome.) (nt:f815; 99 pct identical  
 to phsg\_ecoli sw: p13031) (le:543) (re:2990) (di:complement) AE000419  
 AE000419 g2367228 Escherichia coli 562 -11533307

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829846	8285	30441	537	178

Description

GTC ORF with score 166 to: (fn:involved in rhamnolipids synthesis)  
(db:genpept-bct2) (de:pseudomonas aeruginosa ctra, beta-ketoacyl reductase  
(rhlg), andregulator protein (rcsf) genes, complete cds.) (nt:rhlg)  
(le:1723) (re:2757) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829850	8286	30442	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829852	8287	30443	714	237

Description

6500729450 glga:b3429 glycogen synthase:starch:bacterial glycogen synthase  
(gtcfc:7.2) (ec:2.4.1.21) (keggfc:7.1) (rileyfc:3.1.10) (db:gtc-escherichia  
coli) b3429 b3429 Escherichia coli 562 -11533308 73776 glga (ec:2.4.1.21)  
(de:synthase)) (db:swissprot) GLGA\_ECOLI P08323 ESCHERICHIA COLI 562  
-11533308 7000685395 glga adpglucose--starch bacterial glycogen  
glucosyltransferase::bacterial-glycogen synthase:glycogen synthase  
(cl:starch synthase) (ec:2.4.1.21) (db:pir1.dat) (mp:75 min) SYECGL H65138  
Escherichia coli 562 -11533308 7500882395 glga glycogen synthase  
(db:genpept-bct1) (ec:2.4.1.21) (de:escherichia coli k-12 chromosomal region  
from 67.4 to 76.0 minutes.) (nt:cg site no. 710) (le:347339) (re:348772)  
(di:complement) ECOUW67 U18997 g606364 Escherichia coli 562 -11533308  
236663 glga glycogen synthase (fn:enzyme; macromolecule synthesis,  
modification:) (db:genpept-bct2) (ec:2.4.1.21) (de:escherichia coli k-12  
mg1655 section 309 of 400 of the completegenome.) (nt:f477; cg site no. 710;  
100 pct identical amino) (le:3009) (re:4442) (di:complement) AE000419  
AE000419 g1789836 Escherichia coli 562 -11533308 5000690551  
(de:(ecoli\_3347) (pn:glycogen synthase) (gn:glga) (gtcfc:7.2) (ec:2.4.1.21)  
(glga\_ecoli) (keggfc:7.1) (rileyfc:3.1.10) (db:gtc-escherichia coli))  
ECOLI\_3347 ECOLI\_3347 Escherichia coli 562 10016308

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829866	8288	30444	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829867	8289	30445	1152	383

Description

6500729451 glgc:b3430 glucose-1-phosphate adenylyltransferase:adp-glucose synthase:adp-glucose pyrophosphorylase (gtcfc:7.2) (ec:2.7.7.27) (keggfc:7.1) (rileyfc:3.1.10) (db:gtc-escherichia coli) b3430 b3430 Escherichia coli 562 -11533309 124058 glgc glucose-1-phosphate adenylyltransferase::adp-glucose pyrophosphorylase:adp-glucose synthase (cl:glucose-1-phosphate adenylyltransferase) (ec:2.7.7.27) (db:pir1.dat) (mp:75 min) YUEC A00721 Escherichia coli 562 -11533309 7500953274 glgc glucose-1-phosphate adenylyltransferase (db:genpept-bct1) (ec:1.7.7.27) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 711) (le:348772) (re:350067) (di:complement) ECOUW67 U18997 g606365 Escherichia coli 562 -11533309 236664 glgc glucose-1-phosphate adenylyltransferase (fn:enzyme; macromolecule synthesis, modification:) (db:genpept-bct2) (ec:2.7.7.27) (de:escherichia coli k-12 mg1655 section 309 of 400 of the completegenome.) (nt:f431; cg site no. 711; 100 pct identical amino) (le:4442) (re:5737) (di:complement) AE000419 AE000419 g1789837 Escherichia coli 562 -11533309 5000690552 (de:(ecoli\_3348) (pn:glucose-1-phosphate adenylyltransferase) (gn:glgc) (gtcfc:7.2) (ec:2.7.7.27) (glgc\_ecoli) (keggfc:7.1) (rileyfc:3.1.10) (db:gtc-escherichia coli)) ECOLI\_3348 ECOLI\_3348 Escherichia coli 562 10066018

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829880	8290	30446	1068	355

Description

6500729452 glgb:b3432 1:4-alpha-glucan branching enzyme:glycogen branching enzyme (gtcfc:7.2) (ec:2.4.1.18) (keggfc:7.1) (rileyfc:3.1.10) (db:gtc-escherichia coli) b3432 b3432 Escherichia coli 562 -11533310 73784 glgb (ec:2.4.1.18) (de:enzyme)) (db:swissprot) GLGB\_ECOLI P07762 ESCHERICHIA COLI 562 -11533310 123420 glgb 1:4-alpha-glucan branching enzyme (cl:1,4-alpha-glucan branching enzyme) (ec:2.4.1.18) (db:pir1.dat) (mp:75 min) NQECA A25498 Escherichia coli 562 -11533310 7500882399 glgb (sr:e.coli dna, clone pop12) (db:genpept-bct1) (de:escherichia coli glgb gene encoding a branching enzyme, completedcds.) (nt:branching enzyme (ec 2.4.1.18)) (le:199) (re:2385) (di:direct) ECOGLGBA M13751 g146142 Escherichia coli 562 -11533310 234493 glgb 1:4-alpha-glucan branching enzyme (fn:enzyme; macromolecule synthesis, modification:) (db:genpept-bct2) (ec:2.4.1.18) (de:escherichia coli k-12 mg1655 section 309 of 400 of the completegenome.) (nt:f728; cg site no. 709; 99 pct identical amino) (le:7725) (re:9911) (di:complement) AE000419 AE000419 g1789839 Escherichia coli 562 -11533310 5000690553 (de:(ecoli\_3350) (pn:1,4-alpha-glucan branching enzyme) (gn:glgb) (gtcfc:7.2) (ec:2.4.1.18) (glgb\_ecoli) (keggfc:7.1) (rileyfc:3.1.10) (db:gtc-escherichia coli)) ECOLI\_3350 ECOLI\_3350 Escherichia coli 562 10016316

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829881	8291	30447	897	298

Description

6500729453 mals:b3571 alpha-amylase:alpha-amylase  
precursor:1:4-alpha-d-glucan glucanohydrolase (gtcfc:7.2) (ec:3.2.1.1)  
(keggfc:7.1) (rileyfc:3.2.4) (db:gtc-escherichia coli) b3571 b3571  
Escherichia coli 562 -11533311 236808 mals (ec:3.2.1.1)  
(de:glucanohydrolase)) (db:swissprot) AMY1\_ECOLI P25718 ESCHERICHIA COLI 562  
-11533311 162709 mals alpha-amylase:precursor:periplasmic (ec:3.2.1.1)  
(db:pir2.dat) S23807 S23807 Escherichia coli 562 -11533311 5000690555  
alpha-amylase precursor (db:genpept-bct1) (ec:3.2.1.1) (de:e.coli mals gene  
for 1,4-alpha-d-glucan glucanohydrolase.) (le:798) (re:2828) (di:direct)  
ECMALS X58994 g41966 Escherichia coli 562 -11533311 304586 mals  
alpha-amylase (sr:escherichia coli (sub\_strain mg1655, strain k-12)  
(library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0  
to 81.5 minutes.) (nt:cg site no. 17659) (le:151748) (re:153778) (di:direct)  
ECOUW76 U00039 g466709 Escherichia coli 562 -11533311 233350 mals  
alpha-amylase (fn:enzyme; degradation of polysaccharides) (db:genpept-bct2)  
(ec:3.2.1.1) (de:escherichia coli k-12 mg1655 section 324 of 400 of the  
completegenome.) (nt:o676; 100 pct identical to amy1\_ecoli sw: p25718;)  
(le:6640) (re:8670) (di:direct) AE000434 AE000434 g1789995 Escherichia coli  
562 -11533311 59433 mals (ec:3.2.1.1) (de:glucanohydrolase)) (db:swissprot)  
AMY1\_ECOLI P25718 ESCHERICHIA COLI 562 -11533311

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829886	8292	30448	621	206

Description

6500729454 glgs:b3049 glycogen synthesis protein glgs (gtcfc:7.2)  
(keggfc:14.2) (rileyfc:3.1.10) (db:gtc-escherichia coli) b3049 b3049  
Escherichia coli 562 -11533312 7500882407 glgs (de:glycogen synthesis  
protein glgs) (db:swissprot) GLGS\_ECOLI P26649 ESCHERICHIA COLI 562  
-11533312 163108 glgs glycogen synthesis protein glgs (db:pir2.dat)  
(mp:66.6 min) S25201 S25201 Escherichia coli 562 -11533312 225268 glgs glgs  
protein (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:e.coli  
genomic dna, 68.6-68.8 min.) (nt:similar to (pir accession number s25201))  
(le:4385) (re:4585) (di:complement) D90897 D90897 g1805589 Escherichia coli  
562 -11533312 5000690557 glgs (db:genpept-bct1) (de:e.coli glgs gene.)  
(le:240) (re:440) (di:direct) ECGLGSG Z11885 g41561 Escherichia coli 562  
-11533312 232995 glgs glycogen biosynthesis:rpos dependent (fn:putative  
enzyme; macromolecule synthesis,) (db:genpept-bct2) (de:escherichia coli  
k-12 mg1655 section 276 of 400 of the completegenome.) (nt:f66; 100 pct  
identical to glgs\_ecoli sw: p26649) (le:9277) (re:9477) (di:complement)  
AE000386 AE000386 g1789428 Escherichia coli 562 -11533312 73806 glgs  
(de:glycogen synthesis protein glgs) (db:swissprot) GLGS\_ECOLI P26649  
ESCHERICHIA COLI 562 -11533312

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829898	8293	30449	393	130

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829955	8294	30450	333	110

Description

6500729455 phoa:b0383 alkaline phosphatase precursor  
(gtcfc:8.1:9.13:9.6:12.13:13.10) (ec:3.1.3.1) (keggfc:8.1:9.7:9.12:12.1)  
(rileyfc:1.1.4) (db:gtc-escherichia coli) (gtcfc:metabolism of complex  
lipids-glycerolipid metabolism:metabolism of cofactors and vitamins-other  
cofactors:metabolism of cofactors ... b0383 b0383 Escherichia coli 562  
-11533313 7500974857 phoa alkaline phosphatase (fn:enzyme; central  
intermediary metabolism:) (db:genpept-bct2) (ec:3.1.3.1) (de:escherichia  
coli k-12 mg1655 section 35 of 400 of the completegenome.) (nt:o494; 99 pct  
identical to ppb\_ecoli sw: p00634) (le:554) (re:2038) (di:direct) AE000145  
AE000145 g1786582 Escherichia coli 562 -11533313 5000690559 (de:(ecoli\_367)  
(pn:alkaline phosphatase) (gn:phoa) (gtcfc:8.1:9.13:9.6) (ec:3.1.3.1)  
(ppb\_ecoli) (keggfc:8.1:9.7:9.12) (rileyfc:1.1.4) (db:gtc-escherichia coli))  
ECOLI\_367 ECOLI\_367 Escherichia coli 562 -11533313 7000690853 g64766  
(de:(pn:alkaline phosphatase, precursor) (gn:phoa) (ec:3.1.3.1) (db:pir))  
G64766 G64766 Escherichia coli 562 10122808

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501829956	8295	30451	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829960	8296	30452	339	113

Description

6500729456 pgpa:b0418 hypothetical protein:phosphatidylglycerophosphatase a (gtcfc:8.1:14.1) (ec:3.1.3.27) (keggfc:8.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0418 b0418 Escherichia coli 562 -11533314 89355 pgpa (ec:3.1.3.27) (de:phosphatidylglycerophosphatase a,) (db:swissprot) PGPA\_ECOLI P18200 ESCHERICHIA COLI 562 -11533314 7000686129 pgpa phosphatidylglycerophosphatase (cl:conserved hypothetical protein hil306) (ec:3.1.3.27) (db:pir2.dat) B64771 B64771 Escherichia coli 562 -11533314 240195 (sr:escherichia coli (strain:k-12) dna, clone\_lib:clarke-carbon gen) (db:genpept-bct1) (de:e. coli thil gene, complete cds.) (nt:putative open reading frame) (le:1076) (re:1594) (di:direct) D17333 D17333 g2329841 Escherichia coli 562 -11533314 7500887980 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to h. influenzae hil306) (le:16039) (re:16557) (di:direct) ECU82664 U82664 g1773102 Escherichia coli 562 -11533314 5500687866 pgpa phosphatidylglycerophosphatase (fn:enzyme; macromolecule synthesis, modification:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 38 of 400 of the completegenome.) (nt:o172; 50 pct identical (2 gaps) to 155 residues of) (le:3663) (re:4181) (di:direct) AE000148 AE000148 g1786620 Escherichia coli 562 -11533314 5000691570 (de:(ecoli\_402) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_402 ECOLI\_402 Escherichia coli 562 10122821

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829973	8297	30453	768	256

Description

6500729457 pgpb:b1278 phosphatidylglycerophosphatase b (gtcfc:8.1)  
(ec:3.1.3.27) (keggfc:8.1) (rileyfc:3.1.11) (db:gtc-escherichia coli) b1278  
b1278 Escherichia coli 562 -11533315 89356 pgpb (ec:3.1.3.27)  
(de:phosphatidylglycerophosphatase b,) (db:swissprot) PGPB\_ECOLI P18201  
ESCHERICHIA COLI 562 -11533315 124301 pgpb phosphatidylglycerophosphatase:b  
(cl:phosphatidylglycerophosphatase b) (ec:3.1.3.27) (db:pir1.dat) PAECGB  
A30193 Escherichia coli 562 -11533315 223506 pgpb  
phosphatidylglycerophosphatase b ec 3.1.3.27 . (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #255(28.8-29.2 min.).)  
(nt:orf\_id:o255#3; similar to (swissprot accession) (le:1595) (re:2359)  
(di:direct) D90766 D90766 g1742092 Escherichia coli 562 -11533315 300309  
pgpb phosphatidylglycerophosphate phosphatase b (db:genpept-bct1)  
(ec:3.1.3.27) (de:e. coli phosphatidylglycerophosphate phosphatase b (pgpb)  
gene,complete cds.) (le:272) (re:1036) (di:direct) ECOPGPB M23628 g450384  
Escherichia coli 562 -11533315 235400 pgpb non-essential  
phosphatidylglycerophosphate (fn:enzyme; macromolecule synthesis,  
modification:) (db:genpept-bct2) (ec:3.1.3.27) (de:escherichia coli k-12  
mg1655 section 116 of 400 of the completegenome.) (nt:o254; 100 pct  
identical to pgpb\_ecoli sw: p18201;) (le:822) (re:1586) (di:direct) AE000226  
AE000226 g1787534 Escherichia coli 562 -11533315 5000690561  
(de:(ecoli\_1238) (pn:non-essential phosphatidylglycerophosphate phosphatase,  
membrane bound) (gn:pgpb) (gtcfc:8.1) (ec:3.1.3.27) (pgpb\_ecoli)  
(keggfc:8.1) (rileyfc:3.1.11) (db:gtc-escherichia coli)) ECOLI\_1238  
ECOLI\_1238 Escherichia coli 562 10031479

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829974	8298	30454	516	171

Description

6500729458 pgsa:b1912 phosphatidylglycerophosphate synthetase:cdp-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase:phosphatidylglycerophosphate synthase:pgp synthase (gtcfc:8.1) (ec:2.7.8.5) (keggfc:8.1) (rileyfc:3.1.11) (db:gtc-escherichia coli) b1912 b1912 Escherichia coli 562 -11533316 7000688872 pgsa cdpdiacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase::glycerophosphate phosphatidyltransferase:phosphatidylglycerophosphate synthase (cl:cdpdiacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase) (ec:2.7.8.5) (db:pir1.dat) (mp:42 min) XNECPG E64954 Escherichia coli 562 -11533316 7500953275 pgsa phosphatidylglycerophosphate synthase (sr:e. coli k12 dna) (db:genpept-bct1) (ec:2.7.8.5) (de:e. coli pgsa and glyw genes encoding phosphatidylglycerophosphatesynthase and gly-trna-3, complete cds, and uvrc gene, 3' end.) (nt:product is also known as) (le:82) (re:630) (di:direct) ECOPGSA M12299 g473749 Escherichia coli 562 -11533316 235402 pgsa phosphatidylglycerophosphate synthetase = (fn:enzyme; macromolecule synthesis, modification:) (db:genpept-bct2) (ec:2.7.8.5) (de:escherichia coli k-12 mg1655 section 174 of 400 of the completegenome.) (nt:f182; 100 pct identical to pgsa\_ecoli sw: p06978;) (le:4297) (re:4845) (di:complement) AE000284 AE000284 g1788220 Escherichia coli 562 -11533316 5000690562 (de:(ecoli\_1866) (pn:phosphatidylglycerophosphate synthetase , cdp-1,2-diacyl-sn- glycerol-3-phosphate phosphatidyl transferase:phosphatidylglycerophosphate synthetase ) (gn:pgsa) (gtcfc:8.1) (ec:2.7.8.5) (pgsa\_ecoli) (keggfc:8.1)) ECOLI\_1866 ECOLI\_1866 Escherichia coli 562 10123506

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829984	8299	30455	360	119
<u>Description</u>				
6500729459 plsc:parf:b3018 1-acyl-glycerol-3-phosphate acyltransferase:1-acyl-sn-glycerol-3-phosphate acyltransferase (gtcfc:8.1) (ec:2.3.1.51) (keggfc:8.1) (rileyfc:3.1.11) (db:gtc-escherichia coli) b3018 b3018 Escherichia coli 562 -11533317 90016 plsc:parf (ec:2.3.1.51) (de:lpaat) (db:swissprot) PLSC_ECOLI P26647 ESCHERICHIA COLI 562 -11533317 164344 plsc 1-acylglycerol-3-phosphate o-acyltransferase (ec:2.3.1.51) (db:pir2.dat) S20460 S20460 Escherichia coli 562 -11533317 239232 plsc 1-acyl-glycerol-3-phosphate acyltransferase (fn:produces diacyl-glycerol-3-phosphate) (sr:escherichia coli (strain k-12) (library: clarke-carbon) dna) (db:genpept-bct1) (de:escherichia coli 1-acyl-sn-glycerol-3-phosphate acyltransferase(plsc) gene, complete cds; periplasmic protein (sufi) gene, ... ECOPLSC M63491 g147298 Escherichia coli 562 -11533317 7500888170 plsc 1-acyl-glycerol-3-phosphate acyltransferase (fn:produces diacyl-glycerol-3-phosphate) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (le:117131) (re:117868) (di:complement) ECU28377 U28377 g882548 Escherichia coli 562 -11533317 235502 plsc 1-acyl-sn-glycerol-3-phosphate acyltransferase (fn:enzyme; macromolecule synthesis, modification:) (db:genpept-bct2) (ec:2.3.1.51) (de:escherichia coli k-12 mg1655 section 274 of 400 of the completegenome.) (nt:f245; 100 pct identical to plsc_ecoli sw: p26647) (le:1573) (re:2310) (di:complement) AE000384 AE000384 g1789395 Escherichia coli 562 -11533317 5000690567 (de:(ecoli_2941) (pn:1-acyl-sn-glycerol-3-phosphate acyltransferase) (gn:plsc) (gtcfc:8.1) (ec:2.3.1.51) (plsc_ecoli) (keggfc:8.1) (rileyfc:3.1.11) (db:gtc-escherichia coli)) ECOLI_2941 ECOLI_2941 Escherichia coli 562 10032136				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829985	8300	30456	306	101

Description

6500729460 gpsa:b3608 l-glycerol 3-phosphate  
dehydrogenase:glycerol-3-phosphate dehydrogenase:nad+ (gtcfc:8.1)  
(ec:1.1.1.8) (keggfc:8.1) (rileyfc:3.1.11) (db:gtc-escherichia coli) b3608  
b3608 Escherichia coli 562 -11533318 74346 gpsa (ec:1.1.1.8)  
(de:glycerol-3-phosphate dehydrogenase (nad+),) (db:swissprot) GPDA\_ECOLI  
P37606 ESCHERICHIA COLI 562 -11533318 163979 gpsa glycerol-3-phosphate  
dehydrogenase nad+ (cl:glycerol-3-phosphate dehydrogenase) (ec:1.1.1.8)  
(db:pir2.dat) S47829 S47829 Escherichia coli 562 -11533318 7500882657 gpsa  
l-glycerol 3-phosphate dehydrogenase (sr:escherichia coli (sub\_strain  
mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli  
chromosomal region from 76.0 to 81.5 minutes.) (nt:similar to rabbit  
glycerol-3-phosphate) (le:196892) (re:197911) (di:complement) ECOUW76 U00039  
g1657692 Escherichia coli 562 -11533318 236845 gpsa glycerol-3-phosphate  
dehydrogenase nad+ (fn:enzyme; energy metabolism, carbon: aerobic)  
(db:genpept-bct2) (ec:1.1.1.8) (de:escherichia coli k-12 mg1655 section 329  
of 400 of the completegenome.) (nt:f339; 100 pct identical to gpda\_ecoli sw:  
p37606;) (le:70) (re:1089) (di:complement) AE000439 AE000439 g1790037  
Escherichia coli 562 -11533318 5000690570 (de:(ecoli\_3528)  
(pn:glycerol-3-phosphate dehydrogenase:nad) (gn:gpsa) (gtcfc:8.1)  
(ec:1.1.1.8) (gpda\_ecoli) (keggfc:8.1) (rileyfc:3.1.11) (db:gtc-escherichia  
coli)) ECOLI\_3528 ECOLI\_3528 Escherichia coli 562 10016863

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501829994	8301	30457	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830004	8302	30458	348	115

Description

6500729461 plda:b3821 phospholipase a1 precursor:detergent-resistant phospholipase a:dr-phospholipase a:phosphatidylcholine 1-acylhydrolase:outer membrane phospholipase a:om pla (gtcfc:11.1:8.1:8.4:13.10) (ec:3.1.1.32) (keggfc:8.1:8.4) (rileyfc:1.1.4) (db:gtc-escherichia coli) b3821 b3821 Escherichia coli 562 -11533319 237836 plda (ec:3.1.1.32) (de:acylhydrolase) (outer membrane phospholipase a) (om pla)) (db:swissprot) PA1\_ECOLI P00631 ESCHERICHIA COLI 562 -11533319 124255 plda phospholipase a1:precursor:outer-membrane phospholipase a:phosphatidylcholine 1-acylhydrolase:phospholipase a:detergent-resistant (cl:bacterial phospholipase a1) (ec:3.1.1.32) (db:pir1.dat) (mp:85 min) PSECA1 A22133 Escherichia coli 562 -11533319 7502851920 dr phospholipase a (db:genpept-bct1) (de:escherichia coli k-12 plda gene for dr-phospholipase a.) (le:292) (re:1161) (di:direct) ECPLDA1 X02143 g757840 Escherichia coli 562 -11533319 7500887552 plda outer membrane phospholipase a (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:3.1.1.32) (de:escherichia coli k-12 mg1655 section 348 of 400 of the completegenome.) (nt:o289; 99 pct identical to pa1\_ecoli sw: p00631;) (le:81) (re:950) (di:direct) AE000458 AE000458 g2367300 Escherichia coli 562 -11533319 7500887550 plda (ec:3.1.1.32) (de:acylhydrolase) (outer membrane phospholipase a) (om pla)) (db:swissprot) PA1\_ECOLI P00631 ESCHERICHIA COLI 562 -11533319

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830005	8303	30459	276	91

Description

6500729462 plsb:b4041 glycerol-3-phosphate acyltransferase (gtcfc:8.1) (ec:2.3.1.15) (keggfc:8.1) (rileyfc:3.1.11) (db:gtc-escherichia coli) b4041 b4041 Escherichia coli 562 -11533320 123351 plsb glycerol-3-phosphate o-acyltransferase (cl:glycerol-3-phosphate acyltransferase) (ec:2.3.1.15) (db:pir1.dat) (mp:92 min) XUECAG A00565 Escherichia coli 562 -11533320 7500888168 plsb glycerol-3-phosphate acyltransferase (fn:enzyme; macromolecule synthesis, modification:) (db:genpept-bct2) (ec:2.3.1.15) (de:escherichia coli k-12 mg1655 section 367 of 400 of the completegenome.) (nt:f827; 99 pct identical amino acid sequence and) (le:6138) (re:8621) (di:complement) AE000477 AE000477 g1790474 Escherichia coli 562 -11533320 90013 plsb (ec:2.3.1.15) (de:glycerol-3-phosphate acyltransferase,) (db:swissprot) PLSB\_ECOLI P00482 ESCHERICHIA COLI 562 -11533320 5000690574 (de:(ecoli\_3927) (pn:glycerolphosphate acyltransferase activity) (gn:plsb) (gtcfc:8.1) (ec:2.3.1.15) (plsb\_ecoli) (keggfc:8.1) (rileyfc:3.1.11) (db:gtc-escherichia coli)) ECOLI\_3927 ECOLI\_3927 Escherichia coli 562 10032133

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830030	8304	30460	396	131

Description

6500729463 mdob:b4359 phosphoglycerol transferase  
i:phosphatidylglycerol--membrane-oligosaccharide glycerophosphotransferase  
(gtcfc:8.1:8.4:11.1) (ec:2.7.8.20) (keggfc:8.1) (rileyfc:4.6.0)  
(db:gtc-escherichia coli) b4359 b4359 Escherichia coli 562 -11533321 83348  
mdob (ec:2.7.8.20) (de:membrane-oligosaccharide glycerophosphotransferase))  
(db:swissprot) MDOB\_ECOLI\_P39401 ESCHERICHIA COLI 562 -11533321 164052 mdob  
phosphatidylglycerol--membrane-oligosaccharide  
glycerophosphotransferase::mdob protein (ec:2.7.8.20) (db:pir2.dat) S56586  
S56586 Escherichia coli 562 -11533321 237567 mdob phosphoglycerol  
transferase i (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region  
from 92.8 to 00.1 minutes.) (le:287982) (re:290234) (di:complement) ECOUW93  
U14003 g537202 Escherichia coli 562 -11533321 7500885442 mdob  
phosphoglycerol transferase i activity (db:genpept-bct1) (de:escherichia  
coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no.  
18169) (le:287982) (re:290234) (di:complement) ECOUW93 U14003 g1263175  
Escherichia coli 562 -11533321 237566 mdob phosphoglycerol transferase i  
(fn:enzyme; osmotic adaptation) (db:genpept-bct2) (ec:2.7.8.20)  
(de:escherichia coli k-12 mg1655 section 397 of 400 of the completegenome.)  
(nt:f750; 100 pct identical amino acid sequence and) (le:99) (re:2351)  
(di:complement) AE000507 AE000507 g1790821 Escherichia coli 562 -11533321  
5000691073 (de:(ecoli\_4244) (pn:membrane-derived oligosaccharides;  
phosphoglycerol transferase i activity) (gn:mdob) (gtcfc:12.11)  
(ec:2.7.8.20) (mdob\_ecoli) (keggfc:11.1) (rileyfc:4.6.0) (db:gtc-escherichia  
coli)) ECOLI\_4244 ECOLI\_4244 Escherichia coli 562 10025564

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830031	8305	30461	474	157

Description

6500729464 plsx:b1090 plsx protein:fatty acid/phospholipid synthesis protein  
 plsx homolog (gtcfc:8.1) (keggfc:14.2) (rileyfc:3.1.11) (db:gtc-escherichia  
 coli) b1090 b1090 Escherichia coli 562 -11533322 90024 plsx (de:fatty  
 acid/phospholipid synthesis protein plsx homolog) (db:swissprot) PLSX\_ECOLI  
 P27247 ESCHERICHIA COLI 562 -11533322 7000686153 plsx fatty  
 acid/phospholipid synthesis protein plsx homolog (cl:phospholipid synthesis  
 protein) (db:pir2.dat) G64852 G64852 Escherichia coli 562 -11533322  
 7500888175 plsx (fn:fatty acid or phospholipid synthesis) (sr:escherichia  
 coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli plsx gene,  
 complete cds and beta-ketoacyl-acylcarrier protein synthase iii (fabh) gene,  
 5' end.) (le:93) (re:1133) (di:direct) ECOPLSFABA M96793 g147301 Escherichia  
 coli 562 -11533322 235504 plsx glycerolphosphate auxotrophy in plsb  
 background (fn:phenotype; macromolecule synthesis,) (db:genpept-bct2)  
 (de:escherichia coli k-12 mg1655 section 99 of 400 of the completegenome.)  
 (nt:o346; 100 pct identical to plsx\_ecoli sw: p27247) (le:9336) (re:10376)  
 (di:direct) AE000209 AE000209 g1787331 Escherichia coli 562 -11533322  
 5000690578 (de:(ecoli\_1052) (pn:glycerolphosphate auxotrophy in plsb  
 background) (gn:plsx) (gtcfc:8.4) (ec:) (plsx\_ecoli) (keggfc:11.2)  
 (rileyfc:3.1.11) (db:gtc-escherichia coli)) ECOLI\_1052 ECOLI\_1052  
 Escherichia coli 562 10032144

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830036	8306	30462	390	129

Description

6500729465 lgt:umpa:b2828 prolipoprotein diacylglyceryl transferase (gtcfc:8.1:8.5) (ec:2.4.99.-) (keggfc:8.5) (rileyfc:3.1.11) (db:gtc-escherichia coli) b2828 b2828 Escherichia coli 562 -11533323 82005 lgt:umpa (ec:2.4.99.-) (de:prolipoprotein diacylglyceryl transferase,) (db:swissprot) LGT\_ECOLI P37149 ESCHERICHIA COLI 562 -11533323 164413 lgt:umpa prolipoprotein diacylglyceryl transferase (cl:prolipoprotein diacylglyceryl transferase) (ec:2.4.99.-) (db:pir2.dat) A56149 A56149 Escherichia coli 562 -11533323 7500884983 lgt prolipoprotein diacylglyceryl transferase (db:genpept-bct1) (de:escherichia coli (ygdf) gene, partial cds and prolipoproteindiacylglyceryl transferase (lgt) gene, complete cds.) (le:435) (re:1310) (di:direct) ECOLGT U12289 g516036 Escherichia coli 562 -11533323 234977 lgt phosphatidylglycerol-prolipoprotein (fn:enzyme; macromolecule synthesis, modification:) (db:genpept-bct2) (ec:2.4.99.-) (de:escherichia coli k-12 mg1655 section 256 of 400 of the completegenome.) (nt:f291; 99 pct identical to lgt\_ecoli sw: p37149;) (le:6220) (re:7095) (di:complement) AE000366 AE000366 g1789192 Escherichia coli 562 -11533323 5000690581 (de:(ecoli\_2756) (pn:phosphatidylglycerol-prolipoprotein diacylglyceryl transferase; a major membrane phospholipid) (gn:lgt) (gtcfc:8.4:8.5) (ec:2.4.99.-) (lgt\_ecoli) (keggfc:8.5) (rileyfc:3.1.11) (db:gtc-escherichia coli)) ECOLI\_2756 ECOLI\_2756 Escherichia coli 562 10024239

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830039	8307	30463	228	75

Description

6500729466 yifd:pssr:b3763 pssr:possible regulatory protein pssr (gtcfc:8.1) (keggfc:14.2) (rileyfc:3.1.11) (db:gtc-escherichia coli) b3763 b3763 Escherichia coli 562 -11533324 92030 yifd:pssr (de:possible regulatory protein pssr) (db:swissprot) PSSR\_ECOLI P27826 ESCHERICHIA COLI 562 -11533324 7000686200 pssr pssr protein:hypothetical protein f133 (db:pir2.dat) F65179 F65179 Escherichia coli 562 -11533324 7500888869 f133 (db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (nt:cgsc no. 18010; possible pssr gene) (le:703) (re:1104) (di:complement) ECOUW85 M87049 g148171 Escherichia coli 562 -11533324 236995 pssr regulator of pssa (fn:regulator; macromolecule synthesis,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 343 of 400 of the completegenome.) (nt:f133; cgsc no. 18010) (le:3926) (re:4327) (di:complement) AE000453 AE000453 g1790199 Escherichia coli 562 -11533324 5000690579 (de:(ecoli\_3676) (pn:regulator of pssa) (gn:pssr) (gtcfc:8.4) (ec:) (pssr\_ecoli) (keggfc:11.2) (rileyfc:3.1.11) (db:gtc-escherichia coli)) ECOLI\_3676 ECOLI\_3676 Escherichia coli 562 10034064



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830044	8308	30464	780	259

Description

6500729467 pldb:b3825 lysophospholipase 12:lecithinase b (gtcfc:8.4:13.10) (ec:3.1.1.5) (keggfc:8.4) (rileyfc:1.1.4) (db:gtc-escherichia coli) b3825 b3825 Escherichia coli 562 -11533325 7500888153 pldb (ec:3.1.1.5) (de:lysophospholipase 12, (lecithinase b)) (db:swissprot) PLDB\_ECOLI P07000 ESCHERICHIA COLI 562 -11533325 7000688873 pldb lysophospholipase:12:2-lysophosphatidylcholine acylhydrolase:lecithinase b (cl:lysophospholipase 12) (ec:3.1.1.5) (db:pir1.dat) (mp:85 min) PSECL2 B65187 Escherichia coli 562 -11533325 7500888155 pldb lysophospholipase 1 2 (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:3.1.1.5) (de:escherichia coli k-12 mg1655 section 348 of 400 of the completegenome.) (nt:o340; 99 pct identical amino acid sequence and) (le:4384) (re:5406) (di:direct) AE000458 AE000458 g2367303 Escherichia coli 562 -11533325

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830049	8309	30465	378	125

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830050	8310	30466	1251	416

Description

6500729468 gatz:b2095 putative tagatose 6-phosphate kinase gatz (gtcfc:8.5:9.4:14.3) (ec:2.7.1.-) (keggfc:8.5:9.4) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2095 b2095 Escherichia coli 562 -11533326 73178 gatz (ec:2.7.1.143) (de:putative tagatose 6-phosphate kinase gatz,) (db:swissprot) GATZ\_ECOLI P37191 ESCHERICHIA COLI 562 -11533326 7000685369 gatz probable tagatose 6-phosphate kinase gatz (ec:2.7.1.-) (db:pir2.dat) F64976 F64976 Escherichia coli 562 -11533326 224649 gatz putative tagatose 6-phosphate kinase gatz ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #359(46.8-47.2 min.)) (nt:orf\_id:o359#5; similar to (swissprot accession) (le:2983) (re:4245) (di:complement) D90848 D90848 g1736821 Escherichia coli 562 -11533326 301289 gatz putative tagatose 6-phosphate kinase 1 (fn:putative enzyme; not classified) (db:genpept-bct2) (ec:2.7.1.-) (de:escherichia coli k-12 mg1655 section 188 of 400 of the completegenome.) (nt:f420; residues 1-371 are 98 pct identical to) (le:10013) (re:11275) (di:complement) AE000298 AE000298 g1788411 Escherichia coli 562 -11533326 5000690547 (de:(ecoli\_2043) (pn:putative tagatose 6-phosphate kinase 1) (gn:gatz) (gtcfc:7.2:8.4:8.5:9.4) (ec:2.7.1.-) (gatz\_ecoli) (keggfc:7.1:8.5:9.4) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2043 ECOLI\_2043 Escherichia coli 562 10120008

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830064	8311	30467	375	124
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830065	8312	30468	873	290
<u>Description</u>				

6500729469 agaz:b3132 putative tagatose 6-phosphate kinase agaz  
 (gtcfc:8.5:9.4:14.3) (ec:2.7.1.-) (keggfc:8.5:9.4) (rileyfc:5.8.0)  
 (db:gtc-escherichia coli) b3132 b3132 Escherichia coli 562 -11533327 58937  
 agaz (ec:2.7.1.144) (de:putative tagatose 6-phosphate kinase agaz,)  
 (db:swissprot) AGAZ\_ECOLI P42903 ESCHERICHIA COLI 562 -11533327 7000684538  
 agaz probable tagatose 6-phosphate kinase agaz (ec:2.7.1.-) (db:pir2.dat)  
 H65102 H65102 Escherichia coli 562 -11533327 7500876665 (db:genpept-bct1)  
 (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.)  
 (nt:orf\_o426) (le:59667) (re:60947) (di:direct) ECOUW67 U18997 g606072  
 Escherichia coli 562 -11533327 236371 agaz putative tagatose 6-phosphate  
 kinase 2 (fn:putative enzyme; not classified) (db:genpept-bct2) (ec:2.7.1.-)  
 (de:escherichia coli k-12 mg1655 section 284 of 400 of the completegenome.)  
 (nt:o426; 100 pct identical amino acid sequence and) (le:9312) (re:10592)  
 (di:direct) AE000394 AE000394 g1789520 Escherichia coli 562 -11533327  
 5000690548 (de:(ecoli\_3056) (pn:putative tagatose 6-phosphate kinase agaz)  
 (gn:agaz) (gtcfc:7.2:8.4:8.5:9.4) (ec:2.7.1.-) (agaz\_ecoli)  
 (keggfc:7.1:8.5:9.4) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_3056  
 ECOLI\_3056 Escherichia coli 562 10001681

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830066	8313	30469	1392	464

Description

6500729470 heml:gsa:popc:b0154 glutamate-1-semialdehyde  
2:1-aminomutase:gsa:glutamate-1-semialdehyde aminotransferase:gsa-at  
(gtcfc:9.10) (ec:5.4.3.8) (keggfc:9.10) (rileyfc:1.7.12) (db:gtc-escherichia  
coli) b0154 b0154 Escherichia coli 562 -11533328 74596 heml:gsa:popc  
(ec:5.4.3.8) (de:(glutamate-1-semialdehyde aminotransferase) (gsa-at))  
(db:swissprot) GSA\_ECOLI P23893 ESCHERICHIA COLI 562 -11533328 7000685459  
heml glutamate-1-semialdehyde 2:1-aminomutase (ec:5.4.3.8) (db:pir2.dat)  
B64739 B64739 Escherichia coli 562 -11533328 7500882783 gsa  
glutamine-1-semialdehyde aminotransferase (db:genpept-bct1) (de:escherichia  
coli chromosome minutes 4-6.) (le:4677) (re:5957) (di:complement) ECU70214  
U70214 g1552732 Escherichia coli 562 -11533328 239783 heml  
glutamate-1-semialdehyde aminotransferase (fn:enzyme; biosynthesis of  
cofactors, carriers:) (db:genpept-bct2) (ec:5.4.3.8) (de:escherichia coli  
k-12 mg1655 section 15 of 400 of the completegenome.) (nt:f426; 99 pct  
identical to gsa\_ecoli sw: p23893;) (le:109) (re:1389) (di:complement)  
AE000125 AE000125 g1786349 Escherichia coli 562 -11533328 5000690592  
(de:(ecoli\_154) (pn:glutamate-1-semialdehyde aminotransferase) (gn:heml)  
(gtcfc:9.10) (ec:5.4.3.8) (gsa\_ecoli) (keggfc:9.10) (rileyfc:1.7.12)  
(db:gtc-escherichia coli)) ECOLI\_154 ECOLI\_154 Escherichia coli 562 10122687

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830077	8314	30470	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830078	8315	30471	477	158

Description

6500729471 hemb:b0369 delta-aminolevulinic acid dehydratase (gtcfc:9.10)  
(ec:4.2.1.24) (keggfc:9.10) (rileyfc:1.7.12) (db:gtc-escherichia coli) b0369  
b0369 Escherichia coli 562 -11533329 7000688896 hemb porphobilinogen  
synthase::5-aminolevulinic acid dehydratase:aminolevulinate dehydratase  
(cl:porphobilinogen synthase) (ec:4.2.1.24) (db:pir1.dat) (mp:8 min) SYECPF  
A64765 Escherichia coli 562 -11533329 239985 porphobilinogen synthase  
(sr:escherichia coli (strain k12) (library: kohara) dna, clone 8f10)  
(db:genpept-bct1) (de:escherichia coli hemb gene, complete cds.) (le:14412)  
(re:15419) (di:complement) ECOPS D85613 g1054579 Escherichia coli 562  
-11533329 7500953344 hemb porphobilinogen synthase (db:genpept-bct1)  
(ec:4.2.1.24) (de:escherichia coli chromosome minutes 6-8.) (le:96343)  
(re:97350) (di:complement) ECU73857 U73857 g1657564 Escherichia coli 562  
-11533329 235582 hemb 5-aminolevulinate dehydratase = porphobilinogen  
(fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2)  
(ec:4.2.1.24) (de:escherichia coli k-12 mg1655 section 33 of 400 of the  
completegenome.) (nt:f335; 100 pct identical to gb: ecops\_9) (le:8798)  
(re:9805) (di:complement) AE000143 AE000143 g1786566 Escherichia coli 562  
-11533329 5000690593 (de:(ecoli\_353) (pn:5-aminolevulinate dehydratase ,  
porphobilinogen synthase:5-aminolevulinate dehydratase ) (gn:hemb)  
(gtcfc:9.10) (ec:4.2.1.24) (hem2\_ecoli) (keggfc:9.10) (rileyfc:1.7.12)  
(db:gtc-escherichia coli)) ECOLI\_353 ECOLI\_353 Escherichia coli 562 10122797

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830081	8316	30472	189	62

Description

6500729472 hemh:popa:visa:b0475 ferrochelata:protoheme ferro-lyase:heme synthetase (gtcfc:9.10:14.3) (ec:4.99.1.1) (keggfc:9.10) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0475 b0475 Escherichia coli 562 -11533330 76779 hemh:popa:visa (ec:4.99.1.1) (de:synthetase)) (db:swissprot) HEMZ\_ECOLI P23871 ESCHERICHIA COLI 562 -11533330 7000685518 visa:hemh:popa ferrochelata::heme synthetase:protoheme ferro-lyase (cl:ferrochelata) (ec:4.99.1.1) (db:pir2.dat) (mp:11 min) B64778 B64778 Escherichia coli 562 -11533330 240250 hemh ferrochelata (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:77503) (re:78465) (di:direct) ECU82664 U82664 g1773157 Escherichia coli 562 -11533330 7500883207 hemh ferrochelata:final enzyme of heme (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:4.99.1.1) (de:escherichia coli k-12 mg1655 section 43 of 400 of the completegenome.) (nt:o320; 99 pct identical to hemz\_ecoli sw: p23871;) (le:8081) (re:9043) (di:direct) AE000153 AE000153 g1786681 Escherichia coli 562 -11533330 142059 visa:hemh ferrochelata::protoheme ferro-lyase (cl:ferrochelata) (ec:4.99.1.1) (db:pir) (mp:11 min) B64778 B64778 Escherichia coli 562 -11533330 5000690594 (de:(ecoli\_458) (pn:ferrochelata, final enzyme of haeme biosynthesis) (gn:hemh) (gtcfc:9.10) (ec:4.99.1.1) (hemz\_ecoli) (keggfc:9.10) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_458 ECOLI\_458 Escherichia coli 562 10072751

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830087	8317	30473	723	240

Description

6500729473 btur:coba:b1270 i alamin adenosyltransferase:cob:ialamin  
adenosyltransferase:corrinoid adenosyltransferase (gtcfc:9.10:9.9)  
(ec:2.5.1.17) (keggfc:9.10) (rileyfc:1.7.13) (db:gtc-escherichia coli)  
(gtcfc:metabolism of cofactors and vitamins-porphyrin and chlorophyll  
metabolism:metabolism of cofactors and vitamins-cobalamin (vitamin b12))  
(rileyfc:biosynthesis... b1270 b1270 Escherichia coli 562 -11533331 62077  
btur:coba (ec:2.5.1.17) (de:adenosyltransferase)) (db:swissprot) BTUR\_ECOLI  
P13040 ESCHERICHIA COLI 562 -11533331 7000684735 btur:coba cob i alamin  
adenosyltransferase (ec:2.5.1.17) (db:pir2.dat) A64875 A64875 Escherichia  
coli 562 -11533331 223481 btur:coba cob i alamin adenosyltransferase ec  
2.5.1.17 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda  
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#253(28.4-28.7 min.)) (nt:orf\_id:o253#10; similar to (swissprot accession)  
(le:10387) (re:10977) (di:complement) D90764 D90764 g1742065 Escherichia  
coli 562 -11533331 300299 btur:coba cob i alamin adenosyltransferase ec  
2.5.1.17 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda  
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#254(28.4-28.9 min.)) (nt:orf\_id:o253#10; similar to (swissprot accession)  
(le:7893) (re:8483) (di:complement) D90765 D90765 g1742081 Escherichia coli  
562 -11533331 300284 (sr:e.coli (k12) dna) (db:genpept-bct1) (de:e.coli  
btur gene encoding protein btur, complete cds.) (nt:btur protein) (le:102)  
(re:692) (di:direct) ECOBTUR M21528 g145448 Escherichia coli 562 -11533331  
233927 btur cob i alamin adenolsyltransferase (fn:enzyme; biosynthesis of  
cofactors, carriers:) (db:genpept-bct2) (ec:2.5.1.17) (de:escherichia coli  
k-12 mg1655 section 115 of 400 of the completegenome.) (nt:f196; 100 pct  
identical to btur\_ecoli sw: p13040;) (le:1051) (re:1641) (di:complement)  
AE000225 AE000225 g1787525 Escherichia coli 562 -11533331 223496 btur:coba  
cob i alamin adenosyltransferase ec 2.5.1.17 (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #254(28.4-28.9 min.))  
(nt:orf\_id:o253#10; similar to (swissprot accession) (le:7893) (re:8483)  
(di:complement) D90765 D90765 g1742081 Escherichia coli 562 -11533331  
5000690595 (de:(ecoli\_1230) (pn:cob:ialamin adenolsyltransferase) (gn:btur)  
(gtcfc:9.10) (ec:2.5.1.17) (btur\_ecoli) (keggfc:9.10) (rileyfc:1.7.13)  
(db:gtc-escherichia coli)) ECOLI\_1230 ECOLI\_1230 Escherichia coli 562  
10004777

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830095	8318	30474	534	178

Description

6500729474 hemf:b2436 coproporphyrinogen iii oxidase:coproporphyrinogen iii oxidase:aerobic:coproporphyrinogenase:coprogen oxidase (gtcfc:9.10) (ec:1.3.3.3) (keggfc:9.10) (rileyfc:1.7.12) (db:gtc-escherichia coli) b2436 b2436 Escherichia coli 562 -11533332 7500883170 hemf (ec:1.3.3.3) (de:(coproporphyrinogenase) (coprogen oxidase)) (db:swissprot) HEM6\_ECOLI P36553 ESCHERICHIA COLI 562 -11533332 136557 hemf coproporphyrinogen oxidase:iii:aerobic (cl:coproporphyrinogen oxidase) (ec:1.3.3.3) (db:pir2.dat) B36964 B36964 Escherichia coli 562 -11533332 225007 hemf coproporphyrinogen iii oxidase:aerobic ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #420(54.9-55.2 min.)) (nt:similar to (swissprot accession number p36553)) (le:7163) (re:8062) (di:direct) D90873 D90873 g1799866 Escherichia coli 562 -11533332 225013 hemf coproporphyrinogen iii oxidase:aerobic ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #421(55.1-55.5 min.)) (nt:similar to (swissprot accession number p36553)) (le:59) (re:958) (di:direct) D90874 D90874 g1799873 Escherichia coli 562 -11533332 5000690596 hemf coproporphyrinogen oxidase (db:genpept-bct1) (ec:1.3.3.3) (de:e.coli orf1, orf3 and hemf gene for coproporphyrinogen iii oxidase.) (le:1312) (re:2211) (di:direct) ECHEMF X75413 g453969 Escherichia coli 562 -11533332 233081 hemf coproporphyrinogen iii oxidase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:1.3.3.3) (de:escherichia coli k-12 mg1655 section 221 of 400 of the completegenome.) (nt:o299; 100 pct identical to hem6\_ecoli sw: p36553) (le:955) (re:1854) (di:direct) AE000331 AE000331 g1788777 Escherichia coli 562 -11533332 76517 hemf (ec:1.3.3.3) (de:(coproporphyrinogenase) (coprogen oxidase)) (db:swissprot) HEM6\_ECOLI P36553 ESCHERICHIA COLI 562 -11533332

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830103	8319	30475	645	214

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830106	8320	30476	396	131

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830135	8321	30477	2655	884

Description

GTC ORF with score 116 to: (sr:rattus norvegicus (strain:wistar) brain cdna to mrna) (db:genpept-rod) (de:rat brain mrna for annexin v-binding protein (abp-10), partial cds.) (nt:protein sequence is in conflict with the conceptual) (le:<1) (re:1490) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830145	8322	30478	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830147	8323	30479	282	93

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830152	8324	30480	597	199

Description

6500729475 cysg:b3368 siroheme synthase:contains:uroporphyrin-iii c-methyltransferase:urogen iii methylase:sumt:uroporphyrinogen iii methylase:urom / precorrin-2 oxidase / ferrochelataze (gtcfc:9.10) (keggfc:9.10) (rileyfc:1.7.12) (db:gtc-escherichia coli) b3368 b3368 Escherichia coli 562 -11533333 67654 cysg (ec:2.1.1.107:1.-.-.:4.99.1.-) (de:(ec 4.99.1.-))) (db:swissprot) CYSG\_ECOLI P11098 ESCHERICHIA COLI 562 -11533333 7000684969 cysg cysg protein (db:pir2.dat) (mp:74 min) C65131 C65131 Escherichia coli 562 -11533333 7500879908 cysg uroporphyrinogen iii methylase:sirohaeme (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 302 of 400 of the completegenome.) (nt:o457; cg site no. 893; 99 pct identical amino) (le:8932) (re:10305) (di:direct) AE000412 AE000412 g1789768 Escherichia coli 562 -11533333 5000690597 (de:(ecoli\_3286) (pn:uroporphyrinogen iii methylase; sirohaeme biosynthesis) (gn:cysg) (gtcfc:9.10) (ec:2.1.1.107) (cysg\_ecoli) (keggfc:9.10) (rileyfc:1.7.12) (db:gtc-escherichia coli)) ECOLI\_3286 ECOLI\_3286 Escherichia coli 562 10124018

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830160	8325	30481	195	64

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830175	8326	30482	429	142

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830178	8327	30483	225	74

Description

6500729476 hemx:b3803 uroporphyrinogen iii methylase:putative  
uroporphyrin-iii c-methyltransferase:urogen iii methylase:orf x (gtcfc:9.10)  
(ec:2.1.1.107) (keggfc:9.10) (rileyfc:1.7.12) (db:gtc-escherichia coli)  
b3803 b3803 Escherichia coli 562 -11533334 237027 hemx (ec:2.1.1.107)  
(de:iii methylase) (orf x)) (db:swissprot) HEMX\_ECOLI P09127 ESCHERICHIA  
COLI 562 -11533334 164814 hemx uroporphyrin-iii c-methyltransferase  
(ec:2.1.1.107) (db:pir2.dat) (mp:85 min) S02185 S02185 Escherichia coli 562  
-11533334 233085 (db:genpept-bct1) (de:e. coli genes hemc and hemd for  
porphobilinogen deaminase (ec4.3.1.8) and uroporphyrinogen iii cosynthetase  
(ec 4.2.1.75).) (nt:orf x (aa 1 - 393)) (le:1820) (re:3001) (di:direct)  
ECHEMCD X12614 g41668 Escherichia coli 562 -11533334 5000690598  
(db:genpept-bct1) (de:e. coli hemx gene for putative urogeniii methylase.)  
(nt:put. urogeniii methylase (aa 1 - 393); hemx gene) (le:25) (re:1206)  
(di:direct) ECHENX X13406 g41678 Escherichia coli 562 -11533334 7500883202  
hemx uroporphyrinogen iii methylase (db:genpept-bct1) (de:e. coli genomic  
sequence of the region from 84.5 to 86.5 minutes.) (le:40997) (re:42178)  
(di:complement) ECOUW85 M87049 g148202 Escherichia coli 562 -11533334  
233073 hemx uroporphyrinogen iii methylase (fn:enzyme; biosynthesis of  
cofactors, carriers:) (db:genpept-bct2) (ec:2.1.1.107) (de:escherichia coli  
k-12 mg1655 section 346 of 400 of the completegenome.) (nt:f393; 100 pct  
identical to hemx\_ecoli sw: p09127) (le:5027) (re:6208) (di:complement)  
AE000456 AE000456 g1790235 Escherichia coli 562 -11533334 76769 hemx  
(ec:2.1.1.107) (de:iii methylase) (orf x)) (db:swissprot) HEMX\_ECOLI P09127  
ESCHERICHIA COLI 562 -11533334

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830179	8328	30484	567	188

Description

6500729477 hemd:b3804 uroporphyrinogen iii synthase:uroporphyrinogen-iii synthase:uros:uroporphyrinogen-iii cosynthetase:hydroxymethylbilane hydrolyase:cyclizing (gtcfc:9.10) (ec:4.2.1.75) (keggfc:9.10) (rileyfc:1.7.12) (db:gtc-escherichia coli) b3804 b3804 Escherichia coli 562 -11533335 237028 hemd (ec:4.2.1.75) (de:iii cosynthetase) (hydroxymethylbilane hydrolyase (cyclizing))) (db:swissprot) HEM4\_ECOLI P09126 ESCHERICHIA COLI 562 -11533335 7000685510 hemd uroporphyrinogen-iii synthase::uroporphyrinogen iii cosynthetase (ec:4.2.1.75) (db:pir2.dat) (mp:85 min) E65184 E65184 Escherichia coli 562 -11533335 5000690599 (db:genpept-bct1) (de:e. coli genes hemc and hemd for porphobilinogen deaminase (ec4.3.1.8) and uroporphyrinogen iii cosynthetase (ec 4.2.1.75).) (nt:uroporphyrinogen iii cosynthetase (aa 1 - 246)) (le:1058) (re:1798) (di:direct) ECHEMCD X12614 g41667 Escherichia coli 562 -11533335 7500883160 hemd::cgsc no. 645 uroporphyrinogen iii synthase (db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (le:42200) (re:42940) (di:complement) ECOUW85 M87049 g148203 Escherichia coli 562 -11533335 233072 hemd uroporphyrinogen iii synthase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:4.2.1.75) (de:escherichia coli k-12 mg1655 section 346 of 400 of the completegenome.) (nt:f246; 100 pct identical to hem4\_ecoli sw: p09126) (le:6230) (re:6970) (di:complement) AE000456 AE000456 g1790236 Escherichia coli 562 -11533335 76511 hemd (ec:4.2.1.75) (de:iii cosynthetase) (hydroxymethylbilane hydrolyase (cyclizing))) (db:swissprot) HEM4\_ECOLI P09126 ESCHERICHIA COLI 562 -11533335

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830198	8329	30485	576	192

Description

6500729478 hemc:b3805 porphobilinogen deaminase (gtcfc:9.10) (ec:4.3.1.8) (keggfc:9.10) (rileyfc:1.7.12) (db:gtc-escherichia coli) b3805 b3805 Escherichia coli 562 -11533336 7500974868 hemc porphobilinogen deaminase = hydroxymethylbilane (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:4.3.1.8) (de:escherichia coli k-12 mg1655 section 346 of 400 of the completegenome.) (nt:f320; 98 pct identical to 313 amino acids) (le:6967) (re:7929) (di:complement) AE000456 AE000456 g2367293 Escherichia coli 562 -11533336

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830199	8330	30486	525	174

Description

6500729479 hemg:b3850 hypothetical protein:protoporphyrinogen oxidase:ppo (gtcfc:9.10:14.1) (ec:1.3.3.4) (keggfc:9.10) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3850 b3850 Escherichia coli 562 -11533337  
7500883183 hemg (ec:1.3.3.4) (de:protoporphyrinogen oxidase, (ppo)) (db:swissprot) HEMG\_ECOLI P27863 ESCHERICHIA COLI 562 -11533337 164429 hemg protoporphyrinogen oxidase::hypothetical protein o181 (ec:1.3.3.4) (db:pir2.dat) (mp:86 min) JC2513 JC2513 Escherichia coli 562 -11533337  
5000690601 hemg protoporphyrinogen oxidase (db:genpept-bct1) (de:e.coli hemg gene for protoporphyrinogen oxidase.) (le:98) (re:643) (di:direct) ECHEMGA X68660 g581103 Escherichia coli 562 -11533337 233083 hemg protoporphyrin oxidase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 350 of 400 of the completegenome.) (nt:o181) (le:7348) (re:7893) (di:direct) AE000460 AE000460 g1790285 Escherichia coli 562 -11533337 76731 hemg (ec:1.3.3.4) (de:protoporphyrinogen oxidase, (ppo)) (db:swissprot) HEMG\_ECOLI P27863 ESCHERICHIA COLI 562 -11533337

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830201	8331	30487	1305	434

Description

6500729480 heme:b3997 uroporphyrinogen decarboxylase:upd (gtcfc:9.10) (ec:4.1.1.37) (keggfc:9.10) (rileyfc:1.7.12) (db:gtc-escherichia coli) b3997 b3997 Escherichia coli 562 -11533338 68142 heme (ec:4.1.1.37) (de:uroporphyrinogen decarboxylase, (upd)) (db:swissprot) DCUP\_ECOLI P29680 ESCHERICHIA COLI 562 -11533338 7000684995 heme uroporphyrinogen decarboxylase (cl:uroporphyrinogen decarboxylase) (ec:4.1.1.37) (db:pir2.dat) (mp:90 min) H65206 H65206 Escherichia coli 562 -11533338  
7500880098 heme uroporphyrinogen decarboxylase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:4.1.1.37) (de:escherichia coli k-12 mg1655 section 363 of 400 of the completegenome.) (nt:o354; 100 pct identical to dcup\_ecoli sw: p29680;) (le:8078) (re:9142) (di:direct) AE000473 AE000473 g2367337 Escherichia coli 562 -11533338

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830209	8332	30488	435	145

# Description

6500729481 hemm:b1209 hemm protein (gtcfc:9.10) (keggfc:14.2)  
(rileyfc:1.7.12) (db:gtc-escherichia coli) b1209 b1209 Escherichia coli 562  
-11533339 76741 lolb:hemm (de:outer membrane lipoprotein lolb precursor)  
(db:swissprot) LOLB\_ECOLI P24208 ESCHERICHIA COLI 562 -11533339 162603 hemm  
5-aminolevulinate synthase:hemm protein (db:pir2.dat) (mp:27 min) A47706  
A47706 Escherichia coli 562 -11533339 223411 hemm orf1 3 of hema  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #247)  
(db:genpept-bct1) (de:escherichia coli genomic dna.(27.0 -27.4 min).)  
(le:7139) (re:7762) (di:complement) D90756 D90756 g1651599 Escherichia coli  
562 -11533339 7500883188 (sr:escherichia coli (strain k-12) dna)  
(db:genpept-bct1) (de:e.coli orf1 and orf2 gene, complete cds; prs gene, 5'  
end; hemagene, putative cds.) (nt:orf1) (le:221) (re:844) (di:direct)  
ECOPRSA M77237 g147381 Escherichia coli 562 -11533339 235572 hemm an enzyme  
in main pathway of synthesis of (fn:enzyme; biosynthesis of cofactors,  
carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 109 of  
400 of the completegenome.) (nt:f207; 99 pct identical to hemm\_ecoli sw:  
p24208) (le:6571) (re:7194) (di:complement) AE000219 AE000219 g1787460  
Escherichia coli 562 -11533339 5000690591 hemm 22k hypothetical protein 3  
of hema (sr:escherichia coli(strain:k12) dna, clone:kohara clone #247)  
(db:genpept) (de:escherichia coli genomic dna. (27.1 - 27.5 min).)  
(nt:orf\_id:o247#7; similar to pir accession number) (le:7139) (re:7762)  
(di:complement) D90756 D90756 g1651599 Escherichia coli 562 -11533339

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830212	8333	30489	726	241

Description

6500729482 thil:b0417 hypothetical protein:thiamin-monophosphate kinase:thiamin-phosphate kinase (gtcfc:9.1:14.1) (ec:2.7.4.16) (keggfc:9.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-thiamine metabolism (vitamin b1):unknown-hypothetical) b0417 b0417 Escherichia coli 562 -11533340 1500687056 thil (ec:2.7.4.16) (de:thiamin-monophosphate kinase, (thiamin-phosphate kinase)) (db:swissprot) THIL\_ECOLI P77785 ESCHERICHIA COLI 562 -11533340 7000686793 thil thiamin-phosphate kinase (ec:2.7.4.16) (db:pir2.dat) A64771 A64771 Escherichia coli 562 -11533340 7500893072 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to h. influenzae hil305) (le:15084) (re:16061) (di:direct) ECU82664 U82664 g1773101 Escherichia coli 562 -11533340 240194 thil thiamin-monophosphate kinase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 38 of 400 of the completegenome.) (nt:o325; 56 pct identical to 273 aa of gb:) (le:2708) (re:3685) (di:direct) AE000148 AE000148 g1786619 Escherichia coli 562 -11533340 5000691569 (de:(ecoli\_401) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_401 ECOLI\_401 Escherichia coli 562 10063510

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830223	8334	30490	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830229	8335	30491	894	297

Description

6500729483 thid:b2103 hypothetical protein:phosphomethylpyrimidine kinase:hmp-phosphate kinase:hmp-p kinase (gtcfc:9.1:14.1) (ec:2.7.4.7) (keggfc:9.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-thiamine metabolism (vitamin b1):unknown-hypothetical) b2103 b2103 Escherichia coli 562 -11533341 1500687053 thid (ec:2.7.4.7) (de:(hmp-p kinase)) (db:swissprot) THID\_ECOLI P76422 ESCHERICHIA COLI 562 -11533341 7000686788 hypothetical protein b2103 (cl:phosphomethylpyrimidine phosphate kinase) (db:pir2.dat) F64977 F64977 Escherichia coli 562 -11533341 224655 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #359(46.8-47.2 min.)) (nt:orf\_id:o359#15; similar to (swissprot accession) (le:11637) (re:12437) (di:complement) D90848 D90848 g1736827 Escherichia coli 562 -11533341 301295 thid phosphomethylpyrimidine kinase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 189 of 400 of the completegenome.) (nt:f266; this 266 aa orf is 42 pct identical (7 gaps)) (le:6385) (re:7185) (di:complement) AE000299 AE000299 g1788420 Escherichia coli 562 -11533341 5000692697 (de:(ecoli\_2051) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2051 ECOLI\_2051 Escherichia coli 562 10063506

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830250	8336	30492	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830267	8337	30493	222	74

Description

6500729484 thim:b2104 hypothetical protein:hydroxyethylthiazole  
kinase:4-methyl-5-beta-hydroxyethylthiazole kinase:thz kinase:th kinase  
(gtcfc:9.1:14.1) (ec:2.7.1.50) (keggfc:9.1) (rileyfc:5.7.0)  
(db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and  
vitamins-thiamine metabolism (vitamin b1):unknown-hypothetical) b2104 b2104  
Escherichia coli 562 -11533342 1500687059 thim (ec:2.7.1.50)  
(de:hydroxyethylthiazole kinase) (thz kinase) (th kinase)) (db:swissprot)  
THIM\_ECOLI P76423 ESCHERICHIA COLI 562 -11533342 7000686795  
hydroxyethylthiazole kinase::hypothetical protein b2104  
(cl:hydroxyethylthiazole kinase:hydroxyethylthiazole kinase homology)  
(ec:2.7.1.50) (db:pir2.dat) G64977 G64977 Escherichia coli 562 -11533342  
224656 thi4 protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara  
lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#359(46.8-47.2 min.)) (nt:orf\_id:o359#16; similar to (pir accession number)  
(le:12434) (re:13222) (di:complement) D90848 D90848 g1736828 Escherichia  
coli 562 -11533342 301296 thim hydroxyethylthiazole kinase (fn:enzyme;  
biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli  
k-12 mg1655 section 189 of 400 of the completegenome.) (nt:f262; this 262 aa  
orf is 40 pct identical (6 gaps)) (le:7182) (re:7970) (di:complement)  
AE000299 AE000299 g1788421 Escherichia coli 562 -11533342 5000692698  
(de:(ecoli\_2052) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)  
(keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2052  
ECOLI\_2052 Escherichia coli 562 10063513

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830268	8338	30494	756	251

Description

6500729485 thie:b3993 thie protein:thiamin-phosphate pyrophosphorylase:tmp  
pyrophosphorylase:tmp-ppase:thiamin-phosphate synthase (gtcfc:9.1)  
(ec:2.5.1.3) (keggfc:9.1) (rileyfc:1.7.8) (db:gtc-escherichia coli)  
(gtcfc:metabolism of cofactors and vitamins-thiamine metabolism (vitamin  
b1)) b3993 b3993 Escherichia coli 562 -11533343 101324 thie (ec:2.5.1.3)  
(de:pyrophosphorylase) (tmp-ppase) (thiamin-phosphate synthase))  
(db:swissprot) THIE\_ECOLI P30137 ESCHERICHIA COLI 562 -11533343 164681 thie  
thie protein (cl:thie protein:thiamin-phosphate pyrophosphorylase homology)  
(db:pir2.dat) S35118 S35118 Escherichia coli 562 -11533343 238340 thie  
(db:genpept-bct1) (de:escherichia coli thicefsgh operon, complete cds.)  
(le:2156) (re:2791) (di:direct) ECTHICEFGH M88701 g414233 Escherichia coli  
562 -11533343 237203 thie thiamin biosynthesis:thiazole moiety (fn:enzyme;  
biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli  
k-12 mg1655 section 363 of 400 of the completegenome.) (nt:f211; 100 pct  
identical amino acid sequence and) (le:3931) (re:4566) (di:complement)  
AE000473 AE000473 g1790426 Escherichia coli 562 -11533343 7500893060 thie  
(fn:thiamine biosynthesis) (sr:escherichia coli (sub\_strain mg1655, strain  
k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region  
from 89.2 to 92.8 minutes.) (le:58810) (re:59445) (di:complement) ECOUW89  
U00006 g396332 Escherichia coli 562 -11533343 5000690589 (de:(ecoli\_3883)  
(pn:thiamin biosynthesis, thiazole moiety) (gn:thie) (gtcfc:9.1) (ec:)  
(thie\_ecoli) (keggfc:11.2) (rileyfc:1.7.8) (db:gtc-escherichia coli))  
ECOLI\_3883 ECOLI\_3883 Escherichia coli 562 10043165



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830270	8339	30495	489	162

Description

6500729486 thih:b3990 thih protein (gtcfc:9.1) (keggfc:14.2) (rileyfc:1.7.8) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-thiamine metabolism (vitamin b1)) b3990 b3990 Escherichia coli 562 -11533344 101332 thih (de:thih protein) (db:swissprot) THIH\_ECOLI P30140 ESCHERICHIA COLI 562 -11533344 164682 thih thih protein (db:pir2.dat) S35121 S35121 Escherichia coli 562 -11533344 238344 thih (db:genpept-bct1) (de:escherichia coli thicefsgh operon, complete cds.) (le:4489) (re:5622) (di:direct) ECTHICEFGH M88701 g414236 Escherichia coli 562 -11533344 237200 thih thiamin biosynthesis:thiazole moiety (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 363 of 400 of the completegenome.) (nt:f377; 100 pct identical amino acid sequence and) (le:1097) (re:2230) (di:complement) AE000473 AE000473 g1790423 Escherichia coli 562 -11533344 7500893068 thih (fn:thiamine biosynthesis) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:55976) (re:57109) (di:complement) ECOUW89 U00006 g396329 Escherichia coli 562 -11533344 5000690586 (de:(ecoli\_3880) (pn:thiamin biosynthesis, thiazole moiety) (gn:thih) (gtcfc:9.1) (ec:) (thih\_ecoli) (keggfc:11.2) (rileyfc:1.7.8) (db:gtc-escherichia coli)) ECOLI\_3880 ECOLI\_3880 Escherichia coli 562 10043173

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830278	8340	30496	705	234

# Description

6500729487 thig:b3991 thig protein (gtcfc:9.1) (keggfc:14.2) (rileyfc:1.7.8) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-thiamine metabolism (vitamin b1)) b3991 b3991 Escherichia coli 562 -11533345 101328 thig (de:thig protein) (db:swissprot) THIG\_ECOLI P30139 ESCHERICHIA COLI 562 -11533345 7000686790 thig thig protein:4-methyl-5-beta-hydroxyethyl thiazole monophosphate synthesis protein thig (cl:thiamine biosynthesis protein thig) (db:pir2.dat) B65206 B65206 Escherichia coli 562 -11533345 237201 thig thiamin biosynthesis:thiazole moiety (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 363 of 400 of the completegenome.) (nt:f281; this 281 aa orf is 99 pct identical to) (le:2227) (re:3072) (di:complement) AE000473 AE000473 g1790424 Escherichia coli 562 -11533345 7500893065 thig (fn:thiamine biosynthesis) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:57106) (re:57951) (di:complement) ECOUW89 U00006 g409790 Escherichia coli 562 -11533345 5000690587 (de:(ecoli\_3881) (pn:thiamin biosynthesis, thiazole moiety) (gn:thig) (gtcfc:9.1) (ec:) (thig\_ecoli) (keggfc:11.2) (rileyfc:1.7.8) (db:gtc-escherichia coli)) ECOLI\_3881 ECOLI\_3881 Escherichia coli 562 10124127

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830284	8341	30497	1941	646

# Description

5000690588 thif (gtcfc:9.1) (keggfc:14.2) (rileyfc:1.7.8) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-thiamine metabolism (vitamin b1)) b3992 b3992 Escherichia coli 562 -11533346 7000691920 thif thif protein:4-methyl-5-beta-hydroxyethyl thiazole monophosphate synthesis protein thif (cl:molybdopterin biosynthesis protein moeb) (db:pir2.dat) C65206 C65206 Escherichia coli 562 -11533346 237202 thif thiamin biosynthesis:thiazole moiety (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 363 of 400 of the completegenome.) (nt:f245; this 245 aa orf is 100 pct identical to) (le:3183) (re:3920) (di:complement) AE000473 AE000473 g1790425 Escherichia coli 562 -11533346 7500960467 thif (fn:thiamine biosynthesis) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:similar to e. coli chln) (le:58062) (re:58799) (di:complement) ECOUW89 U00006 g396331 Escherichia coli 562 -11533346 6500729488 thif (gtcfc:9.1) (keggfc:14.2) (rileyfc:1.7.8) (db:gtc-escherichia coli) b3992 b3992 Escherichia coli 562 -11533346

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830285	8342	30498	429	143

Description

6500729489 thic:b3994 thic protein:thiamin biosynthesis protein thic (gtcfc:9.1) (keggfc:14.2) (rileyfc:1.7.8) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-thiamine metabolism (vitamin b1)) b3994 b3994 Escherichia coli 562 -11533347 101323 thic (de:thiamin biosynthesis protein thic) (db:swissprot) THIC\_ECOLI P30136 ESCHERICHIA COLI 562 -11533347 7000686786 thic thic protein (db:pir2.dat) E65206 E65206 Escherichia coli 562 -11533347 237204 thic thiamin biosynthesis:pyrimidine moiety (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 363 of 400 of the completegenome.) (nt:f631; 100 pct identical to thic\_ecoli sw: p30136;) (le:4566) (re:6461) (di:complement) AE000473 AE000473 g1790427 Escherichia coli 562 -11533347 7500893048 thic (fn:thiamine biosynthesis) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 115) (le:59445) (re:61340) (di:complement) ECOUW89 U00006 g396333 Escherichia coli 562 -11533347 5000690590 (de:(ecoli\_3884) (pn:thiamin biosynthesis, pyrimidine moiety) (gn:thic) (gtcfc:9.1) (ec:) (thic\_ecoli) (keggfc:11.2) (rileyfc:1.7.8) (db:gtc-escherichia coli)) ECOLI\_3884 ECOLI\_3884 Escherichia coli 562 10043164

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830286	8343	30499	438	145

Description

6500729490 mog:chlg:b0009 molybdopterin biosynthesis mog protein (gtcfc:9.11) (keggfc:14.2) (rileyfc:1.7.4) (db:gtc-escherichia coli) b0009 b0009 Escherichia coli 562 -11533348 7500885765 mog:chlg (de:molybdopterin biosynthesis mog protein) (db:swissprot) MOG\_ECOLI P28694 ESCHERICHIA COLI 562 -11533348 163189 mog molybdopterin biosynthesis protein mog (db:pir2.dat) B56688 B56688 Escherichia coli 562 -11533348 5000690603 (db:genpept-bct1) (de:e.coli dnaK and htga genes.) (nt:orf1) (le:395) (re:982) (di:direct) ECHTGA X67700 g41755 Escherichia coli 562 -11533348 233158 mog required for the efficient incorporation of (fn:transport; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 1 of 400 of the completegenome.) (nt:o195; 100 pct identical to mog\_ecoli sw: p28694) (le:9306) (re:9893) (di:direct) AE000111 AE000111 g1786190 Escherichia coli 562 -11533348 84005 mog:chlg (de:molybdopterin biosynthesis mog protein) (db:swissprot) MOG\_ECOLI P28694 ESCHERICHIA COLI 562 -11533348

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830303	8344	30500	654	217

Description

6500729491 moaa:chlal:chla:nara:bisa:b0781 molybdenum cofactor biosynthesis protein a (gtcfc:9.11) (keggfc:14.2) (rileyfc:1.7.4) (db:gtc-escherichia coli) b0781 b0781 Escherichia coli 562 -11533349 7500885711  
moaa:chlal:chla:nara:bisa (de:molybdenum cofactor biosynthesis protein a) (db:swissprot) MOAA\_ECOLI P30745 ESCHERICHIA COLI 562 -11533349 164075 moaa molybdenum cofactor biosynthesis protein a:moaa protein (cl:haemophilus influenzae molybdenum cofactor biosynthesis protein a) (db:pir2.dat) (mp:18 min) S31879 S31879 Escherichia coli 562 -11533349 223202 moaa molybdenum cofactor biosynthesis protein a (sr:escherichia coli(strain:k12) dna, clone:kohara clone #203) (db:genpept-bct1) (de:escherichia coli genomic dna.(17.5 - 17.9 min).) (le:3018) (re:4007) (di:direct) D90716 D90716 g1651354 Escherichia coli 562 -11533349 5000690604 moaa (db:genpept-bct1) (de:e.coli moa operon (genes moaa to moae).) (le:205) (re:1194) (di:direct) ECMOAACD X70420 g42008 Escherichia coli 562 -11533349 233392 moaa molybdopterin biosynthesis:protein a (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 71 of 400 of the completegenome.) (nt:o329; 100 pct identical to moaa\_ecoli sw: p30745) (le:229) (re:1218) (di:direct) AE000181 AE000181 g1786999 Escherichia coli 562 -11533349 7502851921 bisa molybdenum cofactor biosynthesis protein a. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #203) (db:genpept) (de:escherichia coli genomic dna. (17.6 - 18.0 min).) (nt:orf\_id:o203#2; similar to swissprot accession) (le:3018) (re:4007) (di:direct) D90716 D90716 g1651354 Escherichia coli 562 -11533349 83946 moaa:chlal:chla:nara:bisa (de:molybdenum cofactor biosynthesis protein a) (db:swissprot) MOAA\_ECOLI P30745 ESCHERICHIA COLI 562 -11533349

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830306	8345	30501	498	165
<u>Description</u>				

6500729492 moab:chla2:b0782 molybdenum cofactor biosynthesis protein b (gtcfc:9.11) (keggfc:14.2) (rileyfc:1.7.4) (db:gtc-escherichia coli) b0782 b0782 Escherichia coli 562 -11533350 164076 moab molybdenum cofactor biosynthesis protein b:moab protein (cl:molybdenum cofactor biosynthesis protein b moab) (db:pir2.dat) (mp:18 min) S31880 S34999 Escherichia coli 562 -11533350 223203 moab moab protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #203) (db:genpept-bct1) (de:escherichia coli genomic dna. (17.5 - 17.9 min).) (le:4029) (re:4541) (di:direct) D90716 D90716 g1651355 Escherichia coli 562 -11533350 7500960386 moab (db:genpept-bct1) (de:e.coli moa operon (genes moaa to moae).) (le:1216) (re:1728) (di:direct) ECMOAACD X70420 g42009 Escherichia coli 562 -11533350 233393 moab molybdopterin biosynthesis:protein b (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 71 of 400 of the completegenome.) (nt:o170; 100 pct identical to moab\_ecoli sw: p30746) (le:1240) (re:1752) (di:direct) AE000181 AE000181 g1787000 Escherichia coli 562 -11533350 5000690605 moab moab protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #203) (db:genpept) (de:escherichia coli genomic dna. (17.6 - 18.0 min).) (nt:orf\_id:o203#3; similar to pir accession number) (le:4029) (re:4541) (di:direct) D90716 D90716 g1651355 Escherichia coli 562 -11533350

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830315	8346	30502	462	153
<u>Description</u>				

6500729493 moac:chla3:b0783 molybdenum cofactor biosynthesis protein c (gtcfc:9.11) (keggfc:14.2) (rileyfc:1.7.4) (db:gtc-escherichia coli) b0783 b0783 Escherichia coli 562 -11533351 7000691866 moac molybdenum cofactor biosynthesis protein c:moac protein (cl:molybdenum cofactor biosynthesis protein c) (db:pir2.dat) (mp:18 min) G64814 G64814 Escherichia coli 562 -11533351 223204 moac moac protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #203) (db:genpept-bct1) (de:escherichia coli genomic dna. (17.5 - 17.9 min).) (le:4544) (re:5029) (di:direct) D90716 D90716 g1651356 Escherichia coli 562 -11533351 7500955521 moac molybdopterin biosynthesis:protein c (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 71 of 400 of the completegenome.) (nt:o161; this 161 aa orf is 95 pct identical (1 gap)) (le:1755) (re:2240) (di:direct) AE000181 AE000181 g1787001 Escherichia coli 562 -11533351 5000690606 moac moac protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #203) (db:genpept) (de:escherichia coli genomic dna. (17.6 - 18.0 min).) (nt:orf\_id:o203#4; similar to pir accession number) (le:4544) (re:5029) (di:direct) D90716 D90716 g1651356 Escherichia coli 562 -11533351

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830329	8347	30503	765	254
<u>Description</u>				

6500729494 moad:chla4:chlm:b0784 molybdopterin converting factor:subunit 1:molybdopterin:mpt converting factor:subunit 1:molybdenum cofactor biosynthesis protein d (gtcfc:9.11) (keggfc:14.2) (rileyfc:1.7.4) (db:gtc-escherichia coli) b0784 b0784 Escherichia coli 562 -11533352 83951 moad:chla4:chlm (de:subunit) (db:swissprot) MOAD\_ECOLI P30748 ESCHERICHIA COLI 562 -11533352 7000685860 moad molybdopterin-converting factor 10k chain (cl:molybdopterin-converting factor chain 1) (db:pir2.dat) (mp:17.7 min) H64814 H64814 Escherichia coli 562 -11533352 223205 moad molybdopterin mpt converting factor:subunit (sr:escherichia coli(strain:k12) dna, clone:kohara clone #203) (db:genpept-bct1) (de:escherichia coli genomic dna. (17.5 - 17.9 min).) (le:5022) (re:5267) (di:direct) D90716 D90716 g1651357 Escherichia coli 562 -11533352 7500885727 moad molybdopterin biosynthesis (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 71 of 400 of the completegenome.) (nt:o81; 98 pct identical moad\_ecoli sw: p30748) (le:2233) (re:2478) (di:direct) AE000181 AE000181 g1787002 Escherichia coli 562 -11533352 5000690607 chla4 molybdopterin mpt converting factor:subunit 1 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #203) (db:genpept) (de:escherichia coli genomic dna. (17.6 - 18.0 min).) (nt:orf\_id:o203#5; similar to swissprot accession) (le:5022) (re:5267) (di:direct) D90716 D90716 g1651357 Escherichia coli 562 -11533352

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830330	8348	30504	510	169
<u>Description</u>				

GTC ORF with score 119 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac f17a22 genomic sequence,complete sequence.) (nt:unknown protein) (le:58530:58713:58897) (re:58629:58804:59052) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830332	8349	30505	903	300

Description

6500729495 moae:chla5:b0785 molybdopterin converting factor:subunit 2:molybdopterin:mpt converting factor:subunit 2:molybdenum cofactor biosynthesis protein e (gtcfc:9.11) (keggfc:14.2) (rileyfc:1.7.4) (db:gtc-escherichia coli) b0785 b0785 Escherichia coli 562 -11533353 164098 moae molybdopterin-converting factor 16k chain (cl:molybdopterin-converting factor chain 2) (db:pir2.dat) (mp:18 min) S31883 S35002 Escherichia coli 562 -11533353 7500960387 moae (db:genpept-bct1) (de:e.coli moa operon (genes moaa to moae).) (le:2453) (re:2905) (di:direct) ECMOAACD X70420 g42012 Escherichia coli 562 -11533353 233396 moae molybdopterin converting factor:subunit 2 (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 71 of 400 of the completegenome.) (nt:o150; 100 pct identical to moae\_ecoli sw: p30749) (le:2480) (re:2932) (di:direct) AE000181 AE000181 g1787003 Escherichia coli 562 -11533353 5000690608 moae molybdopterin-converting factor 16k chain (sr:escherichia coli(strain:k12) dna, clone:kohara clone #203) (db:genpept) (de:escherichia coli genomic dna. (17.6 - 18.0 min).) (nt:orf\_id:o203#6; similar to pir accession number) (le:5269) (re:5721) (di:direct) D90716 D90716 g4062341 Escherichia coli 562 -11533353

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830336	8350	30506	300	99

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830345	8351	30507	561	186

Description

6500729496 moeb:chln:b0826 molybdopterin biosynthesis moeb protein  
 (gtcfc:9.11) (keggfc:14.2) (rileyfc:1.7.4) (db:gtc-escherichia coli) b0826  
 b0826 Escherichia coli 562 -11533354 83998 moeb:chln (de:molybdopterin  
 biosynthesis moeb protein) (db:swissprot) MOEB\_ECOLI P12282 ESCHERICHIA COLI  
 562 -11533354 164100 moeb:chln molybdopterin biosynthesis protein  
 moeb:molybdopterin-converting factor chln (cl:molybdopterin biosynthesis  
 protein moeb) (db:pir2.dat) (mp:18 min) B32352 B32352 Escherichia coli 562  
 -11533354 223219 moeb molybdopterin biosynthesis moeb protein  
 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #207)  
 (db:genpept-bct1) (de:escherichia coli genomic dna.(18.3 - 18.7 min).)  
 (le:10941) (re:11690) (di:complement) D90720 D90720 g1651375 Escherichia  
 coli 562 -11533354 223221 moeb molybdopterin biosynthesis moeb protein  
 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #208)  
 (db:genpept-bct1) (de:escherichia coli genomic dna.(18.5 - 18.9 min).)  
 (le:1398) (re:2147) (di:complement) D90721 D90721 g1651378 Escherichia coli  
 562 -11533354 7500885761 (sr:e.coli k12 dna, clone ptn69) (db:genpept-bct1)  
 (de:e.coli chlen operon encoding two proteins (chle and chln) involved in  
 molybdopterin biosynthesis, complete cds.) (nt:chln protein) (le:1596)  
 (re:2345) (di:direct) ECOCHLEN M21151 g145540 Escherichia coli 562 -11533354  
 233990 moeb molybdopterin biosynthesis (fn:enzyme; biosynthesis of  
 cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655  
 section 75 of 400 of the complete genome.) (nt:f249; 100 pct identical to  
 moeb\_ecoli sw: p12282) (le:68) (re:817) (di:complement) AE000185 AE000185  
 g1787048 Escherichia coli 562 -11533354 5000690609 chln molybdopterin  
 biosynthesis moeb protein. (sr:escherichia coli(strain:k12) dna,  
 clone:kohara clone #207) (db:genpept) (de:escherichia coli genomic dna.  
 (18.4 - 18.8 min).) (nt:orf\_id:o208#2; similar to swissprot accession)  
 (le:10941) (re:11690) (di:complement) D90720 D90720 g1651375 Escherichia  
 coli 562 -11533354 7502851922 chln molybdopterin biosynthesis moeb protein.  
 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #208) (db:genpept)  
 (de:escherichia coli genomic dna. (18.6 - 19.0 min).) (nt:orf\_id:o208#2;  
 similar to swissprot accession) (le:1398) (re:2147) (di:complement) D90721  
 D90721 g1651378 Escherichia coli 562 -11533354



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830346	8352	30508	225	74
<u>Description</u>				

6500729497 moea:chle:bisb:nare:b0827 molybdopterin biosynthesis moea protein (gtcfc:9.11) (keggfc:14.2) (rileyfc:1.7.4) (db:gtc-escherichia coli) b0827 b0827 Escherichia coli 562 -11533355 83996 moea:chle:bisb:nare (de:molybdopterin biosynthesis moea protein) (db:swissprot) MOEA\_ECOLI P12281 ESCHERICHIA COLI 562 -11533355 164099 moea:chle:bisb:nare molybdopterin biosynthesis protein moea:molybdopterin-converting factor chle (db:pir2.dat) (mp:18 min) A32352 A32352 Escherichia coli 562 -11533355 223220 moea molybdopterin biosynthesis moea protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #207) (db:genpept-bct1) (de:escherichia coli genomic dna. (18.3 - 18.7 min).) (le:11690) (re:12925) (di:complement) D90720 D90720 g1651376 Escherichia coli 562 -11533355 223222 moea molybdopterin biosynthesis moea protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #208) (db:genpept-bct1) (de:escherichia coli genomic dna. (18.5 - 18.9 min).) (le:2147) (re:3382) (di:complement) D90721 D90721 g1651379 Escherichia coli 562 -11533355 7500885756 (sr:e.coli k12 dna, clone ptn69) (db:genpept-bct1) (de:e.coli chlen operon encoding two proteins (chle and chln) involved in molybdopterin biosynthesis, complete cds.) (nt:chle protein) (le:361) (re:1596) (di:direct) ECOCHLEN M21151 g145539 Escherichia coli 562 -11533355 233989 moea molybdopterin biosynthesis (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 75 of 400 of the complete genome.) (nt:f411; 100 pct identical to moea\_ecoli sw: p12281) (le:817) (re:2052) (di:complement) AE000185 AE000185 g1787049 Escherichia coli 562 -11533355 5000690610 bisb molybdopterin biosynthesis moea protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #207) (db:genpept) (de:escherichia coli genomic dna. (18.4 - 18.8 min).) (nt:orf\_id:o208#3; similar to swissprot accession) (le:11690) (re:12925) (di:complement) D90720 D90720 g1651376 Escherichia coli 562 -11533355 7502851923 bisb molybdopterin biosynthesis moea protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #208) (db:genpept) (de:escherichia coli genomic dna. (18.6 - 19.0 min).) (nt:orf\_id:o208#3; similar to swissprot accession) (le:2147) (re:3382) (di:complement) D90721 D90721 g1651379 Escherichia coli 562 -11533355

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830347	8353	30509	189	62

Description

6500729498 moba:b3857 molybdopterin-guanine dinucleotide biosynthesis protein a (gtcfc:9.11) (keggfc:14.2) (rileyfc:1.7.4) (db:gtc-escherichia coli) b3857 b3857 Escherichia coli 562 -11533356 83958 moba:mob:chlb:narb (de:fa)) (db:swissprot) MOBA\_ECOLI P32173 ESCHERICHIA COLI 562 -11533356 164078 moba molybdopterin-guanine dinucleotide biosynthesis protein a:mob protein (db:pir2.dat) S40803 S40803 Escherichia coli 562 -11533356 7500885741 mob (fn:biosynthesis of molybdopterin) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 921) (le:3055) (re:3639) (di:complement) ECOUW87 L19201 g304963 Escherichia coli 562 -11533356 237077 moba molybdopterin ---molybdopterin-guanine (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 351 of 400 of the completegenome.) (nt:f194; 100 pct identical to moba\_ecoli sw: p32173;) (le:4014) (re:4598) (di:complement) AE000461 AE000461 g1790288 Escherichia coli 562 -11533356 5000690611 (de:(ecoli\_3757) (pn:molybdopterin ---) (gn:moba) (gtcfc:9.11) (ec:) (moba\_ecoli) (keggfc:11.2) (rileyfc:1.7.4) (db:gtc-escherichia coli)) ECOLI\_3757 ECOLI\_3757 Escherichia coli 562 10026165

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830366	8354	30510	396	131

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830379	8355	30511	429	142

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830386	8356	30512	609	202
<u>Description</u>				
6500729499 entc:b0593 isochorismate synthase entc (gtcfc:9.12:9.13) (ec:5.4.99.6) (keggfc:9.13) (rileyfc:1.7.14) (db:gtc-escherichia coli) b0593 b0593 Escherichia coli 562 -11533357 70232 entc (ec:5.4.99.6) (de:isochorismate synthase entc,) (db:swissprot) ENTC_ECOLI P10377 ESCHERICHIA COLI 562 -11533357 125846 entc:fepf isochorismate synthase::isochorismate synthetase (cl:isochorismate synthase) (ec:5.4.99.6) (db:pir1.dat) (mp:14 min) SYECIK JT0497 Escherichia coli 562 -11533357 409199 entc isochorismate hydroxymutase 2:enterochelin (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:5.4.99.6) (de:escherichia coli k-12 mg1655 section 55 of 400 of the completegenome.) (nt:o391; 100 pct identical to entc_ecoli sw: p10377) (le:218) (re:1393) (di:direct) AE000165 AE000165 g1786809 Escherichia coli 562 -11533357 7500881063 entc isochorismate synthase (db:genpept-una) (ec:5.4.99.6) (de:e. coli isochorismate synthase (entc) gene, complete cds.) (le:380) (re:1555) (di:direct) ECOENTC M24142 g450376 Escherichia coli 562 -11533357 5000690615 (de:(ecoli_574) (pn:isochorismate synthase, enterochelin biosynthesis) (gn:entc) (gtcfc:9.12) (ec:5.4.99.6) (entc_ecoli) (keggfc:9.13) (rileyfc:1.7.14) (db:gtc-escherichia coli)) ECOLI_574 ECOLI_574 Escherichia coli 562 10012810				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830398	8357	30513	216	71

Description

6500729500 entb:entg:b0595 isochorismatase:2:3 dihydro-2:3 dihydroxybenzoate synthase (gtcfc:9.12:9.13) (ec:3.3.2.1) (keggfc:9.13) (rileyfc:1.7.14) (db:gtc-escherichia coli) b0595 b0595 Escherichia coli 562 -11533358 70231 entb:entg (ec:3.3.2.1) (de:synthase)) (db:swissprot) ENTB\_ECOLI P15048 ESCHERICHIA COLI 562 -11533358 124717 entb isochorismatase::2:3 dihydro-2:3 dihydroxybenzoate synthase (cl:isochorismatase) (ec:3.3.2.1) (db:pir1.dat) (mp:14 min) YXECIC C91904 Escherichia coli 562 -11533358 234242 entb 2:3-dihydro-2:3-dihydroxybenzoate synthase (sr:escherichia coli (individual\_isolate mc4100, strain k-12) (clone) (db:genpept-bct1) (ec:3.3.2.1) (de:escherichia coli enterobactin biosynthesis-associated protein (entaand entb), and 15-kda protein (p15) genes, complete cds.) (le:76) (re:933) (di:d... ECOENTAB M24143 g522182 Escherichia coli 562 -11533358 240108 entb isochorismatase (sr:escherichia coli dna) (db:genpept-bct1) (ec:3.3.2.1) (de:e. coli enterobactin biosynthesis genes ente, partial cds, entb,enta, and p15, complete cds.) (le:449) (re:1306) (di:direct) ECOENTEB A M24148 g450381 Escherichia coli 562 -11533358 7500881062 entb isochorismatase (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (le:68325) (re:69182) (di:direct) ECU82598 U82598 g1778512 Escherichia coli 562 -11533358 234236 entb 2:3-dihydro-2:3-dihydroxybenzoate synthetase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:3.3.2.1) (de:escherichia coli k-12 mg1655 section 55 of 400 of the completegenome.) (nt:o285; 100 pct identical to entb\_ecoli sw: p15048) (le:3027) (re:3884) (di:direct) AE000165 AE000165 g1786811 Escherichia coli 562 -11533358 5000690616 (de:(ecoli\_576) (pn:2,3-dihydro-2,3-dihydroxybenzoate synthetase, enterochelin biosynthesis) (gn:entb) (gtcfc:9.12) (ec:3.3.2.1) (entb\_ecoli) (keggfc:9.13) (rileyfc:1.7.14) (db:gtc-escherichia coli)) ECOLI\_576 ECOLI\_576 Escherichia coli 562 10012809

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830402	8358	30514	303	100

Description

GTC ORF with score 99 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1341.) (nt:similar to saccharomyces cerevisiae orf ycr028) (le:<1) (re:916) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830405	8359	30515	423	140

Description

6500729501 enta:b0596 2:3-dihydro-2:3-dihydroxybenzoate dehydrogenase  
 (gtcfc:9.12:9.13) (ec:1.3.1.28) (keggfc:9.13) (rileyfc:1.7.14)  
 (db:gtc-escherichia coli) b0596 b0596 Escherichia coli 562 -11533359 70230  
 enta (ec:1.3.1.28) (de:2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase,)  
 (db:swissprot) ENTA\_ECOLI P15047 ESCHERICHIA COLI 562 -11533359 122504 enta  
 2:3-dihydro-2:3-dihydroxybenzoate dehydrogenase (cl:ribitol  
 dehydrogenase:short-chain alcohol dehydrogenase homology) (ec:1.3.1.28)  
 (db:pir1.dat) (mp:13 min) DEECDB A91904 Escherichia coli 562 -11533359  
 234243 enta 2:3-dihydro-2:3-dihydroxybenzoate dehydrogenase (sr:escherichia  
 coli (individual\_isolate mc4100, strain k-12) (clone) (db:genpept-bct1)  
 (ec:1.3.1.28) (de:escherichia coli enterobactin biosynthesis-associated  
 protein (entaand entb), and 15-kda protein (p15) genes, complete cds.)  
 (le:933) (re:1679) (d... ECOENTAB M24143 g522183 Escherichia coli 562  
 -11533359 7500881061 enta 2:3-dihydro-2:3-dihydroxybenzoate dehydrogenase  
 (sr:escherichia coli dna) (db:genpept-bct1) (ec:1.3.1.28) (de:e. coli  
 enterobactin biosynthesis genes ente, partial cds, entb,enta, and p15,  
 complete cds.) (le:1306) (re:2052) (di:direct) ECOENTEBA M24148 g450382  
 Escherichia coli 562 -11533359 234237 enta  
 2:3-dihydro-2:3-dihydroxybenzoate dehydrogenase (fn:enzyme; biosynthesis of  
 cofactors, carriers:) (db:genpept-bct2) (ec:1.3.1.28) (de:escherichia coli  
 k-12 mg1655 section 55 of 400 of the completegenome.) (nt:o248; 100 pct  
 identical to enta\_ecoli sw: p15047) (le:3884) (re:4630) (di:direct) AE000165  
 AE000165 g1786812 Escherichia coli 562 -11533359 5000690617 (de:(ecoli\_577)  
 (pn:2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase, enterochelin  
 biosynthesis) (gn:enta) (gtcfc:9.12) (ec:1.3.1.28) (enta\_ecoli)  
 (keggfc:9.13) (rileyfc:1.7.14) (db:gtc-escherichia coli)) ECOLI\_577  
 ECOLI\_577 Escherichia coli 562 10012808

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830406	8360	30516	477	158

Description

6500729502 lipb:b0630 lipoate-protein ligase b:lipoate biosynthesis protein b (gtcfc:9.12:9.6:9.7) (ec:6.-.-.-) (keggfc:9.7:9.13) (rileyfc:1.7.3) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-quinone biosynthesis:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolis... b0630 b0630 Escherichia coli 562 -11533360 82179 lipb (ec:6.-.-.-) (de:b)) (db:swissprot) LIPB\_ECOLI P30976 ESCHERICHIA COLI 562 -11533360 7000685753 lipb lipoate--protein ligase:b:lipoate biosynthesis protein b:lipoic acid metabolism protein lipb (ec:6.3.4.-) (db:pir2.dat) D64797 D64797 Escherichia coli 562 -11533360 223118 lipb lipoate biosynthesis protein b (sr:escherichia coli(strain:k12) dna, clone:kohara clone #168) (db:genpept-bct1) (de:escherichia coli genomic dna. (13.9 - 14.3 min).) (le:12700) (re:13275) (di:complement) D90703 D90703 g1651258 Escherichia coli 562 -11533360 7500885042 lipb lipoate biosynthesis protein b (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (le:102267) (re:102842) (di:complement) ECU82598 U82598 g1778547 Escherichia coli 562 -11533360 240143 lipb protein of lipoate biosynthesis (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 57 of 400 of the completegenome.) (nt:f191; 99 pct identical to lipb\_ecoli sw: p30976) (le:9578) (re:10153) (di:complement) AE000167 AE000167 g1786848 Escherichia coli 562 -11533360 5000690618 lipb lipoic acid metabolism protein lipb. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #168) (db:genpept) (de:escherichia coli genomic dna. (14.0 - 14.4 min).) (nt:orf\_id:o168#15; similar to pir accession number) (le:12700) (re:13275) (di:complement) D90703 D90703 g1651258 Escherichia coli 562 -11533360

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830407	8361	30517	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830420	8362	30518	783	260

Description

6500729503 ubig:b2232 3-demethylubiquinone-9  
3-methyltransferase:3:4-dihydroxy-5-hexaprenylbenzoate  
methyltransferase:dhbb methyltransferase (gtcfc:9.12) (ec:2.1.1.64)  
(keggfc:9.13) (rileyfc:1.7.11) (db:gtc-escherichia coli) b2232 b2232  
Escherichia coli 562 -11533361 236245 ubig:pufx (ec:2.1.1.64)  
(de:methyltransferase)) (db:swissprot) UBIG\_ECOLI P17993 ESCHERICHIA COLI  
562 -11533361 162599 ubig 3-demethylubiquinone-9  
3-o-methyltransferase::2-octaprenyl-3-methyl-5-hydroxy-6-methoxy-1:4-benzoqu  
inone methyltransferase:ubig (cl:3-demethylubiquinone-9  
3-o-methyltransferase:bioc homology) (ec:2.1.1.64) (db:pir2.dat) A47682  
A47682 Escherichia coli 562 -11533361 224736  
2-octaprenyl-3-methyl-5-hydroxy-6-methoxy-1 (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #376(50.2-50.6 min.)) (nt:similar to  
(pir accession number a47682)) (le:12808) (re:13530) (di:direct) D90854  
D90854 g1799576 Escherichia coli 562 -11533361 5000690619 pufx pufx protein  
(db:genpept-bct1) (de:escherichia coli gyra, pufx & pufy' genes.) (le:345)  
(re:1067) (di:complement) ECGYRAAM Y00544 g41638 Escherichia coli 562  
-11533361 7500893669 ubig ubiquinone synthesis-related protein  
(sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia  
coli  
s-adenosyl-1-methionine:2-octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoq  
uinone (ubig)gene, complete cds.) (le:155) (re:877) (di:direct) ECOUBIG  
M87509 g148104 Escherichia coli 562 -11533361 233050 ubig  
3-demethylubiquinone-9 3-methyltransferase and (fn:enzyme; biosynthesis of  
cofactors, carriers:) (db:genpept-bct2) (ec:2.1.1.64) (de:escherichia coli  
k-12 mg1655 section 203 of 400 of the completegenome.) (nt:o240; 100 pct  
identical to ubig\_ecoli sw: p17993) (le:104) (re:826) (di:direct) AE000313  
AE000313 g1788564 Escherichia coli 562 -11533361 103077 ubig:pufx  
(ec:2.1.1.64) (de:methyltransferase)) (db:swissprot) UBIG\_ECOLI P17993  
ESCHERICHIA COLI 562 -11533361

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830426	8363	30519	1470	490

# Description

6500729504 mene:b2260 o-succinylbenzoic acid--coa ligase:osb-coa synthetase:o-succinylbenzoate-coa synthase (gtcfc:9.12) (ec:6.2.1.26) (keggfc:9.13) (rileyfc:1.7.11) (db:gtc-escherichia coli) b2260 b2260 Escherichia coli 562 -11533362 83447 mene (ec:6.2.1.26) (de:(o-succinylbenzoate-coa synthase)) (db:swissprot) MENE\_ECOLI P37353 ESCHERICHIA COLI 562 -11533362 7000685822 mene o-succinylbenzoate--coa ligase (cl:o-succinylbenzoate--coa ligase) (ec:6.2.1.26) (db:pir2.dat) B64997 B64997 Escherichia coli 562 -11533362 224771 mene o-succinylbenzoic acid--coa ligase ec 6.2.1.26 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #380(51.1-51.4 min.)) (nt:similar to (swissprot accession number p37353)) (le:6275) (re:7630) (di:complement) D90857 D90857 g1799614 Escherichia coli 562 -11533362 7500885493 mene o-succinylbenzoate-coa ligase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:6.2.1.26) (de:escherichia coli k-12 mg1655 section 206 of 400 of the completegenome.) (nt:f451; 99 pct identical to mene\_ecoli sw: p37353) (le:70) (re:1425) (di:complement) AE000316 AE000316 g1788595 Escherichia coli 562 -11533362 5000690620 (de:(ecoli\_2209) (pn:o-succinylbenzoate-coa ligase) (gn:mene) (gtcfc:9.12) (ec:6.2.1.26) (mene\_ecoli) (keggfc:9.13) (rileyfc:1.7.11) (db:gtc-escherichia coli)) ECOLI\_2209 ECOLI\_2209 Escherichia coli 562 10120064



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830432	8364	30520	414	137

Description

6500729505 menb:b2262 naphthoate synthase:dihydroxynaphthoic acid synthetase:dhna synthetase (gtcfc:9.12) (ec:4.1.3.36) (keggfc:9.13) (rileyfc:1.7.11) (db:gtc-escherichia coli) b2262 b2262 Escherichia coli 562 -11533363 83439 menb (ec:4.1.3.36) (de:(dhna synthetase)) (db:swissprot) MENB\_ECOLI P27290 ESCHERICHIA COLI 562 -11533363 205564 menb naphthoate synthase::dhna synthase:menaquinone biosynthesis enzyme menb:mitochondrial enoyl-coa hydratase homolog (cl:naphthoate synthase:enoyl-coa hydratase homology) (ec:4.1.3.36) (db:pir2.dat) D64997 A42714 Escherichia coli 562 -11533363 224773 naphthoate synthase:dhna synthase (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #380(51.1-51.4 min.)) (nt:similar to (pir accession number a42714)) (le:8589) (re:9446) (di:complement) D90857 D90857 g1799616 Escherichia coli 562 -11533363 7500885485 menb dhna synthase (sr:escherichia coli (individual\_isolate pl2024, strain k-12) dna) (db:genpept-bct1) (de:e.coli dhna synthase (menb) gene, complete cds.) (le:357) (re:1214) (di:direct) ECODHNASYN M93421 g145740 Escherichia coli 562 -11533363 234145 menb dihydroxynaphtoic acid synthetase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:4.1.3.36) (de:escherichia coli k-12 mg1655 section 206 of 400 of the completegenome.) (nt:f285; 100 pct identical to menb\_ecoli sw: p27290) (le:2384) (re:3241) (di:complement) AE000316 AE000316 g1788597 Escherichia coli 562 -11533363 5000690621 (de:(ecoli\_2211) (pn:dihydroxynaphtoic acid synthetase) (gn:menb) (gtcfc:9.12) (ec:4.1.3.36) (menb\_ecoli) (keggfc:9.13) (rileyfc:1.7.11) (db:gtc-escherichia coli)) ECOLI\_2211 ECOLI\_2211 Escherichia coli 562 10025653

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830433	8365	30521	489	162

Description

6500729506 mend:b2264 2-succinyl-6-hydroxy-2:4-cyclohexadiene-1-carboxylate synthase:shchc synthase / 2-oxoglutarate decarboxylase:alpha-ketoglutarate decarboxylase:kdc (gtcfc:9.12) (ec:4.1.1.71) (keggfc:9.13) (rileyfc:1.7.11) (db:gtc-escherichia coli) b2264 b2264 Escherichia coli 562 -11533364 83444 mend (ec:4.1.1.71) (de:ketoglutarate decarboxylase) (kdc)) (db:swissprot) MEND\_ECOLI P17109 ESCHERICHIA COLI 562 -11533364 7000685821 mend mend protein:2-succinyl-6-hydroxy-2:4-cyclohexadiene-1-carboxylic acid synthase / alpha-ketoglutarate decarboxylase -escherichia ...:shchc synthase (cl:mend protein) (db:pir2.dat) F64997 F64997 Escherichia coli 562 -11533364 7500885491 mend 2-oxoglutarate decarboxylase:shchc synthase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 206 of 400 of the completegenome.) (nt:f556; 96 pct identical (1 gap) to 542 residues) (le:4011) (re:5681) (di:complement) AE000316 AE000316 g1788599 Escherichia coli 562 -11533364 5000690622 (de:(ecoli\_2213) (pn:2-oxoglutarate decarboxylase; shchc synthase) (gn:mend) (gtcfc:9.12) (ec:4.1.1.71) (mend\_ecoli) (keggfc:9.13) (rileyfc:1.7.11) (db:gtc-escherichia coli)) ECOLI\_2213 ECOLI\_2213 Escherichia coli 562 10123620

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830443	8366	30522	360	119

Description

6500729507 menf:b2265 isochorismate synthase (gtcfc:9.12:14.3) (ec:5.4.99.6) (keggfc:9.13) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2265 b2265 Escherichia coli 562 -11533365 7000691853 menf isochorismate synthase (ec:5.4.99.6) (db:pir2.dat) G64997 G64997 Escherichia coli 562 -11533365 7500960371 menf isochorismate hydroxymutase 2:menaquinone (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 206 of 400 of the completegenome.) (nt:f356; 99 pct identical to 328 residues of) (le:5770) (re:6840) (di:complement) AE000316 AE000316 g1788600 Escherichia coli 562 -11533365 5000690623 (de:(ecoli\_2214) (pn:isochorismate synthase, menaquinone biosynthesis) (gn:menf) (gtcfc:9.12) (ec:5.4.99.6) (menf\_ecoli) (keggfc:9.13) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2214 ECOLI\_2214 Escherichia coli 562 10123621

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830450	8367	30523	882	293
<u>Description</u>				

6500729508 srmb:rbab:b2576 atp-dependent rna helicase srmb (gtcfc:9.12:10.2) (ec:2.7.7.-) (keggfc:9.13) (rileyfc:3.1.9) (db:gtc-escherichia coli) b2576 b2576 Escherichia coli 562 -11533366 7500892079 srmb:rbab (de:atp-dependent rna helicase srmb) (db:swissprot) SRMB\_ECOLI P21507 ESCHERICHIA COLI 562 -11533366 7000686679 srmb atp-dependent rna helicase srmb (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) G65035 G65035 Escherichia coli 562 -11533366 235691 rbab putative atp dependent rna helicase (sr:escherichia coli (strain k12) (library: kohara) dna, clone 7g4) (db:genpept-bct1) (de:escherichia coli ribonuclease iii and other genes, complete cds.) (le:20357) (re:21691) (di:direct) ECOK12RIII D64044 g987650 Escherichia coli 562 -11533366 238297 rbab putative atp dependent rna helicase (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli genes for l-aspartate oxidase, putative atp dependent rnahelicase, and uracil dna glycosylase.) (le:4117) (re:5451) (di:direct) ECORBAB D13169 g285777 Escherichia coli 562 -11533366 5000690532 srmb srmb protein (db:genpept-bct1) (de:e. coli srmb gene for an eif-4a like protein.) (le:460) (re:1794) (di:direct) ECSRMB X14152 g42996 Escherichia coli 562 -11533366 234900 srmb atp-dependent rna helicase (fn:enzyme; rna synthesis, modification, dna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 234 of 400 of the completengenome.) (nt:o444; 100 pct identical to srmb\_ecoli sw: p21507) (le:2710) (re:4044) (di:direct) AE000344 AE000344 g1788930 Escherichia coli 562 -11533366 99473 srmb:rbab (de:atp-dependent rna helicase srmb) (db:swissprot) SRMB\_ECOLI P21507 ESCHERICHIA COLI 562 -11533366

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830451	8368	30524	435	144

Description

6500729509 dnag:dnap:parb:b3066 dna primase (gtcfc:9.12:10.8) (ec:2.7.7.-) (keggfc:9.13) (rileyfc:3.1.7) (db:gtc-escherichia coli) b3066 b3066  
Escherichia coli 562 -11533367 91034 dnag:dnap:parb (ec:2.7.7.-) (de:dna primase,) (db:swissprot) PRIM\_ECOLI P02923 ESCHERICHIA COLI 562 -11533367 130803 dnag dna primase (cl:dna primase) (ec:2.7.7.-) (db:pir1.dat) (mp:67 min) RYEC2 A03423 Escherichia coli 562 -11533367 235912 dnag dna primase (db:genpept-bct1) (de:e. coli dnag gene.) (le:182) (re:1927) (di:direct) ECDNAG V00274 g1617301 Escherichia coli 562 -11533367 239271 dnag (sr:escherichia coli k12 and hb101 dna) (db:genpept-bct1) (de:e.coli rpsu-dnag-rpod operon with genes coding for ribosomalprotein s21, dna primase and rna polymerase sigma-subunit.) (nt:dna primase) (le:1041) (re:2786) (di:direct) ECORPSRPO J01687 g147755 Escherichia coli 562 -11533367 7500888461 dnag (fn:dna biosynthesis; primase) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 68 minutes.) (nt:cg site no. 847; alternate gen name dnap, parb) (le:15902) (re:17647) (di:direct) ECU28379 U28379 g882589 Escherichia coli 562 -11533367 232697 dnag dna biosynthesis:dna primase (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:2.7.7.-) (de:escherichia coli k-12 mg1655 section 278 of 400 of the completegenome.) (nt:o581; 100 pct identical to prim\_ecoli sw: p02923;) (le:4778) (re:6523) (di:direct) AE000388 AE000388 g1789447 Escherichia coli 562 -11533367 5000690533 (de:(ecoli\_2989) (pn:dna biosynthesis; dna primase) (gn:dnag) (gtcfc:7.1:9.12) (ec:2.7.7.-) (prim\_ecoli) (keggfc:4.4:9.13) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_2989 ECOLI\_2989 Escherichia coli 562 10033143

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830456	8369	30525	945	314

Description

6500729510 lpla:b4386 lipoate-protein ligase a (gtcfc:9.12:9.6:14.3)  
(ec:6.-.-.-) (keggfc:9.7:9.13) (rileyfc:5.8.0) (db:gtc-escherichia coli)  
(gtcfc:metabolism of cofactors and vitamins-quinone biosynthesis:metabolism  
of cofactors and vitamins-biotin metabolism (b8) and folate  
biosynthesis:unknown-... b4386 b4386 Escherichia coli 562 -11533368 163998  
lpla:yjff lipoate--protein ligase:a (cl:lipoate-protein ligase) (ec:6.3.4.-)  
(db:pir2.dat) (mp:100 min) A54035 A54035 Escherichia coli 562 -11533368  
237591 lipoate-protein ligase a (sr:escherichia coli (individual\_isolate  
tm134, sub\_strain w3110) (db:genpept-bct1) (de:escherichia coli  
lipoate-protein ligase a (lpla) gene, completecds; smp gene, 3' end.)  
(le:83) (re:1099) (di:direct) ECOLPLA L27665 g504496 Escherichia coli 562  
-11533368 7500954500 yjff (db:genpept-bct1) (de:escherichia coli k-12  
chromosomal region from 92.8 to 00.1 minutes.) (le:313933) (re:314949)  
(di:complement) ECOUW93 U14003 g537226 Escherichia coli 562 -11533368  
235004 lpla lipoate-protein ligase a (fn:enzyme; macromolecule synthesis,  
modification:) (db:genpept-bct2) (ec:6.-.-.-) (de:escherichia coli k-12  
mg1655 section 398 of 400 of the completegenome.) (nt:f338; 100 pct  
identical amino acid sequence and) (le:13749) (re:14765) (di:complement)  
AE000508 AE000508 g1790846 Escherichia coli 562 -11533368 5000690626  
(de:(ecoli\_4268) (pn:lipoate-protein ligase a) (gn:lpla) (gtcfc:9.12)  
(ec:6.-.-.-) (lpla\_ecoli) (keggfc:9.13) (rileyfc:5.7.0) (db:gtc-escherichia  
coli)) ECOLI\_4268 ECOLI\_4268 Escherichia coli 562 10087125

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830461	8370	30526	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830463	8371	30527	210	69

Description

6500729511 menc:b2261 o-succinylbenzoate-coa synthase:osb  
synthase:4-:2-carboxyphenyl-4-oxybutyric acid synthase (gtcfc:9.12)  
(keggfc:14.2) (rileyfc:1.7.11) (db:gtc-escherichia coli) b2261 b2261  
Escherichia coli 562 -11533369 83441 menc (de:4-oxybutyric acid synthase))  
(db:swissprot) MENC\_ECOLI P29208 ESCHERICHIA COLI 562 -11533369 7000685820  
menc o-succinylbenzoate synthase (db:pir2.dat) C64997 C64997 Escherichia  
coli 562 -11533369 7500885487 menc o-succinylbenzoyl-coa  
synthase:conversion of (fn:enzyme; biosynthesis of cofactors, carriers:)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 206 of 400 of the  
completegenome.) (nt:f320; this 320 aa orf is 99 pct identical (2 gaps))  
(le:1422) (re:2384) (di:complement) AE000316 AE000316 g1788596 Escherichia  
coli 562 -11533369 5000690612 (de:(ecoli\_2210) (pn:o-succinylbenzoyl-coa  
synthase; conversion of chorismate to 2-o-succinylbenzoyl-coa) (gn:menc)  
(gtcfc:9.12) (ec:) (menc\_ecoli) (keggfc:11.2) (rileyfc:1.7.11)  
(db:gtc-escherichia coli)) ECOLI\_2210 ECOLI\_2210 Escherichia coli 562  
10123618

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830476	8372	30528	471	156

Description

6500729512 ubib:fre:flrd:fadi:fsrc:b3844 flavin reductase:nadph-flavin  
reductase:ferrisiderophore reductase c (gtcfc:9.12) (ec:1.6.8.-)  
(keggfc:14.1) (rileyfc:1.7.11) (db:gtc-escherichia coli) b3844 b3844  
Escherichia coli 562 -11533370 164123 ubib:fre nad p h dehydrogenase  
fmn::flavin reductase:fmn reductase (cl:cytochrome-b5 reductase homology)  
(ec:1.6.8.1) (db:pir2.dat) A39434 A39434 Escherichia coli 562 -11533370  
234394 fadi activator protein (sr:escherichia coli (strain k-12) dna)  
(db:genpept-bct1) (de:e.coli activator protein (fadi) gene, complete cds.)  
(nt:activator of fadb and fade genes) (le:253) (re:954) (di:direct) ECOFADI  
M85227 g145908 Escherichia coli 562 -11533370 234395 fre nad p h:fmn  
oxidoreductase (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1)  
(de:escherichia coli nad(p)h:fmn oxidoreductase (fre) gene, completecds.)  
(le:1452) (re:2153) (di:direct) ECOFRE M74448 g1209296 Escherichia coli 562  
-11533370 7500960391 fre flavin oxidoreductase (sr:escherichia coli (strain  
k-12) dna) (db:genpept-bct1) (de:e.coli flavin reductase (fre) gene,  
complete cds.) (le:121) (re:822) (di:direct) ECOFREX M61182 g146002  
Escherichia coli 562 -11533370 234303 ubib ferrisiderophore  
reductase:flavin reductase (fn:enzyme; energy metabolism, carbon: electron)  
(db:genpept-bct2) (ec:1.6.8.-) (de:escherichia coli k-12 mg1655 section 349  
of 400 of the completegenome.) (nt:o233; 99 pct identical amino acid  
sequence and) (le:10267) (re:10968) (di:direct) AE000459 AE000459 g2367314  
Escherichia coli 562 -11533370

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830481	8373	30529	1254	417

Description

6500729513 mena:b3930 menaquinone biosynthesis protein  
mena:1:4-dihydroxy-2-naphthoate octaprenyltransferase (gtcfc:9.12)  
(ec:2.5.-.-) (keggfc:14.1) (rileyfc:1.7.11) (db:gtc-escherichia coli) b3930  
b3930 Escherichia coli 562 -11533371 83436 mena (ec:2.5.1.-)  
(de:octaprenyltransferase)) (db:swissprot) MENA\_ECOLI P32166 ESCHERICHIA  
COLI 562 -11533371 163630 mena menaquinone biosynthesis protein  
mena:hypothetical protein f308 (cl:hypothetical protein hi0509)  
(db:pir2.dat) S40873 S40873 Escherichia coli 562 -11533371 239727  
(sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda)  
(db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.)  
(le:81056) (re:81982) (di:complement) ECOUW87 L19201 g305033 Escherichia  
coli 562 -11533371 7500885475 mena 1:4-dihydroxy-2-naphthoate  
(fn:conversion of 1,4-dihydroxy-2-naphthoate to) (sr:escherichia coli  
strain=k12) (db:genpept-bct1) (de:escherichia coli  
1,4-dihydroxy-2-naphthoate octaprenyltransferase(mena) and  
s-adenosylmethionine:2-demethylmenaquinonemethyltransferase (meng) genes...  
ECU56082 U56082 g1336001 Escherichia coli 562 -11533371 237147 mena  
1:4-dihydroxy-2-naphthoate -- (fn:enzyme; biosynthesis of cofactors,  
carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 357 of  
400 of the completegenome.) (nt:f308; 100 pct identical amino acid sequence  
and) (le:6549) (re:7475) (di:complement) AE000467 AE000467 g1790365  
Escherichia coli 562 -11533371 5000690614 (de:(ecoli\_3828)  
(pn:1,4-dihydroxy-2-naphthoate --) (gn:mena) (gtcfc:9.12) (ec:2.5.-.-)  
(mena\_ecoli) (keggfc:11.1) (rileyfc:1.7.11) (db:gtc-escherichia coli))  
ECOLI\_3828 ECOLI\_3828 Escherichia coli 562 10025650

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830491	8374	30530	309	102

Description

6500729514 yjbp:apha:napa:b4055 hypothetical 26.1 kd protein in tyrb-uvra intergenic region:class b acid phosphatase precursor (gtcfc:9.13:9.2:14.1) (ec:3.1.3.2) (keggfc:9.2:9.12) (rileyfc:5.7.0) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-other cofactors:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2):unknown-hypothetical) b4055 b4055 Escherichia coli 562 -11533372 113630 apha:napa (ec:3.1.3.2) (de:class b acid phosphatase precursor,) (db:swissprot) APHA\_ECOLI P32697 ESCHERICHIA COLI 562 -11533372 162662 yjbp acid phosphatase:hypothetical 26.1k protein tyrb-uvra intergenic region (db:pir2.dat) S54790 S54790 Escherichia coli 562 -11533372 239706 apha acid phosphatase (db:genpept-bct1) (de:e.coli apha gene.) (le:1) (re:714) (di:direct) ECNAPA X86971 g806548 Escherichia coli 562 -11533372 306534 acid phosphatase (sr:escherichia coli strain=w3110) (db:genpept-bct1) (de:escherichia coli acid phosphatase gene, complete cds.) (le:1) (re:714) (di:direct) ECU51210 U51210 g1256442 Escherichia coli 562 -11533372 233450 apha diadenosine tetraphosphatase (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 369 of 400 of the completegenome.) (nt:o237; sequence change joins two orfs relative to) (le:393) (re:1106) (di:direct) AE000479 AE000479 g2367341 Escherichia coli 562 -11533372

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830497	8375	30531	510	169

Description

6500729515 entd:b0583 enterobactin synthetase component d:enterochelin synthase d (gtcfc:9.13) (keggfc:14.2) (rileyfc:1.7.14) (db:gtc-escherichia coli) b0583 b0583 Escherichia coli 562 -11533373 70233 entd (de:enterobactin synthetase component d (enterochelin synthase d)) (db:swissprot) ENT\_D\_ECOLI P19925 ESCHERICHIA COLI 562 -11533373 7000685163 entd enterobactin synthetase component d (db:pir2.dat) (mp:14 min) E64791 E64791 Escherichia coli 562 -11533373 7500881064 entd enterochelin synthetase:component d (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 53 of 400 of the completegenome.) (nt:f209; 100 pct identical to entd\_ecoli sw: p19925) (le:6114) (re:6743) (di:complement) AE000163 AE000163 g1786797 Escherichia coli 562 -11533373 5000690627 (de:(ecoli\_564) (pn:enterochelin synthetase, component d) (gn:entd) (gtcfc:9.13) (ec:) (entd\_ecoli) (keggfc:11.2) (rileyfc:1.7.14) (db:gtc-escherichia coli)) ECOLI\_564 ECOLI\_564 Escherichia coli 562 10012811



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830500	8376	30532	612	203
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830501	8377	30533	861	286
<u>Description</u>				

6500729516 entf:b0586 enterobactin synthetase component f:enterochelin synthase f:serine activating enzyme (gtcfc:9.13) (keggfc:14.2) (rileyfc:1.7.14) (db:gtc-escherichia coli) b0586 b0586 Escherichia coli 562 -11533374 70235 entf (de:(serine activating enzyme)) (db:swissprot) ENTF\_ECOLI P11454 ESCHERICHIA COLI 562 -11533374 7000685165 entf enterobactin synthetase component f:enterochelin synthetase component f (cl:enterobactin synthetase component f:acetate--coa ligase homology:acyl carrier protein homology:gramicidin s synthetase i repeat homology) (db:pir1.dat) (mp:14 min) YGECEF H64791 Escherichia coli 562 -11533374 7500881066 entf atp-dependent serine activating enzyme may be (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 54 of 400 of the completegenome.) (nt:o1293; 100 pct identical to entf\_ecoli sw: p11454) (le:139) (re:4020) (di:direct) AE000164 AE000164 g1786801 Escherichia coli 562 -11533374 5000690628 (de:(ecoli\_567) (pn:atp-dependent serine activating enzyme) (gn:entf) (gtcfc:9.13) (ec:) (entf\_ecoli) (keggfc:11.2) (rileyfc:1.7.14) (db:gtc-escherichia coli)) ECOLI\_567 ECOLI\_567 Escherichia coli 562 10122913

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830503	8378	30534	717	238

Description

6500729517 yaac:ribf:b0025 hypothetical 34.6 kd protein in rpst-iles  
intergenic region:riboflavin kinase:flavokinase / fmn  
adenyltransferase:fad pyrophosphorylase:fad synthetase (gtcfc:9.2:14.1)  
(keggfc:9.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) (gtcfc:metabolism of  
cofactors and vitamins-riboflavin metabolism (vitamin  
b2):unknown-hypothetical) b0025 b0025 Escherichia coli 562 -11533375 109490  
ribf (ec:2.7.1.26:2.7.7.2) (de:synthetase)) (db:swissprot) RIBF\_ECOLI P08391  
ESCHERICHIA COLI 562 -11533375 7000686328 yaac conserved hypothetical  
protein:34.6k rpst-iles intergenic region (cl:conserved hypothetical protein  
hi0963) (db:pir1.dat) (mp:0.5 min) QQECIL A64723 Escherichia coli 562  
-11533375 7500889772 ribf putative regulator (fn:putative regulator; not  
classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 3 of  
400 of the completegenome.) (nt:o312; formerly designated yaac) (le:748)  
(re:1689) (di:direct) AE000113 AE000113 g1786208 Escherichia coli 562  
-11533375 5000691340 (de:(ecoli\_25) (pn:hypothetical 34) (gn:yaac)  
(gtcfc:13.7:14.1) (ec:) (yaac\_ecoli) (keggfc:11.2) (rileyfc:5.7.0)  
(db:gtc-escherichia coli)) ECOLI\_25 ECOLI\_25 Escherichia coli 562 10122622

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830506	8379	30535	891	296

Description

6500729518 ribh:ribe:b0415 probable riboflavin synthase beta chain:6:7-dimethyl-8-ribityllumazine synthase:dmr1 synthase:lumazine synthase:riboflavin synthase beta chain (gtcfc:9.2:14.3) (ec:2.5.1.9) (keggfc:9.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2):unknown-unclassified) b0415 b0415 Escherichia coli 562 -11533376  
7500889815 ribh:ribe (ec:2.5.1.9) (de:(lumazine synthase) (riboflavin synthase beta chain)) (db:swissprot) RISB\_ECOLI P25540 ESCHERICHIA COLI 562 -11533376 163485 ribh:ribe riboflavin synthase:beta chain:6:7-dimethyl-8-ribityllumazine synthase:lumazine synthase (ec:2.5.1.9) (db:pir2.dat) S26202 S26202 Escherichia coli 562 -11533376 233538 homologue of bacillus subtilis ribh (db:genpept-bct1) (de:shigella flexneri homologue of bacillus subtilis ribg, andhomologue of bacillus subtilis ribh genes, complete cds; and nusbgene, partial cds.) (nt:orf3) (le:1967) (re:2437) (di:direct) AF002857 AF002857 g2766597 Shigella flexneri 623 -11533376  
5000690632 (db:genpept-bct1) (de:e.coli genes nusb (ssyb) and 3 orfs.) (nt:orf3, homologue to b.subtilis ribh) (le:2036) (re:2506) (di:direct) ECNUSB X64395 g42150 Escherichia coli 562 -11533376 7000686343 ribh riboflavin synthase:beta chain (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:2.5.1.9) (de:escherichia coli k-12 mg1655 section 38 of 400 of the completegenome.) (nt:o156; 100 pct identical to risb\_ecoli sw:) (le:1721) (re:2191) (di:direct) AE000148 AE000148 g1786617 Escherichia coli 562 -11533376 94485 ribh:ribe (ec:2.5.1.9) (de:(lumazine synthase) (riboflavin synthase beta chain)) (db:swissprot) RISB\_ECOLI P25540 ESCHERICHIA COLI 562 -11533376

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830507	8380	30536	1122	373

#### Description

6500729519 riba:b1277 gtp cyclohydrolase ii (gtcfc:9.2) (ec:3.5.4.25) (keggfc:9.2) (rileyfc:1.7.9) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2)) b1277 b1277 Escherichia coli 562 -11533377 300308 riba (ec:3.5.4.25) (de:gtp cyclohydrolase ii,) (db:swissprot) GCH2\_ECOLI P25523 ESCHERICHIA COLI 562 -11533377 163146 riba gtp cyclohydrolase ii (cl:escherichia coli cyclohydrolase ii:cyclohydrolase homology) (ec:3.5.4.25) (db:pir2.dat) A40654 A40654 Escherichia coli 562 -11533377 223505 riba gtp cyclohydrolase ii ec 3.5.4.25 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #255(28.8-29.2 min.)) (nt:orf\_id:o255#2; similar to (pir accession number) (le:835) (re:1425) (di:complement) D90766 D90766 g1742091 Escherichia coli 562 -11533377 5000690633 riba gtp cyclohydrolase ii (db:genpept-bct1) (de:e.coli riba gene for gtp cyclohydrolase ii.) (le:768) (re:1358) (di:direct) ECRIBA X67876 g42738 Escherichia coli 562 -11533377 238083 riba gtp cyclohydrolase ii (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:3.5.4.25) (de:escherichia coli k-12 mg1655 section 116 of 400 of the completegenome.) (nt:f196; 100 pct identical gch2\_ecoli sw: p25523; cg) (le:62) (re:652) (di:complement) AE000226 AE000226 g1787533 Escherichia coli 562 -11533377 73406 riba (ec:3.5.4.25) (de:gtp cyclohydrolase ii,) (db:swissprot) GCH2\_ECOLI P25523 ESCHERICHIA COLI 562 -11533377

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830528	8381	30537	207	68

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830537	8382	30538	1170	390

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830555	8383	30539	417	139

# Description

6500729520 ribe:ribc:b1662 riboflavin synthase alpha chain (gtcfc:9.2) (ec:2.5.1.9) (keggfc:9.2) (rileyfc:1.7.9) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2)) b1662 b1662 Escherichia coli 562 -11533378 307831 ribe:ribc (ec:2.5.1.9) (de:riboflavin synthase alpha chain,) (db:swissprot) RISA\_ECOLI P29015 ESCHERICHIA COLI 562 -11533378 164544 ribe:ribc riboflavin synthase:alpha chain (cl:riboflavin synthase alpha chain) (ec:2.5.1.9) (db:pir2.dat) S28526 S28526 Escherichia coli 562 -11533378 224107 ribe:ribc riboflavin synthase a chain ec 2.5.1.9 . (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #318(37.2-37.6 min.)) (nt:orf\_id:o319#6; similar to (swissprot accession) (le:14194) (re:14835) (di:complement) D90809 D90809 g1742736 Escherichia coli 562 -11533378 300785 ribe:ribc riboflavin synthase a chain ec 2.5.1.9 . (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #319(37.4-37.8 min.)) (nt:orf\_id:o319#6; similar to (swissprot accession) (le:6588) (re:7229) (di:complement) D90810 D90810 g1742746 Escherichia coli 562 -11533378 239763 ribc riboflavin synthase (db:genpept-bct1) (ec:2.5.1.9) (de:e.coli ribc gene for riboflavin synthase.) (le:905) (re:1546) (di:direct) ECRIBC X69109 g42740 Escherichia coli 562 -11533378 295371 ribc riboflavin synthase:alpha chain (db:genpept-bct1) (ec:2.5.1.9) (de:escherichia coli k-12 mg1655 genome, ribc-pykf region.) (nt:cg site number 11923) (le:5) (re:646) (di:complement) ECU68703 U68703 g1549275 Escherichia coli 562 -11533378 238085 ribe riboflavin synthase:alpha chain (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:2.5.1.9) (de:escherichia coli k-12 mg1655 section 151 of 400 of the completegenome.) (nt:f213; 100 pct identical to risa\_ecoli sw: p29015;) (le:7317) (re:7958) (di:complement) AE000261 AE000261 g1787952 Escherichia coli 562 -11533378 94478 ribe:ribc (ec:2.5.1.9) (de:riboflavin synthase alpha chain,) (db:swissprot) RISA\_ECOLI P29015 ESCHERICHIA COLI 562 -11533378 224116 ribe:ribc riboflavin synthase a chain ec 2.5.1.9 . (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #319(37.4-37.8 min.)) (nt:orf\_id:o319#6; similar to (swissprot accession) (le:6588) (re:7229) (di:complement) D90810 D90810 g1742746 Escherichia coli 562 -11533378 5000690634 (de:(ecoli\_1621) (pn:riboflavin synthase, alpha chain) (gn:ribe) (gtcfc:9.2) (ec:2.5.1.9) (risa\_ecoli) (keggfc:9.2) (rileyfc:1.7.9) (db:gtc-escherichia coli)) ECOLI\_1621 ECOLI\_1621 Escherichia coli 562 10036458

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830556	8384	30540	696	231

Description

6500729521 ribd:ribg:b0414 riboflavin biosynthesis protein  
 ribd:riboflavin-specific deaminase (gtcfc:9.2) (ec:3.5.4.-) (keggfc:14.1)  
 (rileyfc:1.7.9) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and  
 vitamins-riboflavin metabolism (vitamin b2)) b0414 b0414 Escherichia coli  
 562 -11533379 94342 ribd:ribg (ec:3.5.4.-) (de:riboflavin-specific  
 deaminase,) (db:swissprot) RIBD\_ECOLI P25539 ESCHERICHIA COLI 562 -11533379  
 163460 ribd:ribg riboflavin-specific deaminase (ec:3.5.4.-) (db:pir2.dat)  
 S26201 S26201 Escherichia coli 562 -11533379 240191 (db:genpept-bct1)  
 (de:e.coli genes nusB (ssyB) and 3 orfs.) (nt:orf2, homologue to b.subtilis  
 ribg) (le:844) (re:1947) (di:direct) ECNUSB X64395 g581147 Escherichia coli  
 562 -11533379 7500889769 ribg riboflavin biosynthesis protein ribg  
 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.)  
 (le:12905) (re:14008) (di:direct) ECU82664 U82664 g1773098 Escherichia coli  
 562 -11533379 233537 ribd bifunctional pyrimidine deaminase/reductase in  
 (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2)  
 (de:escherichia coli k-12 mg1655 section 38 of 400 of the complete genome.)  
 (nt:o367; 100 pct identical to ribg\_ecoli sw: p25539;) (le:529) (re:1632)  
 (di:direct) AE000148 AE000148 g1786616 Escherichia coli 562 -11533379  
 5000690629 (de:(ecoli\_398) (pn:deaminase in pathway of riboflavin  
 synthesis) (gn:ribd) (gtcfc:9.2) (ec:) (ribd\_ecoli) (keggfc:11.2)  
 (rileyfc:1.7.9) (db:gtc-escherichia coli)) ECOLI\_398 ECOLI\_398 Escherichia  
 coli 562 10036322

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830560	8385	30541	708	235

Description

6500729522 ribb:htrp:b3041 3:4-dihydroxy-2-butanone 4-phosphate synthase:dhbp synthase (gtcfc:9.2) (keggfc:14.2) (rileyfc:1.7.9) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2)) b3041 b3041 Escherichia coli 562 -11533380 238084 ribb:htrp (de:3,4-dihydroxy-2-butanone 4-phosphate synthase (dhbp synthase)) (db:swissprot) RIBB\_ECOLI P24199 ESCHERICHIA COLI 562 -11533380 235029 luxh (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli luxh gene, complete cds; orfa-orfd, complete cds.) (le:4220) (re:4873) (di:complement) ECOLUXH M77129 g455174 Escherichia coli 562 -11533380 5000690630 ribb 3:4-dihydroxy-2-butanone 4-phosphate synthase (db:genpept-bct1) (de:e.coli ribb gene for 3,4-dihydroxy-2-butanone 4-phosphate synthase.) (le:638) (re:1291) (di:direct) ECRIBB X66720 g49100 Escherichia coli 562 -11533380 239255 ribb 3:4-dihydroxy-2-butanone 4-phosphate synthase (fn:block before 6,7-dimethyl-8-ribityllumazine) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:cg site no. 286; alternate names htrp, luxh) (le:138201) (re:138854) (di:complement) ECU28377 U28377 g882571 Escherichia coli 562 -11533380 7500889767 ribb 3:4 dihydroxy-2-butanone-4-phosphate synthase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 276 of 400 of the completegenome.) (nt:f217; 100 pct identical to ribb\_ecoli sw: p24199;) (le:1351) (re:2004) (di:complement) AE000386 AE000386 g1789420 Escherichia coli 562 -11533380 94337 ribb:htrp (de:3,4-dihydroxy-2-butanone 4-phosphate synthase (dhbp synthase)) (db:swissprot) RIBB\_ECOLI P24199 ESCHERICHIA COLI 562 -11533380 162608 (de:3,4-dihydroxy-2-butanone 4-phosphate synthase - escherichiacoli) S22364 S22364 Escherichia coli 562 -11533380

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830582	8386	30542	423	140

#### Description

6500729523 trxa:b3781 thioredoxin (gtcfc:9.2:9.13) (keggfc:14.2) (rileyfc:1.7.9) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2):metabolism of cofactors and vitamins-other cofactors) b3781 b3781 Escherichia coli 562 -11533381 237010 trxa thioredoxin (sr:escherichia coli (sub\_strain sk3983, strain k-12) dna) (db:genpept-bct1) (de:e.coli (clone pbhk10) thioredoxin (trxa) and termination factor(rho) genes, complete cds.) (le:194) (re:577) (di:direct) ECORHOB K02845 g147611 Escherichia coli 562 -11533381 7500974867 trxa::cgsc no. 65 thioredoxin (db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (le:18835) (re:19218) (di:direct) ECOUW85 M87049 g148185 Escherichia coli 562 -11533381 235795 trxa thioredoxin 1 (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 344 of 400 of the completegenome.) (nt:o127; 100 pct identical to 108 amino acids) (le:7792) (re:8175) (di:direct) AE000454 AE000454 g1790215 Escherichia coli 562 -11533381 5000690631 (de:(ecoli\_3691) (pn:thioredoxin) (gn:trxa) (gtcfc:9.2) (ec:)(thio\_ecoli) (keggfc:11.2) (rileyfc:1.7.9) (db:gtc-escherichia coli)) ECOLI\_3691 ECOLI\_3691 Escherichia coli 562 10124093

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830583	8387	30543	258	85

#### Description

6500729524 pdxh:b1638 pyridoxamine 5-phosphate oxidase:pnppmp oxidase (gtcfc:9.3) (ec:1.4.3.5) (keggfc:9.3) (rileyfc:1.7.6) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-pyridoxine metabolism (vitamin b6)) (keggfc:vitamin b6 metabolism) b1638 b1638 Escherichia coli 562 -11533382 164448 pdxh pyridoxamine-phosphate oxidase:pdxh (cl:pyridoxamine-phosphate oxidase) (ec:1.4.3.5) (db:pir2.dat) B43261 B43261 Escherichia coli 562 -11533382 7500953851 pdxh pyridoxamine phosphate oxidase (fn:oxidize pnp and pmp into pyridoxal 5'-phosphate) (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (ec:1.4.3.5) (de:escherichia coli pyridoxamine 5'-phosphate oxidase (pdxh) gene,complete cds, tyrosyl-trna synthetase (tyrs) gene, 3' end, or... ECOTYSPDH M92351 g148097 Escherichia coli 562 -11533382 236237 pdxh pyridoxinephosphate oxidase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:1.4.3.5) (de:escherichia coli k-12 mg1655 section 149 of 400 of the completegenome.) (nt:f218; 100 pct identical to pdxh\_ecoli sw: p28225;) (le:4958) (re:5614) (di:complement) AE000259 AE000259 g1787926 Escherichia coli 562 -11533382 5000690637 (de:(ecoli\_1597) (pn:pyridoxinephosphate oxidase) (gn:pdxh) (gtcfc:9.3) (ec:1.4.3.5) (pdxh\_ecoli) (keggfc:9.3) (rileyfc:1.7.6) (db:gtc-escherichia coli)) ECOLI\_1597 ECOLI\_1597 Escherichia coli 562 10087320



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830584	8388	30544	936	312

Description

6500729525 pdxk:b2418 hypothetical protein:pyridoxine kinase:pyridoxal  
kinase:vitamin b6 kinase:pyridoxamine kinase:pn/pl/pm kinase  
(gtcfc:9.3:14.1) (ec:2.7.1.35) (keggfc:9.3) (rileyfc:5.7.0)  
(db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and  
vitamins-pyridoxine metabolism (vitamin b6):unknown-hypothetical)  
(keggfc:vitamin b6 metabolism) b2418 b2418 Escherichia coli 562 -11533383  
111857 pdxk (ec:2.7.1.35) (de:kinase) (pyridoxamine kinase) (pn/pl/pm  
kinase)) (db:swissprot) PDXK\_ECOLI P40191 ESCHERICHIA COLI 562 -11533383  
7000686107 hypothetical protein b2418 (db:pir2.dat) A65016 A65016  
Escherichia coli 562 -11533383 224980 yfei (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #418(54.6-54.9 min.).) (nt:similar to  
(swissprot accession number p40191)) (le:4754) (re:5605) (di:complement)  
D90871 D90871 g1799837 Escherichia coli 562 -11533383 239722 pdxk  
pyridoxal/pyridoxine/pyridoxamine kinase (fn:enzyme; biosynthesis of  
cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655  
section 219 of 400 of the completegenome.) (nt:f283 was f223; this 223 aa  
orf is 68 pct identical) (le:6205) (re:7056) (di:complement) AE000329  
AE000329 g1788758 Escherichia coli 562 -11533383 7500887784 pdxk  
pyridoxine/pyridoxal/pyridoxamine kinase (sr:escherichia coli strain=k-12  
(w3110)) (db:genpept-bct2) (de:escherichia coli pyridoxine (vitamin  
b6)/pyridoxal/pyridoxaminekinase (pdxk) gene and pts system glucose-specific  
component iia(crr) gene, complete cds.) (nt:pyridoxine(vitamin  
b6)/pyridox... ECU53700 U53700 g1314674 Escherichia coli 562 -11533383  
5000692916 (de:(ecoli\_2359) (pn:function not assigned) (gtcfc:13.7:14.1)  
(ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2359  
ECOLI\_2359 Escherichia coli 562 10120190

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830596	8389	30545	675	224

Description

6500729526 pdxa:b0052 pyridoxal phosphate biosynthetic protein pdxa (gtcfc:9.3) (keggfc:14.2) (rileyfc:1.7.6) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-pyridoxine metabolism (vitamin b6)) b0052 b0052 Escherichia coli 562 -11533384 88901 pdxa (de:pyridoxal phosphate biosynthetic protein pdxa) (db:swissprot) PDXA\_ECOLI P19624 ESCHERICHIA COLI 562 -11533384 131326 pdxa pyridoxal phosphate biosynthetic protein pdxa (cl:pdxa protein) (db:pirl.dat) (mp:1 min) BVECXA JV0026 Escherichia coli 562 -11533384 7500887773 pdxa (fn:required for the novo biosynthesis of) (sr:e.coli (k-12, isolate w3110) dna) (db:genpept-bct1) (de:e.coli pyridoxine (vitamin b6) and pyridoxal phosphate biosynthesis(pdxa) gene, complete cds and 6-m-2-a methyltransferase (ksga)gene, 5' end.) (le:2... ECOPDXA M68521 g147120 Escherichia coli 562 -11533384 235373 pdxa pyridoxine biosynthesis (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 5 of 400 of the completegenome.) (nt:f329; 100 pct identical to pdxa\_ecoli sw: p19624) (le:5265) (re:6254) (di:complement) AE000115 AE000115 g1786237 Escherichia coli 562 -11533384 5000690635 (de:(ecoli\_52) (pn:pyridoxine biosynthesis) (gn:pdxa) (gtcfc:9.3) (ec:) (pdxa\_ecoli) (keggfc:11.2) (rileyfc:1.7.6) (db:gtc-escherichia coli)) ECOLI\_52 ECOLI\_52 Escherichia coli 562 10031028

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830598	8390	30546	405	134

Description

6500729527 pdxj:b2564 pyridoxal phosphate biosynthetic protein pdxj  
 (gtcfc:9.3) (keggfc:14.2) (rileyfc:1.7.6) (db:gtc-escherichia coli)  
 (gtcfc:metabolism of cofactors and vitamins-pyridoxine metabolism (vitamin  
 b6)) b2564 b2564 Escherichia coli 562 -11533385 164828 pdxj pyridoxal  
 phosphate biosynthetic protein pdxj (db:pir2.dat) A42293 A42293 Escherichia  
 coli 562 -11533385 235735 pdxj (sr:escherichia coli (strain k-12) dna)  
 (db:genpept-bct1) (de:escherichia coli pdxj and dpj protein gene, complete  
 cds.) (le:70) (re:801) (di:direct) ECOPDXJDPJ M74526 g147137 Escherichia  
 coli 562 -11533385 239518 pdxj (fn:pyridoxal phosphate biosynthesis)  
 (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia  
 coli recombination and repair protein (reco) gene, 3'end, and pyridoxal  
 phosphate biosynthetic protein (pdxj) gene,complete cds.) (le:244) (...  
 ECORECOPDX M76470 g147555 Escherichia coli 562 -11533385 7500960442 pdxj  
 (fn:pyridoxal phosphate biosynthesis) (db:genpept-bct1) (de:escherichia coli  
 k-12 genome, approximately 55 minutes.) (nt:cg site no. 416) (le:12242)  
 (re:12973) (di:complement) ECU36841 U36841 g1033153 Escherichia coli 562  
 -11533385 235383 pdxj pyridoxine biosynthesis (fn:enzyme; biosynthesis of  
 cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655  
 section 233 of 400 of the completegenome.) (nt:f243; 100 pct identical to  
 pdxj\_ecoli sw: p24223;) (le:758) (re:1489) (di:complement) AE000343 AE000343  
 g1788917 Escherichia coli 562 -11533385 5000690636 (de:(ecoli\_2504)  
 (pn:pyridoxine biosynthesis) (gn:pdxj) (gtcfc:9.3) (ec:) (pdxj\_ecoli)  
 (keggfc:11.2) (rileyfc:1.7.6) (db:gtc-escherichia coli)) ECOLI\_2504  
 ECOLI\_2504 Escherichia coli 562 10087481

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830603	8391	30547	453	150

Description

6500729528 nadc:b0109 nicotinate-nucleotide  
pyrophosphorylase:carboxylating:quinolinate  
phosphoribosyltransferase:decarboxylating:qaprtase (gtcfc:9.4) (ec:2.4.2.19)  
(keggfc:9.4) (rileyfc:1.7.7) (db:gtc-escherichia coli) b0109 b0109  
Escherichia coli 562 -11533386 7000691872 nadc nicotinate-nucleotide  
pyrophosphorylase carboxylating::quinolinate phosphoribosyltransferase  
(cl:nicotinate-nucleotide pyrophosphorylase (carboxylating)) (ec:2.4.2.19)  
(db:pir2.dat) (mp:2.6 min) E64733 E64733 Escherichia coli 562 -11533386  
233785 nadc quinolinate phosphoribosyltransferase (fn:enzyme; biosynthesis  
of cofactors, carriers:) (db:genpept-bct2) (ec:2.4.2.19) (de:escherichia  
coli k-12 mg1655 section 10 of 400 of the completegenome.) (nt:f297; 99 pct  
identical to nadc\_ecoli sw: p30011 but) (le:132) (re:1025) (di:complement)  
AE000120 AE000120 g1786299 Escherichia coli 562 -11533386 7500960397 nadc  
quinolinate phosphoribosyltransferase (sr:escherichia coli (strain k-12)  
dna) (db:genpept-bct2) (de:escherichia coli ampd gene; quinolinate  
phosphoribosyltransferase(nadc) gene; prepilin-like peptidase dependent  
protein (ppdd) gene;hopb, hopc genes; gmp reductase (guac) gene.)  
(nt:putative... ECOAMPHSM L28105 g456041 Escherichia coli 562 -11533386  
5000690640 (de:(ecoli\_109) (pn:quinolinate phosphoribosyltransferase)  
(gn:nadc) (gtcfc:9.4) (ec:2.4.2.19) (nadc\_ecoli) (keggfc:9.4)  
(rileyfc:1.7.7) (db:gtc-escherichia coli)) ECOLI\_109 ECOLI\_109 Escherichia  
coli 562 10122663

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830607	8392	30548	828	275

Description

6500729529 pncb:b0931 nicotinate phosphoribosyltransferase:naprtase  
(gtcfc:9.4) (ec:2.4.2.11) (keggfc:9.4) (rileyfc:1.7.7) (db:gtc-escherichia  
coli) b0931 b0931 Escherichia coli 562 -11533387 138148 pncb nicotinate  
phosphoribosyltransferase (cl:nicotinate phosphoribosyltransferase)  
(ec:2.4.2.11) (db:pir2.dat) JQ0756 JQ0756 Escherichia coli 562 -11533387  
223290 pncb nicotinate phosphoribosyltransferase (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #219) (db:genpept-bct1)  
(de:escherichia coli genomic dna. (21.1 - 21.4 min).) (le:6307) (re:7509)  
(di:complement) D90731 D90731 g1651456 Escherichia coli 562 -11533387  
7500954018 (sr:e.coli (strain k12) dna) (db:genpept-bct1) (de:e.coli  
nicotinic acid phosphoribosyl transferase (pncb) gene,complete cds.)  
(nt:nicotinic acid phosphoribosyl transferase (pncb)) (le:216) (re:1418)  
(di:direct) ECOPNCB J05568 g147307 Escherichia coli 562 -11533387 235507  
pncb nicotinate phosphoribosyltransferase (fn:enzyme; biosynthesis of  
cofactors, carriers:) (db:genpept-bct2) (ec:2.4.2.11) (de:escherichia coli  
k-12 mg1655 section 85 of 400 of the completegenome.) (nt:f400; 100 pct  
identical to pncb\_ecoli sw: p18133) (le:6200) (re:7402) (di:complement)  
AE000195 AE000195 g1787162 Escherichia coli 562 -11533387 5000690641 pncb  
nicotinate phosphoribosyltransferase ec (sr:escherichia coli(strain:k12)  
dna, clone:kohara clone #219) (db:genpept) (de:escherichia coli genomic dna.  
(21.2 - 21.5 min).) (nt:orf\_id:o220#1; similar to pir accession number)  
(le:6307) (re:7509) (di:complement) D90731 D90731 g1651456 Escherichia coli  
562 -11533387

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830609	8393	30549	1047	348

# Description

6500729530 nada:nica:b0750 quinolinate synthetase a protein:quinolinate synthetase a (gtcfc:9.4) (keggfc:14.2) (rileyfc:1.7.7) (db:gtc-escherichia coli) b0750 b0750 Escherichia coli 562 -11533388 85135 nada:nica (de:quinolinate synthetase a) (db:swissprot) NADA\_ECOLI P11458 ESCHERICHIA COLI 562 -11533388 7000685903 nada:nica quinolinate synthetase a (cl:quinolinate synthetase a) (db:pir1.dat) (mp:17 min) SYECQA F64810 Escherichia coli 562 -11533388 223185 nada quinolinate synthetase a (sr:escherichia coli(strain:k12) dna, clone:kohara clone #178) (db:genpept-bct1) (de:escherichia coli genomic dna.(16.5 - 16.8 min).) (le:15275) (re:16318) (di:direct) D90713 D90713 g1651334 Escherichia coli 562 -11533388 223187 nada quinolinate synthetase a (sr:escherichia coli(strain:k12) dna, clone:kohara clone #179) (db:genpept-bct1) (de:escherichia coli genomic dna.(16.8 - 17.1 min).) (le:2149) (re:3192) (di:direct) D90714 D90714 g1651337 Escherichia coli 562 -11533388 7500886227 nada quinolinate synthetase:a protein (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 67 of 400 of the completegenome.) (nt:o347; this 347 aa orf is 98 pct identical to) (le:7870) (re:8913) (di:direct) AE000177 AE000177 g1786964 Escherichia coli 562 -11533388 5000690638 nada quinolinate synthetase a. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #178) (db:genpept) (de:escherichia coli genomic dna. (16.5 - 16.9 min).) (nt:orf\_id:o179#1; similar to swissprot accession) (le:15275) (re:16318) (di:direct) D90713 D90713 g1651334 Escherichia coli 562 -11533388 7502851924 nada quinolinate synthetase a. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #179) (db:genpept) (de:escherichia coli genomic dna. (16.8 - 17.1 min).) (nt:orf\_id:o179#1; similar to swissprot accession) (le:2149) (re:3192) (di:direct) D90714 D90714 g1651337 Escherichia coli 562 -11533388

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830611	8394	30550	189	62

Description

6500729531 nadr:b4390 transcriptional regulator nadr (gtcfc:9.4:10.2) (keggfc:14.2) (rileyfc:1.7.7) (db:gtc-escherichia coli) b4390 b4390 Escherichia coli 562 -11533389 164138 nadr transcription regulator nadr (db:pir2.dat) S56614 S56614 Escherichia coli 562 -11533389 7500960472 nadr (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:318126) (re:319379) (di:direct) ECOUW93 U14003 g537230 Escherichia coli 562 -11533389 237595 nadr probable nadab transcriptional regulator (fn:putative regulator; biosynthesis of cofactors,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 399 of 400 of the completegenome.) (nt:o417b; 100 pct identical to 410 amino acids) (le:2482) (re:3735) (di:direct) AE000509 AE000509 g1790851 Escherichia coli 562 -11533389 5000690639 (de:(ecoli\_4272) (pn:probable nadab transcriptional regulator) (gn:nadr) (gtcfc:9.4) (ec:) (nadr\_ecoli) (keggfc:11.2) (rileyfc:1.7.7) (db:gtc-escherichia coli)) ECOLI\_4272 ECOLI\_4272 Escherichia coli 562 10087188

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830615	8395	30551	294	97

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830622	8396	30552	918	305

# Description

6500729532 panb:b0134 3-methyl-2-oxobutanoate  
hydroxymethyltransferase:ketopantoate hydroxymethyltransferase  
(gtcfc:9.5:9.6) (ec:2.1.2.11) (keggfc:9.5:9.8) (rileyfc:1.7.5)  
(db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and  
vitamins-pantothenate and coa biosynthesis:metabolism of cofactors and  
vitamins-biotin metabolism (b8) and folate biosynthesis) b0134 b0134  
Escherichia coli 562 -11533390 88569 panb (ec:2.1.2.11) (de:(ketopantoate  
hydroxymethyltransferase)) (db:swissprot) PANB\_ECOLI P31057 ESCHERICHIA COLI  
562 -11533390 7000686078 panb 3-methyl-2-oxobutanoate  
hydroxymethyltransferase (cl:3-methyl-2-oxobutanoate  
hydroxymethyltransferase) (ec:2.1.2.11) (db:pir2.dat) F64736 F64736  
Escherichia coli 562 -11533390 7500887641 panb alpha-ketopantoate  
hydroxymethyl transferase (fn:alpha-ketoisovalerate to alpha-ketopantoate)  
(sr:escherichia coli (sub\_strain w3110, strain k-12) dna) (db:genpept-bct1)  
(de:e. coli alpha-ketopantoate hydroxymethyl transferase (panb),pantothenate  
synthetase (panc), aspartate-1-decarboxylase (pand... ECOPANBCD L17086  
g304927 Escherichia coli 562 -11533390 235329 panb 3-methyl-2-oxobutanoate  
(fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2)  
(ec:2.1.2.11) (de:escherichia coli k-12 mg1655 section 12 of 400 of the  
completegenome.) (nt:f264; 100 pct identical to panb\_ecoli sw: p31057)  
(le:10103) (re:10897) (di:complement) AE000122 AE000122 g1786326 Escherichia  
coli 562 -11533390 5000690642 (de:(ecoli\_134) (pn:ketopantoate  
hydroxymethyltransferase) (gn:panb) (gtcfc:9.5:9.6) (ec:2.1.2.11)  
(panb\_ecoli) (keggfc:9.5:9.8) (rileyfc:1.7.5) (db:gtc-escherichia coli))  
ECOLI\_134 ECOLI\_134 Escherichia coli 562 10030696



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830643	8397	30553	441	146

Description

6500729533 coaa:rts:pank:b3974 pantothenate kinase:rts protein (gtcfc:9.5) (ec:2.7.1.33) (keggfc:9.5) (rileyfc:1.7.5) (db:gtc-escherichia coli) b3974 b3974 Escherichia coli 562 -11533391 65055 coaa:rts:pank (ec:2.7.1.33) (de:pantothenate kinase, (rts protein)) (db:swissprot) COAA\_ECOLI P15044 ESCHERICHIA COLI 562 -11533391 123581 coaa:rts pantothenate kinase (cl:pantothenate kinase) (ec:2.7.1.33) (db:pir1.dat) (mp:90 min) BVECRS A45727 Escherichia coli 562 -11533391 237188 coaa pantothenate kinase (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (ec:2.7.1.33) (de:escherichia coli pantothenate kinase (coaa) gene, complete cds.) (nt:large protein) (le:271) (re:1221) (di:direct) ECOCOAA M90071 g145560 Escherichia coli 562 -11533391 234014 coaa pantothenate kinase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:2.7.1.33) (de:escherichia coli k-12 mg1655 section 361 of 400 of the completengenome.) (nt:f316; 100 pct identical to coaa\_ecoli sw: p15044;) (le:10661) (re:11611) (di:complement) AE000471 AE000471 g1790409 Escherichia coli 562 -11533391 7500878983 coaa pantothenate kinase (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (ec:2.7.1.33) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 17731; alternate gene name rts) (le:39318) (re:40268) (di:complement) ECOUW89 U00006 g396317 Escherichia coli 562 -11533391 5000690644 (de:(ecoli\_3868) (pn:pantothenate kinase) (gn:coaa) (gtcfc:9.5) (ec:2.7.1.33) (coaa\_ecoli) (keggfc:9.5) (rileyfc:1.7.5) (db:gtc-escherichia coli)) ECOLI\_3868 ECOLI\_3868 Escherichia coli 562 10007710

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830646	8398	30554	1296	432

Description

6500729534 bioa:b0774 adenosylmethionine-8-amino-7-oxononanoate  
aminotransferase:7:8-diamino-pelargonic acid aminotransferase:dapa  
aminotransferase (gtcfc:9.6) (ec:2.6.1.62) (keggfc:9.6) (rileyfc:1.7.1)  
(db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-biotin  
metabolism (b8) and folate biosynthesis) b0774 b0774 Escherichia coli 562  
-11533392 61708 bioa (ec:2.6.1.62) (de:aminotransferase)) (db:swissprot)  
BIOA\_ECOLI P12995 ESCHERICHIA COLI 562 -11533392 7000684706 bioa  
adenosylmethionine--8-amino-7-oxononanoate  
transaminase::7:8-diaminononanoate  
aminotransferase:adenosylmethionine--8-amino-7-oxononanoate  
aminotransferase:dapa aminotransferase (cl:ornithine--oxo-acid  
aminotransferase) (ec:2.6.1.62) (db:pir1.dat) (mp:17 min) XNECDP F64813  
Escherichia coli 562 -11533392 4000706923 bioa 7:8-diaminopelargonic acid  
synthetase (fn:enzyme; biosynthesis of cofactors, carriers:)  
(db:genpept-bct2) (ec:2.6.1.62) (de:escherichia coli k-12 mg1655 section 70  
of 400 of the completegenome.) (nt:f429; 100 pct identical to bioa\_ecoli sw:  
p12995) (le:2117) (re:3406) (di:complement) AE000180 AE000180 g1786991  
Escherichia coli 562 -11533392 5000690645 bioa dapa synthase  
(db:genpept-pat) (ec:2.6.1.62) (de:sequence 1 from patent wo9408023.)  
(le:3750) (re:5039) (di:direct) A38246 A38246 g2294847 Escherichia coli 562  
-11533392

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830656	8399	30555	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830659	8400	30556	429	142

Description

6500729535 biob:b0775 biotin synthetase (gtcfc:9.6) (ec:2.8.1.-)  
(keggfc:9.6) (rileyfc:1.7.1) (db:gtc-escherichia coli) (gtcfc:metabolism of  
cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) b0775  
b0775 Escherichia coli 562 -11533393 61720 biob (ec:2.8.1.6) (de:biotin  
synthase, (biotin synthetase)) (db:swissprot) BIOB\_ECOLI P12996 ESCHERICHIA  
COLI 562 -11533393 205503 biob biotin synthetase::biob protein (cl:biotin  
synthetase) (ec:2.8.1.-) (db:pir1.dat) (mp:17 min) SYECBB JC2517 Escherichia  
coli 562 -11533393 4000713531 biob biotin synthesis:sulfur insertion?  
(fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2)  
(ec:2.8.1.-) (de:escherichia coli k-12 mg1655 section 70 of 400 of the  
completegenome.) (nt:o346; 99 pct identical to biob\_ecoli sw: p12996)  
(le:3493) (re:4533) (di:direct) AE000180 AE000180 g1786992 Escherichia coli  
562 -11533393 5000690646 biob (db:genpept-pat) (de:biob gene of e.coli with  
primers.) (le:24) (re:1064) (di:direct) A11530 A11530 g490219 Escherichia  
coli 562 -11533393 7502851925 biob biotin synthase (db:genpept-pat)  
(de:sequence 1 from patent wo9408023.) (le:117) (re:1157) (di:direct) A38246  
A38246 g2294845 Escherichia coli 562 -11533393 325118 biob biotin  
synthetase (db:genpept-bct1) (ec:2.8.1.-) (de:escherichia coli k-12 mg1655  
section 70 of 400 of the completegenome.) (nt:o346; 99 pct identical to  
biob\_ecoli sw: p12996) (le:3493) (re:4533) (di:direct) ECAE000180 AE000180  
g1786992 Escherichia coli 562 -11533393

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830674	8401	30557	681	226

Description

6500729536 biof:b0776 8-amino-7-oxononanoate synthase:7-keto-8-amino-pelargonic acid synthetase:7-kap synthetase:l-alanine--pimelyl coa ligase (gtcfc:9.6) (ec:2.3.1.47) (keggfc:9.6) (rileyfc:1.7.1) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) b0776 b0776 Escherichia coli 562 -11533394 61739 biof (ec:2.3.1.47) (de:ligase)) (db:swissprot) BIOF\_ECOLI P12998 ESCHERICHIA COLI 562 -11533394 123371 biof 8-amino-7-oxononanoate synthase::7-kap synthetase:7-keto-8-amino pelargonic acid synthetase (cl:5-aminolevulinate synthase) (ec:2.3.1.47) (db:pir1.dat) (mp:17 min) SYECKP D32025 Escherichia coli 562 -11533394 4000706927 biof 7-keto-8-amino pelargonic acid synthetase (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli 7,8-diamino-pelargonic acid (bioa), biotin synthetase(biob), 7-keto-8-amino-pelargonic acid synthetase (biof), biocprotein, and dethiobiotin synthetase (biob), complete cds.) (le:3049... ECOBIO J04423 g145426 Escherichia coli 562 -11533394 233913 biof 8-amino-7-oxononanoate synthase (fn:enzyme; biosynthesis of cofactors, carriers.) (db:genpept-bct2) (ec:2.3.1.47) (de:escherichia coli k-12 mg1655 section 70 of 400 of the completegenome.) (nt:o384; 100 pct identical to biof\_ecoli sw: p12998) (le:4530) (re:5684) (di:direct) AE000180 AE000180 g1786993 Escherichia coli 562 -11533394 5000690647 biof kapa synthase (db:genpept-pat) (ec:2.3.1.47) (de:sequence 6 from patent wo9408023.) (le:1154) (re:2308) (di:direct) A38251 A38251 g2294850 Escherichia coli 562 -11533394

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830681	8402	30558	1146	381

Description

GTC ORF with score 1148 to: (db:genpept-pln1) (de:aspergillus oryzae putative dna binding protein facb (facb) gene,complete cds.) (nt:description: homologue of the emericella nidulans) (le:1680:2223:2597:2927) (re:2148:2536:2877:3284) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830682	8403	30559	354	117

Description

GTC ORF with score 403 to: (db:genpept-pln1) (de:aspergillus oryzae putative dna binding protein facb (facb) gene,complete cds.) (nt:description: homologue of the emericella nidulans) (le:1680:2223:2597:2927) (re:2148:2536:2877:3284) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830684	8404	30560	822	273

Description

GTC ORF with score 521 to: (db:genpept-pln1) (de:aspergillus oryzae putative dna binding protein facb (facb) gene,complete cds.) (nt:description: homologue of the emericella nidulans) (le:1680:2223:2597:2927) (re:2148:2536:2877:3284) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830687	8405	30561	363	120

Description

GTC ORF with score 451 to: (db:genpept-pln1) (de:aspergillus oryzae putative dna binding protein facb (facb) gene,complete cds.) (nt:description: homologue of the emericella nidulans) (le:1680:2223:2597:2927) (re:2148:2536:2877:3284) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830702	8406	30562	552	184

Description

6500729537 biod:b0778 dethiobiotin synthetase:dtb synthetase:dtbs (gtcfc:9.6) (ec:6.3.3.3) (keggfc:9.6) (rileyfc:1.7.1) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) b0778 b0778 Escherichia coli 562 -11533395 7000688912 biod dethiobiotin synthase::dethiobiotin synthetase (cl:dethiobiotin synthase) (ec:6.3.3.3) (db:pir1.dat) (mp:18 min) SYECDB B64814 Escherichia coli 562 -11533395 7500953384 biod dethiobiotin synthetase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:6.3.3.3) (de:escherichia coli k-12 mg1655 section 70 of 400 of the completegenome.) (nt:o225; 100 pct identical to biod\_ecoli sw: p13000) (le:6419) (re:7096) (di:direct) AE000180 AE000180 g1786995 Escherichia coli 562 -11533395 5000690648 (de:(ecoli\_745) (pn:dethiobiotin synthetase) (gn:biod) (gtcfc:9.6) (ec:6.3.3.3) (biod\_ecoli) (keggfc:9.6) (rileyfc:1.7.1) (db:gtc-escherichia coli)) ECOLI\_745 ECOLI\_745 Escherichia coli 562 10122990

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830706	8407	30563	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830712	8408	30564	420	139
<u>Description</u>				
6500729538 fola:tmra:b0048 dihydrofolate reductase type i (gtcfc:10.7:9.6) (ec:1.5.1.3) (keggfc:9.7:9.8) (rileyfc:1.7.2) (db:gtc-escherichia coli) (gtcfc:metabolism of macromolecules-protein translation and modification:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) b0048 b0048 Escherichia coli 562 -11533396 69424 fola:tmra (ec:1.5.1.3) (de:dihydrofolate reductase,) (db:swissprot) DYR_ECOLI P00379 ESCHERICHIA COLI 562 -11533396 122751 fola dihydrofolate reductase:type i:tetrahydrofolate dehydrogenase (cl:type i dihydrofolate reductase:type i dihydrofolate reductase homology) (ec:1.5.1.3) (db:pir1.dat) (mp:1 min) RDECD A93704 Escherichia coli 562 -11533396 234385 fola dehydrofolate reductase:type i (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (ec:1.5.1.3) (de:e.coli k12 genome, 0-2.4min. region.) (le:49482) (re:49961) (di:direct) ECO110K D10483 g216473 Escherichia coli 562 -11533396 7500880745 fola dihydrofolate reductase (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli dihydrofolate reductase (fola) gene, complete cds.) (le:558) (re:1037) (di:direct) ECOFOLA J01609 g146006 Escherichia coli 562 -11533396 233583 fola dihydrofolate reductase type i:trimethoprim (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:1.5.1.3) (de:escherichia coli k-12 mg1655 section 5 of 400 of the completegenome.) (nt:o159; 100 pct identical to dyra_ecoli sw: p00379) (le:2661) (re:3140) (di:direct) AE000115 AE000115 g1786233 Escherichia coli 562 -11533396 5000690649 (de:(ecoli_48) (pn:dihydrofolate reductase; trimethoprim resistance) (gn:fola) (gtcfc:9.6) (ec:1.5.1.3) (dyra_ecoli) (keggfc:9.7:9.8) (rileyfc:1.7.2) (db:gtc-escherichia coli)) ECOLI_48 ECOLI_48 Escherichia coli 562 10012006				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830713	8409	30565	450	149
<u>Description</u>				
GTC ORF with score 248 to: (fn:golgi retention and vacuolar protein sorting) (sr:baker's yeast) (db:genpept-pln1) (de:saccharomyces cerevisiae vps5p (vps5) gene, complete cds.) (nt:sorting nexin family member; grd2p) (le:290) (re:2317) (di:direct)				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501830714	8410	30566	504	167

#### Description

6500729539 folk:b0142 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine  
 pyrophosphokinase:2-amino-4-hydroxy-6-hydroxymethyldihydropteridine  
 pyrophosphokinase:7:8-dihydro-6-hydroxymethylpterin-pyrophosphokinase:hppk:6  
 -hydroxymethyl-7:8-dihydropterin pyrophosphokinase:pppk (gtcfc:9.6)  
 (ec:2.7.6.3) (keggfc:9.7) (rileyfc:1.7.2) (db:gtc-escherichia coli)  
 (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and  
 folate biosynthesis) b0142 b0142 Escherichia coli 562 -11533397 139049 folk  
 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine  
 pyrophosphokinase::6-hydroxymethyl-7:8-dihydropterin  
 pyrophosphokinase:7:8-dihydro-6-hydroxymethylpterin-pyrophosphokinase  
 (cl:2-amino-4-hydroxy-6-hydroxymethyldihydropteridine  
 pyrophosphokinase:2-amino-4-hydroxy-6-hydroxymethyldihydropteridine  
 pyrophosphokinase homology) (ec:2.7.6.3) (db:pir2.dat) (mp:4 min) A43325  
 A43325 Escherichia coli 562 -11533397 234389 folk  
 7:8-dihydro-6-hydroxymethylpterin-pyrophosphoki (sr:escherichia coli  
 (sub\_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1)  
 (ec:2.3.1.15) (de:escherichia coli genome, 2.4-4.1 min region  
 (110,917-193,643 bpfrom 0 min).) (le:45850) (re:46329) (di:complement)  
 EC082K D26562 g473801 Escherichia coli 562 -11533397 301612 folk  
 hydroxymethyldihydropterin pyrophosphokinase (db:genpept-bct1) (ec:2.7.6.3)  
 (de:escherichia coli hydroxymethylpterin pyrophosphokinase (folk)  
 gene,complete cds.) (le:133) (re:612) (di:direct) ECOFOLK L06495 g146013  
 Escherichia coli 562 -11533397 233674 folk  
 7:8-dihydro-6-hydroxymethylpterin- (fn:enzyme; biosynthesis of cofactors,  
 carriers:) (db:genpept-bct2) (ec:2.7.6.3) (de:escherichia coli k-12 mg1655  
 section 13 of 400 of the completegenome.) (nt:f159; 100 pct identical to  
 hppk\_ecoli sw: p26281) (le:7625) (re:8104) (di:complement) AE000123 AE000123  
 g1786335 Escherichia coli 562 -11533397 5000690651 (de:(ecoli\_142)  
 (pn:7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase) (gn:folk)  
 (gtcfc:9.6) (ec:2.7.6.3) (hppk\_ecoli) (keggfc:9.7) (rileyfc:1.7.2)  
 (db:gtc-escherichia coli)) ECOLI\_142 ECOLI\_142 Escherichia coli 562 10071055

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501830739	8411	30567	192	63

#### Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501830742	8412	30568	207	68

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830743	8413	30569	1248	415

Description

GTC ORF with score 157 to: (or:Ustilago maydis) (sr:smut fungus)  
(db:genpept-pln1) (de:ustilago maydis exodeoxyribonuclease (rec1) gene,  
complete cds.) (nt:continuous orf 810..2378; c-terminal region removed)  
(le:810:2351) (re:2165:2386) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830744	8414	30570	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830764	8415	30571	198	65

Description

Hypothetical protein



ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501830766	8416	30572	198	65

# Description

6500729540 nfnb:nfsi:nfsb:ntr:dpra:b0578 ph  
nitroreductase:oxygen-insensitive nadph nitroreductase / dihydropteridine  
reductase (gtcfc:9.6:13.3) (keggfc:9.7) (rileyfc:5.4.0) (db:gtc-escherichia  
coli) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and  
folate biosynthesis:drug--analog sensitivity) b0578 b0578 Escherichia coli  
562 -11533398 85725 nfnb:nfsi:nfsb:ntr:dpra (ec:1.-.-.:1.6.99.7)  
(de:dihydropteridine reductase,) (db:swissprot) NFNB\_ECOLI P38489  
ESCHERICHIA COLI 562 -11533398 164224 nfnb:nfsb  
nitroreductase:ib1:oxygen-insensitive nad p h nitroreductase  
(cl:nitroreductase) (ec:1.6.6.-) (db:pir2.dat) I67685 I67685 Escherichia  
coli 562 -11533398 223103 nfnb oxygen-insensitive nad p h nitroreductase  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #163)  
(db:genpept-bct1) (de:escherichia coli genomic dna. (12.7 - 13.2 min).)  
(le:10109) (re:10762) (di:complement) D90700 D90700 g1651240 Escherichia  
coli 562 -11533398 4000707218 nfsb/nfnb oxygen-insensitive nad p h  
nitroreductase (fn:reduction of nitroaromatic compounds) (sr:escherichia  
coli (sub\_strain c600, strain k-12) (library: y.kohara) (db:genpept-bct1)  
(de:escherichia coli dna for oxygen-insensitive nad(p)h  
nitroreductase,complete cds.) (le:202) (re:855) (di:direct) ECONR D25414  
g538227 Escherichia coli 562 -11533398 240089 nfnb oxygen-insensitive nad p  
h nitroreductase (db:genpept-bct1) (de:escherichia coli genomic sequence of  
minutes 9 to 12.) (le:45402) (re:46055) (di:complement) ECU82598 U82598  
g1778493 Escherichia coli 562 -11533398 235246 nfnb oxygen-insensitive nad  
p h nitroreductase (fn:enzyme; drug/analog sensitivity) (db:genpept-bct2)  
(ec:1.-.-.-) (de:escherichia coli k-12 mg1655 section 53 of 400 of the  
completegenome.) (nt:f217; 100 pct identical to nfnb\_ecoli sw: p38489;)  
(le:1426) (re:2079) (di:complement) AE000163 AE000163 g1786792 Escherichia  
coli 562 -11533398 325739 nfnb nitroreductase (fn:reduction of mutagenic  
nitroarenes) (db:genpept-bct2) (de:escherichia coli nitroreductase (nfnb)  
gene, complete cds.) (le:176) (re:829) (di:direct) ECU07860 U07860 g533421  
Escherichia coli 562 -11533398 5000691318 nitroreductase (db:genpept-pat)  
(de:nitroreductase gene.) (le:176) (re:829) (di:direct) A23284 A23284  
g809616 Escherichia coli 562 -11533398 7502851926 (db:genpept-pat)  
(de:sequence 1 from patent wo9512678.) (nt:unnamed protein product) (le:176)  
(re:829) (di:direct) A44585 A44585 g2299369 Escherichia coli 562 -11533398  
7502851927 (db:genpept-pat) (de:sequence 1 from patent wo9614420.)  
(nt:unnamed protein product) (le:176) (re:829) (di:direct) A50868 A50868  
g2303708 Escherichia coli 562 -11533398 7502851928 nfnb oxygen-insensitive  
nad p h nitroreductase ec (sr:escherichia coli(strain:k12) dna, clone:kohara  
clone #163) (db:genpept) (de:escherichia coli genomic dna. (12.8 - 13.2  
min).) (nt:orf\_id:ol63#8; similar to swissprot accession) (le:10109)  
(re:10762) (di:complement) D90700 D90700 g1651240 Escherichia coli 562  
-11533398 238532 nfsb/nfnb oxygen-insensitive nad p h nitroreductase  
(fn:reduction of nitroaromatic compounds) (sr:escherichia coli (sub\_strain  
c600, strain k-12) (library: y.kohara) (db:genpept-bct1) (de:escherichia  
coli dna for oxygen-insensitive nad(p)h nitroreductase,complete cds.)

coli dna for oxygen-insensitive nad(p)h nitroreductase, complete cds.)

(le:202) (re:855) (di:direct) ECONF D25414 g538227 Escherichia coli 562

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501830767	8417	30573	645	214

#### Description

6500729541 held:b0962 helicase iv:75 kd helicase (gtcfc:9.6:10.8)  
(ec:3.6.1.-) (keggfc:9.7) (rileyfc:3.1.7) (db:gtc-escherichia coli)  
(gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and  
folate biosynthesis:metabolism of macromolecules-dna  
replication--recombination/repair) b0962 b0962 Escherichia coli 562  
-11533399 76431 held (ec:3.6.1.-) (de:helicase iv, (75 kd helicase))  
(db:swissprot) HELD\_ECOLI P15038 ESCHERICHIA COLI 562 -11533399 7000685502  
held helicase:iv:75k helicase (cl:helicase iv) (ec:3.6.1.-) (db:pir1.dat)  
(mp:22 min) HJECD4 A64837 Escherichia coli 562 -11533399 223303 held  
helicase iv (sr:escherichia coli(strain:k12) dna, clone:kohara clone #223)  
(db:genpept-bct1) (de:escherichia coli genomic dna. (21.9 - 22.2 min).)  
(le:5994) (re:8048) (di:direct) D90734 D90734 g1651471 Escherichia coli 562  
-11533399 7500883126 held dna helicase iv (fn:enzyme; dna - replication,  
repair,) (db:genpept-bct2) (ec:3.6.1.-) (de:escherichia coli k-12 mg1655  
section 88 of 400 of the completegenome.) (nt:o684; 98 pct identical to  
held\_ecoli sw: p15038) (le:6109) (re:8163) (di:direct) AE000198 AE000198  
g1787196 Escherichia coli 562 -11533399 5000690652 held helicase ec 3.6.1.-  
iv. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #223)  
(db:genpept) (de:escherichia coli genomic dna. (22.0 - 22.3 min).)  
(nt:orf\_id:o223#7; similar to pir accession number) (le:5994) (re:8048)  
(di:direct) D90734 D90734 g1651471 Escherichia coli 562 -11533399

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501830769	8418	30574	252	83

#### Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501830772	8419	30575	258	85

#### Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501830782	8420	30576	282	93

# Description

6500729542 lhr:rhlf:b1653 probable atp-dependent helicase lhr:large  
helicase-related protein (gtcfc:9.6:14.3) (ec:3.6.1.-) (keggfc:9.7)  
(rileyfc:5.8.0) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and  
vitamins-biotin metabolism (b8) and folate  
biosynthesis:unknown-unclassified) b1653 b1653 Escherichia coli 562  
-11533400 82078 lhr:rhlf (ec:3.6.1.-) (de:related protein)) (db:swissprot)  
LHR\_ECOLI P30015 ESCHERICHIA COLI 562 -11533400 7000685749 lhr probable  
atp-dependent helicase lhr (cl:dead/h box helicase homology) (ec:3.6.1.-)  
(db:pir2.dat) G64922 G64922 Escherichia coli 562 -11533400 224097 lhr:rhlf  
probable atp-dependent helicase lhr ec 3.6.1.- (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #318(37.2-37.6 min.).)  
(nt:orf\_id:o317#9; similar to (swissprot accession) (le:679) (re:5295)  
(di:direct) D90809 D90809 g1742726 Escherichia coli 562 -11533400 235859  
lhr member of atp-dependent helicase superfamily ii (fn:enzyme; dna -  
replication, repair,) (db:genpept-bct2) (ec:3.6.1.-) (de:escherichia coli  
k-12 mg1655 section 150 of 400 of the completegenome.) (nt:o1538; 100 pct  
identical to lhr\_ecoli sw: p30015;) (le:4422) (re:9038) (di:direct) AE000260  
AE000260 g1787942 Escherichia coli 562 -11533400 7500885011 lhr rna  
helicase-like protein (sr:escherichia coli (strain k-12) dna)  
(db:genpept-bct2) (de:e. coli rnaset (rnt) gene, long helicase-related (lhr)  
gene,complete cds, and glutaredoxin-like (yhdd) gene, 3' end.) (le:933)  
(re:5549) (di:direct) ECORNTLHR L01622 g993028 Escherichia coli 562  
-11533400 5000690653 (de:(ecoli\_1612) (pn:large helicase-related protein;  
probable atp-dependent helicase) (gn:lhr) (gtcfc:9.6) (ec:3.6.1.-)  
(lhr\_ecoli) (keggfc:9.7) (rileyfc:5.7.0) (db:gtc-escherichia coli))  
ECOLI\_1612 ECOLI\_1612 Escherichia coli 562 10024312

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830783	8421	30577	1065	354

Description

6500729543 ntpa:b1865 datp pyrophosphohydrolase (gtcfc:9.6:14.3)  
(ec:3.6.1.-) (keggfc:9.7) (rileyfc:5.8.0) (db:gtc-escherichia coli)  
(gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and  
folate biosynthesis:unknown-unclassified) b1865 b1865 Escherichia coli 562  
-11533401 235945 ntpa (ec:3.6.1.-) (de:datp pyrophosphohydrolase,)  
(db:swissprot) NTPA\_ECOLI P24236 ESCHERICHIA COLI 562 -11533401 162594 ntpa  
datp pyrophosphohydrolase::17k hypothetical protein asps 3 region (cl:mutt  
domain homology) (ec:3.6.1.-) (db:pir2.dat) B38113 B38113 Escherichia coli  
562 -11533401 224359 ntpa datp pyrophosphohydrolase ec 3.6.1.-  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #337(41.9-42.3  
min.)) (nt:orf\_id:o337#6; similar to (swissprot accession) (le:4982)  
(re:5434) (di:complement) D90829 D90829 g1736512 Escherichia coli 562  
-11533401 5000690654 orf150 (db:genpept-bct1) (de:e.coli orf150, orf246,  
orf11 and ruvc gene for resolvase of holliday junction intermediates.)  
(nt:alternative) (le:18) (re:470) (di:direct) ECORFRUFC X59551 g581152  
Escherichia coli 562 -11533401 300999 orf17 (sr:escherichia coli  
(strain:k-12) dna) (db:genpept-bct1) (de:e. coli dna for orf17, orf26, ruvc  
and orf23 genes.) (le:511) (re:963) (di:direct) ECORUVC D10165 g912430  
Escherichia coli 562 -11533401 235773 ntpa datp pyrophosphohydrolase  
(fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (ec:3.6.1.-)  
(de:escherichia coli k-12 mg1655 section 170 of 400 of the complete genome.)  
(nt:f150; 100 pct identical to ntpa\_ecoli sw: p24236;) (le:6599) (re:7051)  
(di:complement) AE000280 AE000280 g1788172 Escherichia coli 562 -11533401  
86614 ntpa (ec:3.6.1.-) (de:datp pyrophosphohydrolase,) (db:swissprot)  
NTPA\_ECOLI P24236 ESCHERICHIA COLI 562 -11533401

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501830789	8422	30578	1077	358

#### Description

6500729544 fole:b2153 gtp cyclohydrolase i:gtp-ch-i (gtcfc:9.6)  
(ec:3.5.4.16) (keggfc:9.7) (rileyfc:1.7.2) (db:gtc-escherichia coli)  
(gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and  
folate biosynthesis) b2153 b2153 Escherichia coli 562 -11533402 7000690902  
fole gtp cyclohydrolase i (cl:gtp cyclohydrolase i) (ec:3.5.4.16)  
(db:pir2.dat) H64983 H64983 Escherichia coli 562 -11533402 234760 fole gtp  
cyclohydrolase i (db:genpept-bct1) (ec:3.5.4.16) (de:e.coli fole gene for  
gtp cyclohydrolase i.) (le:232) (re:900) (di:direct) ECFOLE X63910 g312964  
Escherichia coli 562 -11533402 7500959759 gtp cyclohydrolase i  
(sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome  
region of e.coli k12 bhb2600.) (nt:gtp cyclohydrolase i.) (le:50729)  
(re:51397) (di:complement) ECOHU47 U00007 g405902 Escherichia coli 562  
-11533402 232908 fole gtp cyclohydrolase i (fn:enzyme; biosynthesis of  
cofactors, carriers:) (db:genpept-bct2) (ec:3.5.4.16) (de:escherichia coli  
k-12 mg1655 section 194 of 400 of the completegenome.) (nt:f222; 100 pct  
identical to gch1\_ecoli sw: p27511) (le:6393) (re:7061) (di:complement)  
AE000304 AE000304 g1788476 Escherichia coli 562 -11533402 5000690655  
(de:(ecoli\_2102) (pn:gtp cyclohydrolase i) (gn:fole) (gtcfc:9.6)  
(ec:3.5.4.16) (gch1\_ecoli) (keggfc:9.7) (rileyfc:1.7.2) (db:gtc-escherichia  
coli)) ECOLI\_2102 ECOLI\_2102 Escherichia coli 562 10123586

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501830798	8423	30579	228	75

#### Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501830800	8424	30580	498	165

#### Description

6500729545 folc:dedc:b2315 folylpolyglutamate synthase:folylpoly-gamma-glutamate synthetase:fpgs / dihydrofolate synthase (gtcfc:9.6:5.1) (keggfc:9.7) (rileyfc:1.7.2) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:l-amino acid metabolism-glutamate metabolism) b2315 b2315 Escherichia coli 562 -11533403 72231 folc:dedc (ec:6.3.2.17:6.3.2.12) (de:synthetase) (fpgs) / dihydrofolate synthase,) (db:swissprot) FOLC\_ECOLI P08192 ESCHERICHIA COLI 562 -11533403 7000685315 folc:dedc tetrahydrofolylpolyglutamate synthase:dihydrofolate synthase (cl:folylpolyglutamate synthase) (ec:6.3.2.17:6.3.2.12) (db:pir1.dat) (mp:50 min) SYECFG A65004 Escherichia coli 562 -11533403 224851 dedc folylpolyglutamate synthase ec 6.3.2.17 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #406(52.2-52.5 min.)) (nt:similar to (swissprot accession number p08192)) (le:15251) (re:16519) (di:complement) D90862 D90862 g1799699 Escherichia coli 562 -11533403 224859 dedc folylpolyglutamate synthase ec 6.3.2.17 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #407(52.4-52.8 min.)) (nt:similar to (swissprot accession number p08192)) (le:2316) (re:3584) (di:complement) D90863 D90863 g1799708 Escherichia coli 562 -11533403 7500881706 folc dihydrofolate:folylpolyglutamate synthetase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:6.3.2.17) (de:escherichia coli k-12 mg1655 section 210 of 400 of the completegenome.) (nt:f422; 99 pct identical to folc\_ecoli sw: p08192) (le:5743) (re:7011) (di:complement) AE000320 AE000320 g1788654 Escherichia coli 562 -11533403 5000690656 (de:(ecoli\_2264) (pn:dihydrofolate:folylpolyglutamate synthetase ; dihydrofolate synthetase:dihydrofolate, folylpolyglutamate synthetase ; dihydrofolate synthetase) (gn:folc) (gtcfc:9.6) (ec:6.3.2.17) (folc\_ecoli) (keggfc:9.7) ( ECOLI\_2264 ECOLI\_2264 Escherichia coli 562 10120113

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501830808	8425	30581	264	87

#### Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501830819	8426	30582	204	67

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830823	8427	30583	507	168

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830825	8428	30584	315	104

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830830	8429	30585	219	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830837	8430	30586	246	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830845	8431	30587	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830847	8432	30588	342	114

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830849	8433	30589	735	244

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830867	8434	30590	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830868	8435	30591	525	174

Description

6500729546 folp:b3177 dihydropteroate synthase (gtcfc:9.6) (ec:2.5.1.15) (keggfc:9.7) (rileyfc:1.7.2) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) b3177 b3177 Escherichia coli 562 -11533404 7500974865 folp dihydropteroate synthase (db:genpept-bct1) (ec:2.5.1.15) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 29566; alternate name dhps; gtg start) (le:104815) (re:105708) (di:complement) ECOUW67 U18997 g606115 Escherichia coli 562 -11533404 236414 folp 7:8-dihydropteroate synthase (fn:enzyme; biosynthesis of cofactors, carriers;) (db:genpept-bct2) (ec:2.5.1.15) (de:escherichia coli k-12 mg1655 section 288 of 400 of the completegenome.) (nt:f297; cg site no. 29566; alternate name dhps;) (le:5924) (re:6817) (di:complement) AE000398 AE000398 g1789567 Escherichia coli 562 -11533404 5000690658 (de:(ecoli\_3099) (pn:7,8-dihydropteroate synthase) (gn:folp) (gtcfc:9.6) (ec:2.5.1.15) (dhps\_ecoli) (keggfc:9.7) (rileyfc:1.7.2) (db:gtc-escherichia coli)) ECOLI\_3099 ECOLI\_3099 Escherichia coli 562 10123988



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830902	8436	30592	480	159

Description

6500729547 yhhob3469 hypothetical protein:probable cation-transporting  
atpase yhhob (gtcfc:12.5:9.6) (ec:3.6.1.-) (keggfc:9.7) (rileyfc:5.7.0)  
(db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations  
(na\_k\_ca\_nh4\_etc\_):metabolism of cofactors and vitamins-biotin metabolism  
(b8) and folate biosynthesis) b3469 b3469 Escherichia coli 562 -11533405  
112828 znta (ec:3.6.1.-) (de:atpase)) (db:swissprot) ATZN\_ECOLI P37617  
ESCHERICHIA COLI 562 -11533405 163868 hypothetical protein  
o732: hypothetical protein b3469 (cl:atpase nucleotide-binding domain  
homology) (db:pir2.dat) S47688 S47688 Escherichia coli 562 -11533405  
7500877609 (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library:  
lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5  
minutes.) (le:20713) (re:22911) (di:direct) ECOUW76 U00039 g466605  
Escherichia coli 562 -11533405 236704 znta zinc-transporting atpase  
(fn:transport; transport of small molecules:) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 312 of 400 of the completegenome.)  
(nt:o732) (le:8571) (re:10769) (di:direct) AE000422 AE000422 g1789879  
Escherichia coli 562 -11533405 5000690659 (de:(ecoli\_3387) (pn:probable  
cation-transporting atpase yhhob372) (gtcfc:9.6) (ec:3.6.1.-) (yhhob\_ecoli)  
(keggfc:9.7) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_3387  
ECOLI\_3387 Escherichia coli 562 10054556

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830908	8437	30593	612	203

Description

6500729548 recg:b3652 dna recombinase:atp-dependent dna helicase recg (gtcfc:9.6:10.8) (ec:3.6.1.-) (keggfc:9.7) (rileyfc:3.1.7) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of macromolecules-dna replication--recombination/repair) b3652 b3652 Escherichia coli 562 -11533406 7500889575 recg (ec:3.6.1.-) (de:atp-dependent dna helicase recg,) (db:swissprot) RECG\_ECOLI P24230 ESCHERICHIA COLI 562 -11533406 164458 recg dna recombinase::recg protein (cl:dna helicase recg:dead/h box helicase homology) (ec:3.6.1.-) (db:pir2.dat) (mp:82 min) JH0265 JH0265 Escherichia coli 562 -11533406 238024 recg dna recombinase (sr:escherichia coli (library: lambda 447) dna) (db:genpept-bct1) (de:escherichia coli dna recombinase (recg) gene, complete cds, spougene, 3' end, and glts gene, 3' end.) (nt:atp-binding motif aa295-303 (position 901-927)) (le:19) (re:2100) (di:direct) ECORECG M64367 g147545 Escherichia coli 562 -11533406 7502851929 recg (db:genpept-bct1) (de:e.coli recg dna.) (le:428) (re:2509) (di:direct) ECRCG X59550 g42669 Escherichia coli 562 -11533406 235727 recg dna helicase:resolution of holliday junctions (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:3.6.1.-) (de:escherichia coli k-12 mg1655 section 332 of 400 of the completegenome.) (nt:o693; 99 pct identical amino acid sequence and) (le:6601) (re:8682) (di:direct) AE000442 AE000442 g2367254 Escherichia coli 562 -11533406 93809 recg (ec:3.6.1.-) (de:atp-dependent dna helicase recg,) (db:swissprot) RECG\_ECOLI P24230 ESCHERICHIA COLI 562 -11533406

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830926	8438	30594	483	160

Description

GTC ORF with score 330 to: (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to cytochrome p450 / nadph-cytochrome p450) (le:173710) (re:176874) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501830927	8439	30595	945	315

Description

GTC ORF with score 587 to: (or:Bacillus subtilis) (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:alternate gene name: yfnj; similar to cytochrome) (le:191490) (re:194675) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830928	8440	30596	279	92

Description

GTC ORF with score 187 to: (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to cytochrome p450 / nadph-cytochrome p450) (le:173710) (re:176874) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830945	8441	30597	234	77

Description

6500729549 rep:b3778 atp-dependent dna helicase rep (gtcfc:9.6:10.8) (ec:3.6.1.-) (keggfc:9.7) (rileyfc:3.1.7) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of macromolecules-dna replication--recombination/repair) b3778 b3778 Escherichia coli 562 -11533407 93972 rep (ec:3.6.1.-) (de:atp-dependent dna helicase rep,) (db:swissprot) REP\_ECOLI P09980 ESCHERICHIA COLI 562 -11533407 7000686297 rep atp-dependent dna helicase rep (cl:helicase ii) (ec:3.6.1.-) (db:pir1.dat) (mp:85 min) HJECDR E65181 Escherichia coli 562 -11533407 7500889637 rep::cgsc no. 303 rep helicase (db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (le:13805) (re:15826) (di:direct) ECOUW85 M87049 g148182 Escherichia coli 562 -11533407 237007 rep rep helicase:a single-stranded dna dependent (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:3.6.1.-) (de:escherichia coli k-12 mg1655 section 344 of 400 of the completegenome.) (nt:o673; 100 pct identical to rep\_ecoli sw: p09980) (le:2762) (re:4783) (di:direct) AE000454 AE000454 g1790212 Escherichia coli 562 -11533407 5000690661 (de:(ecoli\_3688) (pn:helicase, a single-stranded dna dependent atpase) (gn:rep) (gtcfc:9.6) (ec:3.6.1.-) (rep\_ecoli) (keggfc:9.7) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_3688 ECOLI\_3688 Escherichia coli 562 10035956

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830951	8442	30598	1098	365

Description

6500729550 uvrD:mutu:pdeb:rad:recl:b3813 dna helicase ii (gtcfc:9.6:10.8) (ec:3.6.1.-) (keggfc:9.7) (rileyfc:3.1.7) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of macromolecules-dna replication--recombination/repair) b3813 b3813 Escherichia coli 562 -11533408 7500893923 uvrD:mutu:pdeb:rad:recl (ec:3.6.1.-) (de:dna helicase ii,) (db:swissprot) UVRD\_ECOLI P03018 ESCHERICHIA COLI 562 -11533408 7000686915 uvrD dna helicase ii (cl:helicase ii) (ec:3.6.1.-) (db:pir1.dat) (mp:86 min) HJEC2 F65185 Escherichia coli 562 -11533408 240375 uvrD dna-dependent atpase i and helicase ii (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:3.6.1.-) (de:escherichia coli k-12 mg1655 section 347 of 400 of the completegenome.) (nt:o720; 100 pct identical to uvrD\_ecoli sw: p03018) (le:3615) (re:5777) (di:direct) AE000457 AE000457 g2367296 Escherichia coli 562 -11533408 7502851930 (db:genpept-bct2) (de:escherichia coli uvrD gene for helicase ii.) (nt:helicase ii) (le:430) (re:2592) (di:direct) ECUVRD02 X04037 g43299 Escherichia coli 562 -11533408 104052 uvrD:mutu:pdeb:rad:recl (ec:3.6.1.-) (de:dna helicase ii,) (db:swissprot) UVRD\_ECOLI P03018 ESCHERICHIA COLI 562 -11533408

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830981	8443	30599	378	125

Description

6500729551 recQ:b3822 dna-dependent atpase:dna helicase:atp-dependent dna helicase recQ (gtcfc:9.6:10.8) (ec:3.6.1.-) (keggfc:9.7) (rileyfc:3.1.7) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of macromolecules-dna replication--recombination/repair) b3822 b3822 Escherichia coli 562 -11533409 7000688983 recQ dna helicase recQ:dna-dependent atpase recQ (cl:recQ protein:dead/h box helicase homology:recQ helicase homology) (ec:3.6.1.-) (db:pir1.dat) (mp:85 min) BVECRQ G65186 Escherichia coli 562 -11533409 7500953322 recQ atp-dependent dna helicase (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:3.6.1.-) (de:escherichia coli k-12 mg1655 section 348 of 400 of the completegenome.) (nt:o610; 99 pct identical to 607 amino acids) (le:1077) (re:2909) (di:direct) AE000458 AE000458 g2367301 Escherichia coli 562 -11533409

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830983	8444	30600	501	166

Description

GTC ORF with score 268 to: (fn:hydrolysis of beta-1,2-glucose residue from) (sr:tomato leaf spot fungus) (db:genpept-pln1) (ec:3.2.1.21) (de:septoria lycopersici beta-1,2-d-glucosidase (b2tom) gene, completecds.) (nt:involved in the detoxification of ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830984	8445	30601	198	65

Description

GTC ORF with score 90 to: (fn:hydrolysis of beta-1,2-glucose residue from) (sr:tomato leaf spot fungus) (db:genpept-pln1) (ec:3.2.1.21) (de:septoria lycopersici beta-1,2-d-glucosidase (b2tom) gene, completecds.) (nt:involved in the detoxification of ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830986	8446	30602	225	74

Description

6500729552 dnab:grop:grpa:b4052 replicative dna helicase (gtcfc:9.6:10.8) (ec:3.6.1.-) (keggfc:9.7) (rileyfc:3.1.7) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of macromolecules-dna replication--recombination/repair) b4052 b4052 Escherichia coli 562 -11533410 68853 dnab:grop:grpa (ec:3.6.1.-) (de:replicative dna helicase,) (db:swissprot) DNAB\_ECOLI P03005 ESCHERICHIA COLI 562 -11533410 7000685070 dnab replicative dna helicase:dnab:helicase (cl:phage p22 gene 12 protein) (ec:3.6.1.-) (db:pir1.dat) (mp:92 min) IQECDB C65213 Escherichia coli 562 -11533410 237258 (sr:escherichia coli (strain yslreca) dna, clone pkal) (db:genpept-bct1) (de:e.coli dnab gene coding for a replication protein.) (nt:dnab replication protein (dnab)) (le:121) (re:1536) (di:direct) ECODNAB K01174 g145763 Escherichia coli 562 -11533410 234181 dnab replicative dna helicase:part of primosome (fn:factor; dna - replication, repair,) (db:genpept-bct2) (ec:3.6.1.-) (de:escherichia coli k-12 mg1655 section 368 of 400 of the completegenome.) (nt:o471; 100 pct identical to dnab\_ecoli sw: p03005;) (le:5153) (re:6568) (di:direct) AE000478 AE000478 g1790486 Escherichia coli 562 -11533410 7500880403 dnab (fn:replication protein) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 850) (le:129558) (re:130973) (di:direct) ECOUW89 U00006 g396387 Escherichia coli 562 -11533410 5000690664 (de:(ecoli\_3938) (pn:chromosome replication; chain elongation; part of primosome) (gn:dnab) (gtcfc:9.6) (ec:3.6.1.-) (dnab\_ecoli) (keggfc:9.7) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_3938 ECOLI\_3938 Escherichia coli 562 10011438

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830987	8447	30603	249	82

Description

GTC ORF with score 131 to: (fn:hydrolysis of beta-1,2-glucose residue from) (sr:tomato leaf spot fungus) (db:genpept-pln1) (ec:3.2.1.21) (de:septoria lycopersici beta-1,2-d-glucosidase (b2tom) gene, completecds.) (nt:involved in the detoxification of ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501830989	8448	30604	345	114

Description

GTC ORF with score 173 to: (fn:hydrolysis of beta-1,2-glucose residue from) (sr:tomato leaf spot fungus) (db:genpept-pln1) (ec:3.2.1.21) (de:septoria lycopersici beta-1,2-d-glucosidase (b2tom) gene, completecds.) (nt:involved in the detoxification of ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831002	8449	30605	858	285

Description

GTC ORF with score 193 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome ii cosmid c21h7.) (nt:spbc21h7.05, len:582aa, similarity: h. sapiens,) (le:10390:11375:11535:11786) (re:11332:11491:11738:12270) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831013	8450	30606	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831014	8451	30607	672	223

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831025	8452	30608	543	180

#### Description

6500729553 mgta:mgt:corb:b4242 mg2+ transport atpase:p-type 1  
 (gtcfc:12.5:9.6) (ec:3.6.1.-) (keggfc:9.7) (rileyfc:4.1.2)  
 (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations  
 (na\_k\_ca\_nh4\_etc\_):metabolism of cofactors and vitamins-biotin metabolism  
 (b8) and folate biosynthesis) b4242 b4242 Escherichia coli 562 -11533411  
 60552 mgta:mgt:corb (ec:3.6.1.-) (de:mg(2+) transport atpase, p-type 1,)  
 (db:swissprot) ATMA\_ECOLI P39168 ESCHERICHIA COLI 562 -11533411 7000684656  
 mgta mg 2+ transport atpase mgta:p-type 1 (cl:na+/k+-transporting atpase  
 alpha chain:atpase nucleotide-binding domain homology) (ec:3.6.1.-)  
 (db:pir2.dat) E65236 E65236 Escherichia coli 562 -11533411 7500877329 mgta  
 mg2+ transport atpase:p-type 1 (fn:enzyme; transport of small molecules:  
 cations) (db:genpept-bct2) (ec:3.6.1.-) (de:escherichia coli k-12 mg1655  
 section 385 of 400 of the completegenome.) (nt:o898; 100 pct identical to  
 atma\_ecoli sw:) (le:8267) (re:10963) (di:direct) AE000495 AE000495 g2367363  
 Escherichia coli 562 -11533411

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831036	8453	30609	1920	640

#### Description

6500729554 bioc:b0777 biotin synthesis protein bioc (gtcfc:9.6)  
 (keggfc:14.2) (rileyfc:1.7.1) (db:gtc-escherichia coli) (gtcfc:metabolism of  
 cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) b0777  
 b0777 Escherichia coli 562 -11533412 61727 bioc (de:biotin synthesis  
 protein bioc) (db:swissprot) BIOC\_ECOLI P12999 ESCHERICHIA COLI 562  
 -11533412 7000684708 bioc biotin biosynthesis protein bioc (cl:bioc  
 protein:bioc homology) (db:pir1.dat) (mp:17 min) BVECBC A64814 Escherichia  
 coli 562 -11533412 4000714807 bioc biotin biosynthesis:reaction prior to  
 pimeloyl (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2)  
 (de:escherichia coli k-12 mg1655 section 70 of 400 of the completegenome.)  
 (nt:o251; 100 pct identical to bioc\_ecoli sw: p12999) (le:5671) (re:6426)  
 (di:direct) AE000180 AE000180 g1786994 Escherichia coli 562 -11533412  
 5000690667 bioc (db:genpept-pat) (de:bioc gene of e.coli with primers.)  
 (le:24) (re:779) (di:direct) A11534 A11534 g490221 Escherichia coli 562  
 -11533412 7502851931 bioc protein (fn:involved in pimeloyl-coa synthesis)  
 (db:genpept-pat) (de:sequence 1 from patent wo9408023.) (le:2295) (re:3050)  
 (di:direct) A38246 A38246 g2294846 Escherichia coli 562 -11533412 325119  
 bioc biotin synthesis protein bioc (db:genpept-bct1) (de:escherichia coli  
 k-12 mg1655 section 70 of 400 of the completegenome.) (nt:o251; 100 pct  
 identical to bioc\_ecoli sw: p12999) (le:5671) (re:6426) (di:direct)  
 EC AE000180 AE000180 g1786994 Escherichia coli 562 -11533412

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831058	8454	30610	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831059	8455	30611	858	286

Description

6500729555 bioh:biob:b3412 bioh:bioh protein (gtcfc:9.6) (keggfc:14.2) (rileyfc:1.7.1) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) b3412 b3412 Escherichia coli 562 -11533413 236646 bioh:biob (de:bioh protein) (db:swissprot) BIOH\_ECOLI P13001 ESCHERICHIA COLI 562 -11533413 131324 bioh bioh protein (cl:bioh protein) (db:pir1.dat) (mp:75 min) BVECBH JQ0081 Escherichia coli 562 -11533413 5000690668 (db:genpept-bct1) (de:escherichia coli bioh gene.) (nt:bioh protein (aa 1-256)) (le:76) (re:846) (di:direct) ECBIOH X15587 g41068 Escherichia coli 562 -11533413 7500877837 bioh (fn:biotin synthesis, block prior to pimeloyl coa) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 954; alternate name biob) (le:324817) (re:325587) (di:complement) ECOUW67 U18997 g606347 Escherichia coli 562 -11533413 232466 bioh biotin biosynthesis:reaction prior to pimeloyl (fn:putative enzyme; biosynthesis of cofactors,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 307 of 400 of the completegenome.) (nt:f256; cg site no. 954; alternate name biob; 100 pct) (le:1039) (re:1809) (di:complement) AE000417 AE000417 g1789817 Escherichia coli 562 -11533413 61743 bioh:biob (de:bioh protein) (db:swissprot) BIOH\_ECOLI P13001 ESCHERICHIA COLI 562 -11533413



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831066	8456	30612	1113	370

Description

6500729556 bisc:b3551 biotin sulfoxide reductase:biotin sulfoxide reductase  
1:bds reductase 1:bsr reductase 1 (gtcfc:9.6) (ec:1.-.-.-) (keggfc:14.1)  
(rileyfc:1.7.1) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and  
vitamins-biotin metabolism (b8) and folate biosynthesis) b3551 b3551  
Escherichia coli 562 -11533414 61756 bisc (ec:1.-.-.-) (de:reductase 1))  
(db:swissprot) BISC\_ECOLI P20099 ESCHERICHIA COLI 562 -11533414 162790 bisc  
biotin sulfoxide reductase:1 (cl:trimethylamine-n-oxide reductase)  
(ec:1.8.4.-) (db:pir2.dat) (mp:79 min) S47772 S47772 Escherichia coli 562  
-11533414 7500877842 bisc biotin sulfoxide reductase (sr:escherichia coli  
(sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e.  
coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 951; c  
term is different and some) (le:128313) (re:130532) (di:complement) ECOUW76  
U00039 g466689 Escherichia coli 562 -11533414 236788 bisc biotin sulfoxide  
reductase (fn:enzyme; biosynthesis of cofactors, carriers:)  
(db:genpept-bct2) (ec:1.-.-.-) (de:escherichia coli k-12 mg1655 section 322  
of 400 of the completegenome.) (nt:f739; 100 pct identical amino acid  
sequence and) (le:6300) (re:8519) (di:complement) AE000432 AE000432 g1789973  
Escherichia coli 562 -11533414 5000690669 (de:(ecoli\_3471) (pn:biotin  
sulfoxide reductase 1) (gn:bisc) (gtcfc:9.6) (ec:1.-.-.-) (bisc\_ecoli)  
(keggfc:11.1) (rileyfc:1.7.1) (db:gtc-escherichia coli)) ECOLI\_3471  
ECOLI\_3471 Escherichia coli 562 10004464

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831079	8457	30613	882	293

Description

6500729557 bira: bior: dhbb: b3973 bifunctional protein: biotin operon repressor and biotin-acetyl-coa carboxylase: bira bifunctional protein: biotin--protein ligase (gtcfc:9.6) (ec:6.3.4.15) (keggfc:14.1) (rileyfc:1.7.1) (db:gtc-escherichia coli) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) b3973 b3973 Escherichia coli 562 -11533415 61752 bira: bior: dhbb (ec:6.3.4.15) (de:coa-carboxylase) synthetase), (biotin--protein ligase)) (db:swissprot) BIRA\_ECOLI P06709 ESCHERICHIA COLI 562 -11533415 126043 bira bira bifunctional protein (cl:bira bifunctional protein) (db:pir1.dat) (mp:89 min) BVECBF B24029 Escherichia coli 562 -11533415 233918 bira bifunctional protein (sr:e.coli dna, clone pba11) (db:genpept-bct1) (de:e.coli bira gene coding for bira, a bifunctional protein with biotin operon-repressor and biotin-operon-synthetase activity.) (le:1326) (re:2291) (di:direct) ECOBIRA M10123 g145432 Escherichia coli 562 -11533415 237187 bira biotin-holoenzyme synthetase (sr:e.coli (strain bm2661 derivatives) dna) (db:genpept-bct1) (ec:6.3.4.15) (de:e.coli bira gene coding for bira protein, wt and mutant alleles.) (le:15) (re:980) (di:direct) ECOBIRAA M15820 g145434 Escherichia coli 562 -11533415 233917 bira biotin-acetylcoa carboxylase holoenzyme (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:6.3.4.15) (de:escherichia coli k-12 mg1655 section 361 of 400 of the complete genome.) (nt:o321; 100 pct identical to bira\_ecoli sw: p06709;) (le:9667) (re:10632) (di:di... AE000471 AE000471 g1790408 Escherichia coli 562 -11533415 7000684713 bira bifunctional protein: biotin operon repressor (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (ec:6.3.4.15) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 952; alternate gene name bior) (le:38324) (re:39289) (di:direct) ECOUW89 U00006 g396316 Escherichia coli 562 -11533415 7500877840 bira escherichia coli biotin-holoenzyme synthetase (db:genpept-syn) (de:cloning vector pbiotrx-bira, complete sequence.) (le:3154) (re:4119) (di:direct) AF044308 AF044308 g2852398 Cloning vector pBIOTRX-BirA 72145 -11533415 5000690670 (de:(ecoli\_3867) (pn:biotin-acetylcoa carboxylase holoenzyme synthetase, biotin operon repressor: biotin-acetylcoa carboxylase holoenzyme synthetase; biotin operon repressor) (gn:bira) (gtcfc:9.6) (ec:6.3.4.15) (bira\_ecoli) (keggf) ECOLI\_3867 ECOLI\_3867 Escherichia coli 562 10004460

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831084	8458	30614	531	176

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831085	8459	30615	438	145

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831088	8460	30616	390	129

Description

GTC ORF with score 112 to: (sr:plasmid ptrab4) (db:genpept-bct1)  
(de:agrobacterium vitis plasmid ptrab4 putative lysr-type protein(ttua),  
putative tartrate transport protein (ttub), putativetartrate dehydrogenase  
(ttuc), putative hydroxypyruvate ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831089	8461	30617	462	153

Description

6500729558 pabc:b1096 4-amino-4-deoxychorismate lyase:adc lyase (gtcfc:9.6)  
(ec:4.-.-.-) (keggfc:14.1) (rileyfc:1.7.2) (db:gtc-escherichia coli)  
(gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and  
folate biosynthesis) b1096 b1096 Escherichia coli 562 -11533416 88422 pabc  
(ec:4.-.-.-) (de:4-amino-4-deoxychorismate lyase, (adc lyase))  
(db:swissprot) PABC\_ECOLI P28305 ESCHERICHIA COLI 562 -11533416 162622 pabc  
4-amino-4-deoxychorismate lyase (ec:4.-.-.-) (db:pir2.dat) A42954 A42954  
Escherichia coli 562 -11533416 223360 pabc 4-amino-4-deoxychorismate lyase  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #236)  
(db:genpept-bct1) (de:escherichia coli genomic dna.(24.7 - 25.1 min).)  
(le:3943) (re:4752) (di:direct) D90745 D90745 g1651539 Escherichia coli 562  
-11533416 7500887591 pabc 4-amino-4-deoxychorismate lyase  
(fn:4-amino-4-deoxychorismate -- 4-aminobenzoate +) (sr:escherichia coli  
(sub\_strain w3110, strain k-12) (library: kohar) (db:genpept-bct1)  
(de:escherichia coli aminodeoxychorismate lyase (pabc) gene, completecds.)  
(nt:amino-terminal sequence -) (le:12... ECOPABC M93135 g147060 Escherichia  
coli 562 -11533416 235325 pabc 4-amino-4-deoxychorismate lyase (fn:enzyme;  
biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:4.-.-.-)  
(de:escherichia coli k-12 mgl655 section 100 of 400 of the completegenome.)  
(nt:o269; 100 pct identical to pabc\_ecoli sw: p28305) (le:4605) (re:5414)  
(di:direct) AE000210 AE000210 g1787338 Escherichia coli 562 -11533416  
5000690671 pabc 4-amino-4-deoxychorismate lyase. (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #236) (db:genpept) (de:escherichia  
coli genomic dna. (24.8 - 25.2 min).) (nt:orf\_id:o236#5; similar to pir  
accession number) (le:3943) (re:4752) (di:direct) D90745 D90745 g1651539  
Escherichia coli 562 -11533416

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831101	8462	30618	219	72

Description

6500729559 lipa:lip:b0628 lipoic acid synthetase:lip-syn (gtcfc:9.7)  
(keggfc:14.2) (rileyfc:1.7.3) (db:gtc-escherichia coli) b0628 b0628  
Escherichia coli 562 -11533417 82172 lipa:lip (de:lipoic acid synthetase  
(lip-syn) (lipoate synthase)) (db:swissprot) LIPA\_ECOLI P25845 ESCHERICHIA  
COLI 562 -11533417 7000685752 lipa:lip lipoic acid synthase (cl:lipoic acid  
synthase) (ec:2.8.1.-) (db:pir2.dat) (mp:15 min) B64797 B64797 Escherichia  
coli 562 -11533417 223117 lipa lipoic acid synthetase (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #168) (db:genpept-bct1)  
(de:escherichia coli genomic dna. (13.9 - 14.3 min).) (le:10314) (re:11279)  
(di:complement) D90703 D90703 g1651257 Escherichia coli 562 -11533417  
7500885025 lipa lipoic acid synthetase (db:genpept-bct1) (de:escherichia  
coli genomic sequence of minutes 9 to 12.) (le:99881) (re:100846)  
(di:complement) ECU82598 U82598 g1778545 Escherichia coli 562 -11533417  
240141 lipa lipoate synthesis:sulfur insertion? (fn:putative enzyme;  
biosynthesis of cofactors,) (db:genpept-bct2) (de:escherichia coli k-12  
mg1655 section 57 of 400 of the completengenome.) (nt:f321; 99 pct identical  
to lipa\_ecoli sw: p25845) (le:7192) (re:8157) (di:complement) AE000167  
AE000167 g1786846 Escherichia coli 562 -11533417 5000690672 lip lipoic acid  
synthetase lip-syn . (sr:escherichia coli(strain:k12) dna, clone:kohara  
clone #168) (db:genpept) (de:escherichia coli genomic dna. (14.0 - 14.4  
min).) (nt:orf\_id:ol68#13; similar to swissprot accession) (le:10314)  
(re:11279) (di:complement) D90703 D90703 g1651257 Escherichia coli 562  
-11533417

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831126	8463	30619	489	163

Description

6500729560 hupb:hopd:b0440 dna-binding protein hu-beta:ns1:hu-1 (gtcfc:10.1) (keggfc:14.2) (rileyfc:3.1.6) (db:gtc-escherichia coli) b0440 b0440 Escherichia coli 562 -11533418 240217 hupb:hopd (de:dna-binding protein hu-beta (ns1) (hu-1)) (db:swissprot) DBHB\_ECOLI P02341 ESCHERICHIA COLI 562 -11533418 128607 hupb:hopd dna-binding protein hu-1:dna-binding protein ns1:histone-like protein hupb (cl:bacterial dna-binding protein) (db:pir1.dat) DNECS1 S06880 Escherichia coli 562 -11533418 5000690694 (db:genpept-bct1) (de:e.coli hupb gene encoding hu-1 protein.) (nt:hu-1 protein (aa 1-90)) (le:103) (re:375) (di:direct) ECHUPB X16540 g581106 Escherichia coli 562 -11533418 7500880015 dbhb dna-binding protein ns1 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:40901) (re:41173) (di:direct) ECU82664 U82664 g1773124 Escherichia coli 562 -11533418 233169 hupb dna-binding protein hu-beta:ns1 hu-1 (fn:factor; basic proteins - synthesis,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 40 of 400 of the completegenome.) (nt:o90; 100 pct identical to dbhb\_ecoli sw: p02341;) (le:6520) (re:6792) (di:direct) AE000150 AE000150 g1786644 Escherichia coli 562 -11533418 7502851932 (db:genpept) (de:e.coli hupb gene encoding hu-1 protein.) (nt:hu-1 protein (aa 1-90)) (le:103) (re:372) (di:direct) ECHUPB X16540 g581106 Escherichia coli 562 -11533418 67918 hupb:hopd (de:dna-binding protein hu-beta (ns1) (hu-1)) (db:swissprot) DBHB\_ECOLI P02341 ESCHERICHIA COLI 562 -11533418

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831137	8464	30620	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831142	8465	30621	366	121

Description

6500729561 tpr:b1229 protamine-like protein (gtcfc:10.1) (keggfc:14.2) (rileyfc:3.1.6) (db:gtc-escherichia coli) b1229 b1229 Escherichia coli 562 -11533419 91367 tpr (de:protamine-like protein) (db:swissprot) PRTL\_ECOLI P02338 ESCHERICHIA COLI 562 -11533419 128579 tpr protamine-like protein (cl:protamine-like protein) (db:pir1.dat) (mp:27 min) WRECP1 A90813 Escherichia coli 562 -11533419 223434 tpr protamine-like protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #249) (db:genpept-bct1) (de:escherichia coli genomic dna(27.5-27.8 min).) (le:8426) (re:8527) (di:complement) D90758 D90758 g1651624 Escherichia coli 562 -11533419 223442 tpr protamine-like protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #250) (db:genpept-bct1) (de:escherichia coli genomic dna (27.6-28.0 min).) (le:4083) (re:4184) (di:complement) D90759 D90759 g1651633 Escherichia coli 562 -11533419 224709 tpr protamine-like protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #251(27.7-28.2 min).) (nt:orf\_id:o249#7; similar to (pir accession number) (le:4083) (re:4184) (di:complement) D90852 D90852 g1805508 Escherichia coli 562 -11533419 301349 (sr:e.coli dna cloned in bacteriophage phi-80su3+, phi-80su3+-, an) (db:genpept-bct1) (de:e.coli tyrt locus containing two tyr-trna-1 genes.) (nt:protamine-like protein) (le:993) (re:1094) (di:direct) ECOTGY1 K01197 g147972 Escherichia coli 562 -11533419 236090 tpr a protaminelike protein (fn:factor; basic proteins - synthesis,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 111 of 400 of the completgenome.) (nt:f33; 100 pct identical to prtl\_ecoli sw: p02338) (le:7511) (re:7612) (di:complement) AE000221 AE000221 g1787482 Escherichia coli 562 -11533419 5000690695 tpr protamine-like protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #249) (db:genpept) (de:escherichia coli genomic dna. (27.6 - 27.9 min).) (nt:orf\_id:o250#5; similar to pir accession number) (le:8426) (re:8527) (di:complement) D90758 D90758 g1651624 Escherichia coli 562 -11533419 7502851933 tpr protamine-like protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #250) (db:genpept) (de:escherichia coli genomic dna. (27.7 - 28.1 min).) (nt:orf\_id:o250#5; similar to pir accession number) (le:4083) (re:4184) (di:complement) D90759 D90759 g1651633 Escherichia coli 562 -11533419

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831166	8466	30622	1275	424

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831180	8467	30623	723	240

Description

GTC ORF with score 100 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome i cosmid c31g5.) (nt:spac31g5.15, anomaly: splicing may be incorrectly) (le:24696:24950:25237:25745) (re:24893:25177:25702:26790) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831183	8468	30624	837	278

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831190	8469	30625	294	98

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831197	8470	30626	261	86

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831206	8471	30627	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501831208	8472	30628	195	64

# Description

6500729562 hns:hnsa:drdx:osmz:bgly:msya:cur:pilg:tops:b1237 dna-binding protein:dna-binding protein h-ns:histone-like protein hlp-ii:protein h1:protein b1 (gtcfc:10.1) (keggfc:14.2) (rileyfc:3.1.6) (db:gtc-escherichia coli) b1237 b1237 Escherichia coli 562 -11533420 148291 virr:kcpa dna-binding protein h-ns homolog virr (cl:dna-binding protein h-ns) (db:pir2.dat) (mp:27 min) S24755 S24755 Shigella flexneri 623 -11533420 148292 hns:drdx:osmz:bgly dna-binding protein h-ns:histone-like protein hlp-ii (cl:dna-binding protein h-ns) (db:pir2.dat) (mp:27.5 min) S00903 S00903 Escherichia coli 562 -11533420 223446 osmz dna-binding protein h-ns (sr:escherichia coli(strain:k12) dna, clone:kohara clone #250) (db:genpept-bct1) (de:escherichia coli genomic dna (27.6-28.0 min).) (le:9505) (re:9918) (di:complement) D90759 D90759 g1651637 Escherichia coli 562 -11533420 224715 bgly dna-binding protein h-ns (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #251(27.7-28.2 min).) (nt:orf\_id:o250#1; similar to (pir accession number) (le:9505) (re:9918) (di:complement) D90852 D90852 g1805514 Escherichia coli 562 -11533420 233413 (db:genpept-bct1) (de:e. coli hns gene for dna-binding protein h-ns.) (nt:hns gene (aa 1-137)) (le:862) (re:1275) (di:direct) ECHNS X07688 g41736 Escherichia coli 562 -11533420 236005 msya histone-like protein h-ns (db:genpept-bct1) (de:e.coli msya gene for histone-like protein h-ns.) (le:1286) (re:1699) (di:complement) ECMSYA X59940 g42027 Escherichia coli 562 -11533420 304601 osmz::bgly dna-binding protein osmz h-ns h1a ) (db:genpept-bct1) (de:e.coli osmz (bgly) gene for dna-binding protein osmz.) (le:296) (re:709) (di:direct) ECOSMZ X57231 g42183 Escherichia coli 562 -11533420 301355 virr (db:genpept-bct1) (de:s.flexneri virr gene.) (le:94) (re:507) (di:direct) SFVIRR X66848 g47070 Shigella flexneri 623 -11533420 233129 hns dna-binding protein hlp-ii hu:bh2:hd:ns (fn:regulator; basic proteins - synthesis,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 112 of 400 of the completgenome.) (nt:f137; 99 pct identical to hns\_ecoli sw: p08936) (le:2343) (re:2756) (di:complement) AE000222 AE000222 g1787489 Escherichia coli 562 -11533420 5000690696 bgly dna-binding protein h-ns. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #250) (db:genpept) (de:escherichia coli genomic dna. (27.7 - 28.1 min).) (nt:orf\_id:o251#3; similar to pir accession number) (le:9505) (re:9918) (di:complement) D90759 D90759 g1651637 Escherichia coli 562 -11533420 260416 osmz::bgly dna-binding protein osmz h-ns h1a ) (db:genpept-bct1) (de:e.coli osmz (bgly) gene for dna-binding protein osmz.) (le:296) (re:709) (di:direct) ECOSMZ X57231 g42183 Escherichia coli 562 -11533420



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831209	8473	30629	234	77

# Description

6500729563 stpa:hnsb:b2669 dna-binding protein stpa (gtcfc:10.1)  
(keggfc:14.2) (rileyfc:3.1.6) (db:gtc-escherichia coli) b2669 b2669  
Escherichia coli 562 -11533421 7500892193 stpa:hnsb (de:dna-binding protein  
stpa (h-ns homolog stpa)) (db:swissprot) STPA\_ECOLI P30017 ESCHERICHIA COLI  
562 -11533421 148293 stpa dna-binding protein h-ns homolog stpa  
(cl:dna-binding protein h-ns) (db:pir2.dat) (mp:58 min) JH0774 JH0774  
Escherichia coli 562 -11533421 225225 hnsb dna-binding protein stpa.  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #445(60.2-60.6  
min.)) (nt:similar to (swissprot accession number p30017)) (le:1561)  
(re:1965) (di:complement) D90891 D90891 g1800058 Escherichia coli 562  
-11533421 238305 stpa h-nsb (db:genpept-bct1) (de:escherichia coli ygac  
(ygac) gene, complete cds, and h-nsb (stpa)gene, complete cds.) (le:1629)  
(re:2033) (di:direct) ECOSTPAA U07823 g469172 Escherichia coli 562 -11533421  
5000690697 stpa h-ns-like protein (db:genpept-bct1) (de:e.coli stpa gene  
for h-ns-like protein.) (le:121) (re:525) (di:direct) ECSTPA X69210 g43008  
Escherichia coli 562 -11533421 236044 stpa dna-binding protein:h-ns-like  
protein (fn:regulator; basic proteins - synthesis,) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 241 of 400 of the completegenome.)  
(nt:fl134; 100 pct identical to stpa\_ecoli sw: p30017) (le:9814) (re:10218)  
(di:complement) AE000351 AE000351 g1789023 Escherichia coli 562 -11533421  
99718 stpa:hnsb (de:dna-binding protein stpa (h-ns homolog stpa))  
(db:swissprot) STPA\_ECOLI P30017 ESCHERICHIA COLI 562 -11533421

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831212	8474	30630	465	154

#### Description

6500729564 hupa:b4000 histonelike dna-binding protein hu-alpha:dna-binding protein hu-alpha:ns2:hu-2 (gtcfc:10.1) (keggfc:14.2) (rileyfc:3.1.6) (db:gtc-escherichia coli) b4000 b4000 Escherichia coli 562 -11533422 237210 hupa (de:dna-binding protein hu-alpha (ns2) (hu-2)) (db:swissprot) DBHA\_ECOLI P02342 ESCHERICHIA COLI 562 -11533422 128608 hupa dna-binding protein hu-2:dna-binding protein ns2:histone-like protein hupa (cl:bacterial dna-binding protein) (db:pir1.dat) DNECS2 S06269 Escherichia coli 562 -11533422 5000690698 (db:genpept-bct1) (de:e.coli hu2 gene.) (nt:hu 2-protein (aa 1-90)) (le:169) (re:441) (di:direct) ECHU2 X05994 g41765 Escherichia coli 562 -11533422 233167 hupa dna-binding protein hu-alpha hu-2 (fn:factor; basic proteins - synthesis,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 363 of 400 of the completegenome.) (nt:o90; 100 pct identical amino acid sequence and) (le:10643) (re:10915) (di:direct) AE000473 AE000473 g1790433 Escherichia coli 562 -11533422 7500880014 hupa histonelike dna-binding protein hu-alpha ns2 (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:65522) (re:65794) (di:direct) ECOUW89 U00006 g396339 Escherichia coli 562 -11533422 67914 hupa (de:dna-binding protein hu-alpha (ns2) (hu-2)) (db:swissprot) DBHA\_ECOLI P02342 ESCHERICHIA COLI 562 -11533422

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831214	8475	30631	264	88

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831220	8476	30632	237	78

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831223	8477	30633	330	109

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831224	8478	30634	384	127

Description

GTC ORF with score 108 to: (fn:mrna turnover) (sr:baker's yeast)  
(db:genpept-pln1) (de:saccharomyces cerevisiae upf2p (upf2) gene, complete  
cds.) (nt:allosuppressor of his4-38, omnipotent suppressor of)  
(le:1181:1300) (re:1186:4563) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831228	8479	30635	438	145

Description

GTC ORF with score 151 to: (sr:lithospermum erythrorhizon dedifferentiated  
cells cell\_line:m1) (db:genpept-pln1) (de:lithospermum erythrorhizon mrna  
for lec14b protein, complete cds.) (nt:single copy gene in the lithospermum  
genome) (le:153) (re:1574) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831241	8480	30636	270	89

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831272	8481	30637	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831279	8482	30638	810	270

Description

6500729565 sbcc:b0397 exonuclease sbcc (gtcfc:10.10) (keggfc:14.2) (rileyfc:3.2.2) (db:gtc-escherichia coli) b0397 b0397 Escherichia coli 562 -11533423 240014 sbcc (de:exonuclease sbcc) (db:swissprot) SBCC\_ECOLI P13458 ESCHERICHIA COLI 562 -11533423 131427 sbcc exonuclease:sbcc (cl:sbcc protein) (ec:3.1.15.-) (db:pir1.dat) (mp:9 min) BVECSC JS0350 Escherichia coli 562 -11533423 5000690673 (db:genpept-bct1) (de:e. coli sbcc gene (orf-45) for sbcc.) (nt:sbcc (aa 1-1048)) (le:1309) (re:4455) (di:direct) ECSBCC X15981 g42914 Escherichia coli 562 -11533423 7500891335 sbcc exonuclease sbcc (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (le:120197) (re:123343) (di:complement) ECU73857 U73857 g1657593 Escherichia coli 562 -11533423 238215 sbcc atp-dependent dsdna exonuclease (fn:enzyme; degradation of dna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 36 of 400 of the completegenome.) (nt:f1048; 100 pct identical to sbcc\_ecoli sw: p13458) (le:93) (re:3239) (di:complement) AE000146 AE000146 g1786597 Escherichia coli 562 -11533423 97992 sbcc (de:exonuclease sbcc) (db:swissprot) SBCC\_ECOLI P13458 ESCHERICHIA COLI 562 -11533423

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831282	8483	30639	345	114

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831285	8484	30640	696	231

Description

6500729566 sbcd:b0398 exonuclease sbcd (gtcfc:10.10) (keggfc:14.2) (rileyfc:3.2.2) (db:gtc-escherichia coli) b0398 b0398 Escherichia coli 562 -11533424 7500891336 sbcd (de:exonuclease sbcd) (db:swissprot) SBDC\_ECOLI P13457 ESCHERICHIA COLI 562 -11533424 163281 sbcd exonuclease:sbcd (cl:exonuclease sbcd:phosphoesterase core homology) (ec:3.1.-.-) (db:pir1.dat) (mp:9 min) JS0349 JS0349 Escherichia coli 562 -11533424 5000690674 (db:genpept-bct1) (de:e. coli sbcc gene (orf-45) for sbcc.) (nt:orf 45 peptide (aa 1-400)) (le:110) (re:1312) (di:direct) ECSBCC X15981 g42913 Escherichia coli 562 -11533424 238214 sbcd atp-dependent dsdna exonuclease (fn:enzyme; degradation of dna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 36 of 400 of the completegenome.) (nt:f400; 100 pct identical to sbcd\_ecoli sw: p13457) (le:3236) (re:4438) (di:complement) AE000146 AE000146 g1786598 Escherichia coli 562 -11533424 97994 sbcd (de:exonuclease sbcd) (db:swissprot) SBDC\_ECOLI P13457 ESCHERICHIA COLI 562 -11533424

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831286	8485	30641	447	148

Description

6500729567 xseb:b0422 exodeoxyribonuclease small subunit:exonuclease vii small subunit (gtcfc:10.10) (ec:3.1.11.6) (keggfc:14.1) (rileyfc:3.2.2) (db:gtc-escherichia coli) b0422 b0422 Escherichia coli 562 -11533425 163294 xseb exodeoxyribonuclease vii:small chain (cl:exodeoxyribonuclease vii small chain) (ec:3.1.11.6) (db:pir2.dat) (mp:10 min) JQ0664 JQ0664 Escherichia coli 562 -11533425 240199 (sr:e.coli (strain k12) genomic dna, clone lambda2h5) (db:genpept-bct1) (de:e.coli ispa gene for farnesyl diphosphate synthase (ec 2.5.1.1).) (nt:orf1) (le:242) (re:484) (di:direct) ECOISPA D00694 g216583 Escherichia coli 562 -11533425 7500959733 ex7s exodeoxyribonuclease small subunit (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:20551) (re:20793) (di:complement) ECU82664 U82664 g1773106 Escherichia coli 562 -11533425 234884 xseb exonuclease vii:small subunit (fn:enzyme; degradation of dna) (db:genpept-bct2) (ec:3.1.11.6) (de:escherichia coli k-12 mg1655 section 38 of 400 of the completegenome.) (nt:f80; 100 pct identical to ex7s\_ecoli sw: p22938) (le:8175) (re:8417) (di:complement) AE000148 AE000148 g1786624 Escherichia coli 562 -11533425 5000690675 (de:(ecoli\_406) (pn:exonuclease vii, small subunit) (gn:xseb) (gtcfc:10.10) (ec:3.1.11.6) (ex7s\_ecoli) (keggfc:11.1) (rileyfc:3.2.2) (db:gtc-escherichia coli)) ECOLI\_406 ECOLI\_406 Escherichia coli 562 10086849

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831301	8486	30642	849	282

Description

6500729568 uvr:b0779 excision nuclease abc subunit b:excinuclease abc subunit b (gtcfc:10.10) (keggfc:14.2) (rileyfc:3.2.2) (db:gtc-escherichia coli) b0779 b0779 Escherichia coli 562 -11533426 7500893896 uvr:b (de:excinuclease abc subunit b) (db:swissprot) UVRB\_ECOLI P07025 ESCHERICHIA COLI 562 -11533426 131424 uvr:b excinuclease abc:chain b:excision endonuclease abc chain b:uvrb protein (cl:excinuclease abc chain b:dead/h box helicase homology) (ec:3.1.-.-) (db:pir1.dat) (mp:18 min) BVECUB A93613 Escherichia coli 562 -11533426 5000690676 (db:genpept-bct1) (de:e. coli uvr:b gene.) (nt:uvrb gene product (aa 1 - 673)) (le:133) (re:2154) (di:direct) ECUVRB2 X03722 g43286 Escherichia coli 562 -11533426 240367 uvr:b dna repair:excision nuclease subunit b (fn:enzyme; degradation of dna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 70 of 400 of the completegenome.) (nt:o673; 100 pct identical to uvr:b\_ecoli sw: p07025) (le:7675) (re:9696) (di:direct) AE000180 AE000180 g1786996 Escherichia coli 562 -11533426 104043 uvr:b (de:excinuclease abc subunit b) (db:swissprot) UVRB\_ECOLI P07025 ESCHERICHIA COLI 562 -11533426

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501831306	8487	30643	420	139

#### Description

6500729569 mcra:rgla:b1159 5-methylcytosine-specific restriction enzyme a (gtcfc:10.10) (ec:3.1.21.-) (keggfc:14.1) (rileyfc:3.2.2) (db:gtc-escherichia coli) b1159 b1159 Escherichia coli 562 -11533427 235094 mcra:rgla (ec:3.1.21.-) (de:5-methylcytosine-specific restriction enzyme a,) (db:swissprot) MCRA\_ECOLI P24200 ESCHERICHIA COLI 562 -11533427 164095 mcra:mcr:rgla 5-methylcytosine-specific restriction enzyme a (ec:3.1.21.-) (db:pir2.dat) (mp:25 min) A41424 A41424 Escherichia coli 562 -11533427 223388 mcra modified cytosine restriction protein a (sr:escherichia coli(strain:k12) dna, clone:kohara clone #241) (db:genpept-bct1) (de:escherichia coli genomic dna. (25.8 - 26.2 min).) (le:8544) (re:9377) (di:direct) D90750 D90750 g1651571 Escherichia coli 562 -11533427 5000690677 mcra methyl cytosine restriction enzyme (fn:restriction of mc & hmc dna) (db:genpept-bct1) (de:e.coli mcra gene for methyl cytosine restriction enzyme.) (le:124) (re:957) (di:direct) ECMCRAGNA Z19104 g41985 Escherichia coli 562 -11533427 7500885392 mcra (fn:restriction of 5-methyl and hydroxymethyl dna) (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli mcra gene (encoding the restriction of 5-methyl andhydroxymethyl dna), complete cds.) (le:61) (re:894) (di:direct) ECOMCRA M76667 g146794 Escherichia coli 562 -11533427 233361 mcra restriction of dna at 5-methylcytosine residues (fn:enzyme; degradation of dna) (db:genpept-bct2) (ec:3.1.21.-) (de:escherichia coli k-12 mg1655 section 105 of 400 of the completegenome.) (nt:o277; 99 pct identical to mcra\_ecoli sw: p24200) (le:84) (re:917) (di:direct) AE000215 AE000215 g1787406 Escherichia coli 562 -11533427 7502851934 mcr modified cytosine restriction protein a (sr:escherichia coli(strain:k12) dna, clone:kohara clone #241) (db:genpept) (de:escherichia coli genomic dna. (26.0 - 26.3 min).) (nt:orf\_id:o241#15; similar to pir accession number) (le:8544) (re:9377) (di:direct) D90750 D90750 g1651571 Escherichia coli 562 -11533427 83231 mcra:rgla (ec:3.1.21.-) (de:5-methylcytosine-specific restriction enzyme a,) (db:swissprot) MCRA\_ECOLI P24200 ESCHERICHIA COLI 562 -11533427

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501831332	8488	30644	576	191

#### Description

GTC ORF with score 152 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831333	8489	30645	441	146

Description

GTC ORF with score 133 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831339	8490	30646	354	118

Description

GTC ORF with score 102 to: (fn:involved in soraphen a biosynthesis) (db:genpept-bct1) (de:sorangium cellulosum soraphen a polyketide synthase gene, partialcds including the ketoreductase, acyl carrier protein,beta-ketoacyl synthase, acyltransferase, ...)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831341	8491	30647	306	101

Description

6500729570 rece:b1350 exodeoxyribonuclease viii:exo viii (gtcfc:10.10) (ec:3.1.11.-) (keggfc:14.1) (rileyfc:3.2.2) (db:gtc-escherichia coli) b1350 b1350 Escherichia coli 562 -11533428 93793 rece (ec:3.1.11.-) (de:exodeoxyribonuclease viii, (exo viii)) (db:swissprot) RECE\_ECOLI P15032 ESCHERICHIA COLI 562 -11533428 7000686287 rece exodeoxyribonuclease viii (cl:exodeoxyribonuclease viii) (ec:3.1.11.-) (db:pir1.dat) (mp:30 min) NCECX8 A64885 Escherichia coli 562 -11533428 223625 rece exodeoxyribonuclease viii ec 3.1.11.- exo (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #263(30.5-30.9 min.)) (nt:orf\_id:o263#1; similar to (swissprot accession) (le:698) (re:3298) (di:complement) D90774 D90774 g1742219 Escherichia coli 562 -11533428 300398 rece exonuclease viii:ds dna exonuclease:5 --3 (fn:enzyme; degradation of dna) (db:genpept-bct2) (ec:3.1.11.-) (de:escherichia coli k-12 mg1655 section 122 of 400 of the completegenome.) (nt:f866; 99 pct identical to rece\_ecoli sw: p15032; cg) (le:10156) (re:12756) (di:complement) AE000232 AE000232 g1787612 Escherichia coli 562 -11533428 5000690678 (de:(ecoli\_1310) (pn:exonuclease viii, ds dna exonuclease,:5" to 3" specific) (gn:rece) (gtcfc:10.10) (ec:3.1.11.-) (rece\_ecoli) (keggfc:11.1) (rileyfc:3.2.2) (db:gtc-escherichia coli)) ECOLI\_1310 ECOLI\_1310 Escherichia coli 562 10119550





ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501831379	8494	30650	423	140
Description				
<p>6500729571 nth:b1633 endonuclease iii:dna-:apurinic or apyrimidinic site lyase (gtcfc:10.10) (ec:4.2.99.18) (keggfc:14.1) (rileyfc:3.2.2) (db:gtc-escherichia coli) b1633 b1633 Escherichia coli 562 -11533429 70153 nth (ec:4.2.99.18) (de:lyase)) (db:swissprot) END3_ECOLI P20625 ESCHERICHIA COLI 562 -11533429 162914 nth dna-apurinic or apyrimidinic site lyase:nth:endonuclease iii (cl:apurinic/apyrimidinic endonuclease class ii) (ec:4.2.99.18) (db:pir2.dat) A32412 A32412 Escherichia coli 562 -11533429 224065 nth deoxyribonuclease pyrimidine dimer ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #315(36.6-36.9 min.)) (nt:orf_id:o316#12; similar to (pir accession number) (le:14519) (re:15154) (di:direct) D90806 D90806 g1742691 Escherichia coli 562 -11533429 224072 nth deoxyribonuclease pyrimidine dimer ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #316(36.7-37.1 min.)) (nt:orf_id:o316#12; similar to (pir accession number) (le:9129) (re:9764) (di:direct) D90807 D90807 g1742699 Escherichia coli 562 -11533429 300778 nth deoxyribonuclease pyrimidine dimer ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #317(36.6-36.9 min.)) (nt:orf_id:o316#12; similar to (pir accession number) (le:14620) (re:15255) (di:direct) D90808 D90808 g1742723 Escherichia coli 562 -11533429 300755 (sr:e.coli (strain k12) dna) (db:genpept-bct1) (de:e.coli nth gene encoding endonuclease iii, complete cds.) (nt:endonuclease iii) (le:85) (re:720) (di:direct) ECONTJ J02857 g146972 Escherichia coli 562 -11533429 235252 nth endonuclease iii:specific for apurinic and/or (fn:enzyme; degradation of dna) (db:genpept-bct2) (ec:4.2.99.18) (de:escherichia coli k-12 mg1655 section 148 of 400 of the completegenome.) (nt:o211; 100 pct identical to end3_ecoli sw: p20625;) (le:12244) (re:12879) (di:direct) AE000258 AE000258 g1787920 Escherichia coli 562 -11533429 224095 nth deoxyribonuclease pyrimidine dimer ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #317(36.6-36.9 min.)) (nt:orf_id:o316#12; similar to (pir accession number) (le:14620) (re:15255) (di:direct) D90808 D90808 g1742723 Escherichia coli 562 -11533429 5000690679 (de:(ecoli_1592) (pn:endonuclease iii; specific for apurinic and) (gn:nth) (gtcfc:10.10) (ec:4.2.99.18) (end3_ecoli) (keggfc:11.1) (rileyfc:3.2.2) (db:gtc-escherichia coli)) ECOLI_1592 ECOLI_1592 Escherichia coli 562 10012731</p>				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831382	8495	30651	303	100

Description

6500729572 xtha:xth:b1749 exodeoxyribonuclease iii:exonuclease iii:ap  
endonuclease vi (gtcfc:10.10) (ec:3.1.11.2) (keggfc:14.1) (rileyfc:3.2.2)  
(db:gtc-escherichia coli) b1749 b1749 Escherichia coli 562 -11533430 304643  
xtha:xth (ec:3.1.11.2) (de:endonuclease vi)) (db:swissprot) EX3\_ECOLI P09030  
ESCHERICHIA COLI 562 -11533430 7000685201 xtha:xth exodeoxyribonuclease  
iii::e. coli exonuclease iii (cl:exodeoxyribonuclease iii) (ec:3.1.11.2)  
(db:pir1.dat) (mp:38 min) NCECX3 E64934 Escherichia coli 562 -11533430  
224220 xtha:xth exodeoxyribonuclease iii ec 3.1.11.2 (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #327(39.2-39.5 min..))  
(nt:orf\_id:o327#6; similar to (pir accession number) (le:12156) (re:12962)  
(di:direct) D90818 D90818 g1742858 Escherichia coli 562 -11533430 300866  
xtha:xth exodeoxyribonuclease iii ec 3.1.11.2 (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #328(39.4-39.8 min..))  
(nt:orf\_id:o327#6; similar to (pir accession number) (le:3943) (re:4749)  
(di:direct) D90819 D90819 g1742863 Escherichia coli 562 -11533430  
5000690680 exonuclease iii (db:genpept-bct1) (de:e. coli xtha gene for  
exonuclease iii.) (le:189) (re:995) (di:direct) ECXTHA X13002 g43312  
Escherichia coli 562 -11533430 240386 xtha exonuclease iii (fn:enzyme;  
degradation of dna) (db:genpept-bct2) (ec:3.1.11.2) (de:escherichia coli  
k-12 mg1655 section 160 of 400 of the completegenome.) (nt:o268; 99 pct  
identical to ex3\_ecoli sw: p09030; cg) (le:253) (re:1059) (di:direct)  
AE000270 AE000270 g1788046 Escherichia coli 562 -11533430 70772 xtha:xth  
(ec:3.1.11.2) (de:endonuclease vi)) (db:swissprot) EX3\_ECOLI P09030  
ESCHERICHIA COLI 562 -11533430 224224 xtha:xth exodeoxyribonuclease iii ec  
3.1.11.2 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda  
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#328(39.4-39.8 min..)) (nt:orf\_id:o327#6; similar to (pir accession number)  
(le:3943) (re:4749) (di:direct) D90819 D90819 g1742863 Escherichia coli 562  
-11533430 300862 exonuclease iii (db:genpept-bct1) (de:e. coli xtha gene  
for exonuclease iii.) (le:189) (re:995) (di:direct) ECXTHA X13002 g43312  
Escherichia coli 562 -11533430

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831399	8496	30652	696	231

Description

6500729573 uvrc:b1913 excinuclease abc subunit c (gtcfc:10.10) (keggfc:14.2) (rileyfc:3.2.2) (db:gtc-escherichia coli) b1913 b1913 Escherichia coli 562 -11533431 7000690875 uvrc excinuclease abc:chain c:excision nuclease abc:chain c:uvrc protein (cl:excinuclease abc chain c) (db:pir1.dat) (mp:42 min) BVECUC F64954 Escherichia coli 562 -11533431 7500953658 uvrc excinuclease abc:subunit c:repair of uv damage (fn:enzyme; degradation of dna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 174 of 400 of the completegenome.) (nt:f588; 99 pct identical to 588 residues of) (le:4902) (re:6668) (di:complement) AE000284 AE000284 g1788221 Escherichia coli 562 -11533431 5000690681 (de:(ecoli\_1867) (pn:repair of uv damage to dna; excision nuclease subunit c) (gn:uvrc) (gtcfc:10.10) (ec:) (uvrc\_ecoli) (keggfc:11.2) (rileyfc:3.2.2) (db:gtc-escherichia coli)) ECOLI\_1867 ECOLI\_1867 Escherichia coli 562 10123507

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831400	8497	30653	1137	378

Description

6500729574 vsr:b1960 patch repair protein:dna mismatch endonuclease (gtcfc:10.10) (ec:3.1.-.-) (keggfc:14.1) (rileyfc:3.2.2) (db:gtc-escherichia coli) b1960 b1960 Escherichia coli 562 -11533432 234132 vsr (ec:3.1.-.-) (de:patch repair protein (dna mismatch endonuclease),) (db:swissprot) VSR\_ECOLI P09184 ESCHERICHIA COLI 562 -11533432 164831 vsr patch repair protein (ec:3.1.-.-) (db:pir2.dat) JS0264 JS0264 Escherichia coli 562 -11533432 224470 vsr patch repair protein dna mismatch endonuclease (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #344(43.5-43.9 min.)) (nt:orf\_id:o344#7; similar to (pir accession number) (le:8853) (re:9323) (di:complement) D90835 D90835 g1736629 Escherichia coli 562 -11533432 5000690682 (db:genpept-bct1) (de:e. coli dcm gene for dna-cytosine methyltransferase and 3 orfs.) (nt:orf 2 (aa 1 - 156)) (le:1697) (re:2167) (di:direct) ECDCM X13330 g41241 Escherichia coli 562 -11533432 301110 (sr:e.coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli dna cytosine methylase (dcm) and patch repair protein genes,complete cds.) (nt:pot. patch repair protein; putative) (le:1649) (re:2119) (di:direct) ECODCMA M32307 g145720 Escherichia coli 562 -11533432 232649 vsr dna mismatch endonuclease:patch repair protein (fn:enzyme; degradation of dna) (db:genpept-bct2) (ec:3.1.-.-) (de:escherichia coli k-12 mg1655 section 177 of 400 of the completegenome.) (nt:f156; 100 pct identical to vsr\_ecoli sw: p09184) (le:8946) (re:9416) (di:complement) AE000287 AE000287 g1788270 Escherichia coli 562 -11533432 107771 vsr (ec:3.1.-.-) (de:patch repair protein (dna mismatch endonuclease),) (db:swissprot) VSR\_ECOLI P09184 ESCHERICHIA COLI 562 -11533432

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501831406	8498	30654	1455	484

#### Description

6500729575 sbcb:xona:cpea:b2011 exodeoxyribonuclease i:exonuclease i:dna deoxyribophosphodiesterase:drpase (gtcfc:10.10) (ec:3.1.11.1) (keggfc:14.1) (rileyfc:3.2.2) (db:gtc-escherichia coli) b2011 b2011 Escherichia coli 562 -11533433 70770 sbcb:xona:cpea (ec:3.1.11.1) (de:deoxyribophosphodiesterase) (drpase)) (db:swissprot) EX1\_ECOLI P04995 ESCHERICHIA COLI 562 -11533433 7000685200 sbcb exodeoxyribonuclease i::exonuclease i (cl:exodeoxyribonuclease i) (ec:3.1.11.1) (db:pir1.dat) (mp:44 min) NCECX1 B64966 Escherichia coli 562 -11533433 224522 sbcb:xona:cpea exodeoxyribonuclease i ec 3.1.11.1 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #349(44.6-45.0 min..)) (nt:orf\_id:o349#2; similar to (swissprot accession) (le:11408) (re:12835) (di:direct) D90839 D90839 g1736685 Escherichia coli 562 -11533433 301167 sbcb:xona:cpea exodeoxyribonuclease i ec 3.1.11.1 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #350(44.9-45.2 min..)) (nt:orf\_id:o349#2; similar to (swissprot accession) (le:99) (re:1526) (di:direct) D90840 D90840 g1736691 Escherichia coli 562 -11533433 301162 exonuclease i (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:sbcb region of e.coli k12 bhb2600.) (le:2613) (re:4040) (di:direct) ECOHU3 U00009 g405954 Escherichia coli 562 -11533433 234713 sbcb exonuclease i:3 --5 specific (fn:enzyme; degradation of dna) (db:genpept-bct2) (ec:3.1.11.1) (de:escherichia coli k-12 mg1655 section 182 of 400 of the completegenome.) (nt:o475; 100 pct identical to ex1\_ecoli sw: p04995; cg) (le:8071) (re:9498) (di:direct) AE000292 AE000292 g1788321 Escherichia coli 562 -11533433 224527 sbcb:xona:cpea exodeoxyribonuclease i ec 3.1.11.1 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #350(44.9-45.2 min..)) (nt:orf\_id:o349#2; similar to (swissprot accession) (le:99) (re:1526) (di:direct) D90840 D90840 g1736691 Escherichia coli 562 -11533433 5000690683 (de:(ecoli\_1959) (pn:3" to 5" specific deoxyribophosphodiesterase:exonuclease i,:3" to 5" specific; deoxyribophosphodiesterase) (gn:sbcb) (gtcfc:10.10) (ec:3.1.11.1) (ex1\_ecoli) (keggfc:11.1) (rileyfc:3.2.2) (db:gtc-escherichia) ECOLI\_1959 ECOLI\_1959 Escherichia coli 562 10013345

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501831412	8499	30655	378	125

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831417	8500	30656	456	151

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831418	8501	30657	846	281

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831419	8502	30658	330	109

Description

6500729576 nfo:b2159 endonuclease iv:endonuclease iv (gtcfc:10.10) (ec:3.1.21.2) (keggfc:14.1) (rileyfc:3.2.2) (db:gtc-escherichia coli) b2159 b2159 Escherichia coli 562 -11533434 70159 nfo (ec:3.1.21.2) (de:endonuclease iv, (endonuclease iv)) (db:swissprot) END4\_ECOLI P12638 ESCHERICHIA COLI 562 -11533434 7000685159 nfo deoxyribonuclease iv phage-t4-induced::endonuclease iv:escherichia coli endonuclease iv (cl:deoxyribonuclease iv (phage t4-induced)) (ec:3.1.21.2) (db:pir1.dat) NDEC4 F64984 Escherichia coli 562 -11533434 7500881024 nfo endonuclease iv (fn:enzyme; degradation of dna) (db:genpept-bct2) (ec:3.1.21.2) (de:escherichia coli k-12 mg1655 section 195 of 400 of the completegenome.) (nt:o285; 99 pct identical to end4\_ecoli sw: p12638) (le:3954) (re:4811) (di:direct) AE000305 AE000305 g1788483 Escherichia coli 562 -11533434 5000690684 (de:(ecoli\_2108) (pn:endonuclease iv) (gn:nfo) (gtcfc:10.10) (ec:3.1.21.2) (end4\_ecoli) (keggfc:11.1) (rileyfc:3.2.2) (db:gtc-escherichia coli)) ECOLI\_2108 ECOLI\_2108 Escherichia coli 562 10123589

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831450	8503	30659	402	133
<u>Description</u>				
6500729577 xsea:b2509 exodeoxyribonuclease large subunit:exonuclease vii large subunit (gtcfc:10.10) (ec:3.1.11.6) (keggfc:14.1) (rileyfc:3.2.2) (db:gtc-escherichia coli) b2509 b2509 Escherichia coli 562 -11533435 70781 xsea (ec:3.1.11.6) (de:large subunit)) (db:swissprot) EX7L_ECOLI P04994 ESCHERICHIA COLI 562 -11533435 7000685204 xsea exodeoxyribonuclease vii:large chain:exonuclease vii large chain (cl:exodeoxyribonuclease vii) (ec:3.1.11.6) (db:pir1.dat) (mp:54 min) NCEC7 D65027 Escherichia coli 562 -11533435 225084 xsea exodeoxyribonuclease vii ec 3.1.11.6 large (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #427(56.5-56.9 min.)) (nt:similar to (pir accession number a25940)) (le:9070) (re:10440) (di:direct) D90880 D90880 g1805569 Escherichia coli 562 -11533435 7500881225 xsea exonuclease vii:large subunit (fn:enzyme; degradation of dna) (db:genpept-bct2) (ec:3.1.11.6) (de:escherichia coli k-12 mg1655 section 227 of 400 of the completengenome.) (nt:o456; 99 pct identical to ex7l_ecoli sw: p04994) (le:5148) (re:6518) (di:direct) AE000337 AE000337 g1788856 Escherichia coli 562 -11533435 5000690685 (de:(ecoli_2449) (pn:exonuclease vii, large subunit) (gn:xsea) (gtcfc:10.10) (ec:3.1.11.6) (ex7l_ecoli) (keggfc:11.1) (rileyfc:3.2.2) (db:gtc-escherichia coli)) ECOLI_2449 ECOLI_2449 Escherichia coli 562 10120233				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831453	8504	30660	306	101

#### Description

6500729578 recd:b2819 exonuclease v alpha-subunit:exodeoxyribonuclease v 67 kd polypeptide:exonuclease v alpha chain (gtcfc:10.10) (ec:3.1.11.5) (keggfc:14.1) (rileyfc:3.2.2) (db:gtc-escherichia coli) b2819 b2819 Escherichia coli 562 -11533436 70774 recd (ec:3.1.11.5) (de:alpha chain) (db:swissprot) EX5A\_ECOLI P04993 ESCHERICHIA COLI 562 -11533436 7000685202 recd exodeoxyribonuclease v:67k chain:exonuclease v alpha chain:recbc dnase alpha chain (cl:exodeoxyribonuclease v 67k chain) (ec:3.1.11.5) (db:pir1.dat) (mp:61 min) NCECXF D65064 Escherichia coli 562 -11533436 7500881217 recd exonuclease v alpha-subunit (db:genpept-bct1) (ec:3.1.11.5) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:cg site no. 4975) (le:32190) (re:34016) (di:complement) ECU29581 U29581 g882711 Escherichia coli 562 -11533436 239390 recd dna helicase:atp-dependent dsdna/ssdna (fn:enzyme; degradation of dna) (db:genpept-bct2) (ec:3.1.11.5) (de:escherichia coli k-12 mg1655 section 255 of 400 of the completegenome.) (nt:f608; 99 pct identical to ex5a\_ecoli sw: p04993; cg) (le:4704) (re:6530) (di:complement) AE000365 AE000365 g1789182 Escherichia coli 562 -11533436 5000690686 (de:(ecoli\_2747) (pn:dna helicase, atp-dependent dsdna) (gn:recd) (gtcfc:10.10) (ec:3.1.11.5) (ex5a\_ecoli) (keggfc:11.1) (rileyfc:3.2.2) (db:gtc-escherichia coli)) ECOLI\_2747 ECOLI\_2747 Escherichia coli 562 10123847

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831461	8505	30661	189	62

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831469	8506	30662	303	100

Description

6500729579 recb:rora:b2820 exonuclease v subunit:exodeoxyribonuclease v 135  
kd polypeptide:exonuclease v beta chain (gtcfc:10.10) (ec:3.1.11.5)  
(keggfc:14.1) (rileyfc:3.2.2) (db:gtc-escherichia coli) b2820 b2820  
Escherichia coli 562 -11533437 239391 recb:rora (ec:3.1.11.5) (de:beta  
chain)) (db:swissprot) EX5B\_ECOLI P08394 ESCHERICHIA COLI 562 -11533437  
124361 recb exodeoxyribonuclease v:135k chain:exonuclease 135k  
polypeptide:recbc dnase 135k polypeptide (cl:exodeoxyribonuclease v 135k  
chain) (ec:3.1.11.5) (db:pir1.dat) (mp:61 min) NCECX5 A25532 Escherichia  
coli 562 -11533437 5000690687 (db:genpept-bct1) (de:e.coli recb gene for  
exonuclease v.) (nt:exonuclease v (aa 1-1180)) (le:327) (re:3869)  
(di:direct) ECRECB X04581 g42682 Escherichia coli 562 -11533437 7500881219  
recb exonuclease v subunit (fn:recombination and dna repair)  
(db:genpept-bct1) (ec:3.1.11.5) (de:escherichia coli k-12 genome;  
approximately 63 to 64 minutes.) (nt:cg site no. 311; alternate name rora)  
(le:34016) (re:37558) (di:complement) ECU29581 U29581 g882712 Escherichia  
coli 562 -11533437 238028 recb dna helicase:atp-dependent dsdna/ssdna  
(fn:enzyme; degradation of dna) (db:genpept-bct2) (ec:3.1.11.5)  
(de:escherichia coli k-12 mg1655 section 255 of 400 of the completegenome.)  
(nt:f1180; 100 pct identical to ex5b\_ecoli sw:) (le:6530) (re:10072)  
(di:complement) AE000365 AE000365 g1789183 Escherichia coli 562 -11533437  
70776 recb:rora (ec:3.1.11.5) (de:beta chain)) (db:swissprot) EX5B\_ECOLI  
P08394 ESCHERICHIA COLI 562 -11533437



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831480	8507	30663	1527	508

Description

6500729580 recc:b2822 exonuclease v subunit:exodeoxyribonuclease v 125 kd polypeptide:exonuclease v gamma chain (gtcfc:10.10) (ec:3.1.11.5) (keggfc:14.1) (rileyfc:3.2.2) (db:gtc-escherichia coli) b2822 b2822 Escherichia coli 562 -11533438 239393 recc (ec:3.1.11.5) (de:v gamma chain)) (db:swissprot) EX5C\_ECOLI P07648 ESCHERICHIA COLI 562 -11533438 124362 recc exodeoxyribonuclease v:125k chain:e. coli exonuclease v 125k polypeptide:rebc dnase 125k polypeptide (cl:exodeoxyribonuclease v 125k chain) (ec:3.1.11.5) (db:pir1.dat) (mp:61 min) NCECXV A24137 Escherichia coli 562 -11533438 5000690688 recc protein aa 1-1122 (db:genpept-bct1) (de:e. coli recc gene and thya-recc intergenic region including urf1-3.) (le:2542) (re:5910) (di:direct) ECRECC X03966 g42689 Escherichia coli 562 -11533438 7500881221 recc exonuclease v subunit (fn:recombination and dna repair) (db:genpept-bct1) (ec:3.1.11.5) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:cg site no. 310) (le:40615) (re:43983) (di:complement) ECU29581 U29581 g882714 Escherichia coli 562 -11533438 238034 recc dna helicase:atp-dependent dsdna/ssdna (fn:enzyme; degradation of dna) (db:genpept-bct2) (ec:3.1.11.5) (de:escherichia coli k-12 mg1655 section 256 of 400 of the completegenome.) (nt:f1122; 100 pct identical to ex5c\_ecoli sw:) (le:118) (re:3486) (di:complement) AE000366 AE000366 g1789186 Escherichia coli 562 -11533438 70778 recc (ec:3.1.11.5) (de:v gamma chain)) (db:swissprot) EX5C\_ECOLI P07648 ESCHERICHIA COLI 562 -11533438

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831482	8508	30664	270	89

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831490	8509	30665	654	217

Description

6500729581 recj:b2892 single-stranded dna-specific exonuclease:single-stranded-dna-specific exonuclease recj (gtcfc:10.10) (ec:3.1.-.-) (keggfc:14.1) (rileyfc:3.2.2) (db:gtc-escherichia coli) b2892 b2892 Escherichia coli 562 -11533439 93811 recj (ec:3.1.-.-) (de:single-stranded-dna-specific exonuclease recj,) (db:swissprot) RECJ\_ECOLI P21893 ESCHERICHIA COLI 562 -11533439 7000686288 recj single-stranded dna-specific exonuclease (ec:3.1.-.-) (db:pir2.dat) (mp:62 min) D65073 D65073 Escherichia coli 562 -11533439 7500889577 recj single-stranded dna-specific exonuclease (fn:recombination and dna repair) (db:genpept-bct1) (ec:3.1.-.-) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:gtg start; cg site no. 17965) (le:46187) (re:47920) (di:complement) ECU28375 U28375 g887842 Escherichia coli 562 -11533439 239105 recj ssdna exonuclease:5 --3 specific (fn:enzyme; degradation of dna) (db:genpept-bct2) (ec:3.1.-.-) (de:escherichia coli k-12 mg1655 section 263 of 400 of the completegenome.) (nt:f577; 99 pct identical (1 gap) to recj\_ecoli) (le:76) (re:1809) (di:complement) AE000373 AE000373 g1789259 Escherichia coli 562 -11533439 5000690689 (de:(ecoli\_2816) (pn:ssdna exonuclease,5" to 3" specific) (gn:recj) (gtcfc:10.10) (ec:3.1.-.-) (recj\_ecoli) (keggfc:11.1) (rileyfc:3.2.2) (db:gtc-escherichia coli)) ECOLI\_2816 ECOLI\_2816 Escherichia coli 562 10123899

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831500	8510	30666	1800	599

Description

6500729582 enda:b2945 endonuclease i (gtcfc:10.10) (ec:3.1.21.1) (keggfc:14.1) (rileyfc:3.2.2) (db:gtc-escherichia coli) b2945 b2945 Escherichia coli 562 -11533440 239158 enda (ec:3.1.21.1) (de:endonuclease i precursor, (endo i)) (db:swissprot) END1\_ECOLI P25736 ESCHERICHIA COLI 562 -11533440 162984 enda deoxyribonuclease i (ec:3.1.21.1) (db:pir2.dat) A38966 A38966 Escherichia coli 562 -11533440 5000690690 enda endonuclease i (db:genpept-bct1) (de:e.coli enda gene for endonuclease i.) (le:387) (re:1094) (di:direct) ECENDAG X65169 g41342 Escherichia coli 562 -11533440 7500881011 enda (fn:endonuclease i) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:cg site no. 824) (le:44741) (re:45448) (di:direct) ECU28377 U28377 g882474 Escherichia coli 562 -11533440 232765 enda dna-specific endonuclease i (fn:enzyme; degradation of dna) (db:genpept-bct2) (ec:3.1.21.1) (de:escherichia coli k-12 mg1655 section 267 of 400 of the completegenome.) (nt:o235; 100 pct identical to end1\_ecoli sw: p25736;) (le:8665) (re:9372) (di:direct) AE000377 AE000377 g1789314 Escherichia coli 562 -11533440 70147 enda (ec:3.1.21.1) (de:endonuclease i,) (db:swissprot) END1\_ECOLI P25736 ESCHERICHIA COLI 562 -11533440

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831506	8511	30667	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831507	8512	30668	786	261

Description

6500729583 mcrb:b4345 mcrb protein (gtcfc:10.10) (ec:3.1.21.4) (keggfc:14.1) (rileyfc:3.2.2) (db:gtc-escherichia coli) b4345 b4345 Escherichia coli 562 -11533441 83247 mcrb (de:mcrb protein) (db:swissprot) MCRC\_ECOLI P15006 ESCHERICHIA COLI 562 -11533441 131357 mcrb mcrb protein (cl:mcrb protein) (db:pir1.dat) (mp:99 min) BVECMB JS0121 Escherichia coli 562 -11533441 237551 mcrb (sr:e.coli (strain k12) cr63 dna clone prab13) (db:genpept-bct1) (de:e.coli mcrb and mcrb protein genes, complete cds.) (nt:mcrb protein (gtg start codon)) (le:1514) (re:2560) (di:direct) ECOMCR M24927 g146792 Escherichia coli 562 -11533441 7500885397 mcrb (fn:modifies specificity of mcrb restriction by) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:267745) (re:268791) (di:complement) ECOUW93 U14003 g537187 Escherichia coli 562 -11533441 235093 mcrb component of mcrbc 5-methylcytosine restriction (fn:enzyme; degradation of dna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 395 of 400 of the completegenome.) (nt:f348; 100 pct identical amino acid sequence and) (le:2923) (re:3969) (di:complement) AE000505 AE000505 g1790804 Escherichia coli 562 -11533441 5000690691 (de:(ecoli\_4229) (pn:component of mcrbc 5-methylcytosine restriction system) (gn:mcrb) (gtcfc:10.10) (ec:3.1.21.4) (mcrb\_ecoli) (keggfc:11.1) (rileyfc:3.2.2) (db:gtc-escherichia coli)) ECOLI\_4229 ECOLI\_4229 Escherichia coli 562 10025466

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501831530	8513	30669	1596	531
<u>Description</u>				
<p>6500729584 mcrb:rglb:b4346 5-methylcytosine-specific restriction enzyme b (gtcfc:10.10) (ec:3.1.21.-) (keggfc:14.1) (rileyfc:3.2.2) (db:gtc-escherichia coli) b4346 b4346 Escherichia coli 562 -11533442 124390 mcrb 5-methylcytosine-specific restriction enzyme b (cl:5-methylcytosine-specific restriction enzyme b) (ec:3.1.21.-) (db:pir1.dat) (mp:99 min) XEYECMB A36708 Escherichia coli 562 -11533442 237552 mcrb (fn:mediates sequence-specific restriction of) (sr:e.coli k-12 dna) (db:genpept-bct1) (de:e.coli mcrb and mcrb genes, complete cds.) (le:129) (re:1526) (di:direct) ECOMCRBC M58752 g146796 Escherichia coli 562 -11533442 7500885396 mcrb (fn:restriction of dna at 5-methylcytosine) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 4978; alternate gene name rg1b) (le:268791) (re:270188) (di:complement) ECOUW93 U14003 g537188 Escherichia coli 562 -11533442 235095 mcrb component of mcrbc 5-methylcytosine restriction (fn:enzyme; degradation of dna) (db:genpept-bct2) (ec:3.1.21.-) (de:escherichia coli k-12 mg1655 section 395 of 400 of the completegenome.) (nt:f465; 100 pct identical to mcrb_ecoli sw: p15005;) (le:3969) (re:5366) (di:complement) AE000505 AE000505 g1790805 Escherichia coli 562 -11533442 83239 mcrb:rglb (ec:3.1.21.-) (de:5-methylcytosine-specific restriction enzyme b,) (db:swissprot) MCRB_ECOLI P15005 ESCHERICHIA COLI 562 -11533442 5000690692 (de:(ecoli_4230) (pn:component of mcrbc 5-methylcytosine restriction system) (gn:mcrb) (gtcfc:10.10) (ec:3.1.21.4) (mcrb_ecoli) (keggfc:11.1) (rileyfc:3.2.2) (db:gtc-escherichia coli)) ECOLI_4230 ECOLI_4230 Escherichia coli 562 10025458</p>				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501831550	8514	30670	705	235
<u>Description</u>				
Hypothetical protein				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501831564	8515	30671	234	77
<u>Description</u>				
Hypothetical protein				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831565	8516	30672	1041	346

Description

6500729585 hsdR:hsr:b4350 type i restriction enzyme ecok i r protein:type i restriction enzyme ecok i r protein (gtcfc:10.10) (ec:3.1.21.3) (keggfc:14.1) (rileyfc:3.2.2) (db:gtc-escherichia coli) b4350 b4350 Escherichia coli 562 -11533443 100262 hsdR:hsr (ec:3.1.21.3) (de:type i restriction enzyme ecok i r protein,) (db:swissprot) T1R\_ECOLI P08956 ESCHERICHIA COLI 562 -11533443 139836 hsdR type i site-specific deoxyribonuclease:ecok chain r:type i restriction enzyme ecok r chain:type i restriction-modification system ecok r chain (cl:type i site-specific deoxyribonuclease ecok chain r:dead/h box helicase homology) (ec:3.1.21.3) (db:pirl.dat) (mp:99 min) NDECKR S56576 Escherichia coli 562 -11533443 7500892669 hsdR (fn:endonuclease r; host restriction) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 620; alternate gene names hs, hsp, hsr,) (le:274082) (re:277648) (di:complement) ECOUW93 U14003 g537192 Escherichia coli 562 -11533443 237556 hsdR host restriction:endonuclease r (fn:enzyme; degradation of dna) (db:genpept-bct2) (ec:3.1.21.3) (de:escherichia coli k-12 mg1655 section 395 of 400 of the completegenome.) (nt:f1188; 100 pct identical to t1r\_ecoli sw: p08956;) (le:9260) (re:12826) (di:complement) AE000505 AE000505 g1790809 Escherichia coli 562 -11533443 5000690693 (de:(ecoli\_4234) (pn:host restriction; endonuclease r) (gn:hsdR) (gtcfc:10.10) (ec:3.1.21.3) (t1r\_ecoli) (keggfc:11.1) (rileyfc:3.2.2) (db:gtc-escherichia coli)) ECOLI\_4234 ECOLI\_4234 Escherichia coli 562 10042116

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831577	8517	30673	651	216

Description

6500729586 htra:degp:ptd:b0161 heat shock protein htra:protease do precursor (gtcfc:10.11:12.7) (ec:3.4.21.-) (keggfc:14.1) (rileyfc:3.2.3) (db:gtc-escherichia coli) b0161 b0161 Escherichia coli 562 -11533444 163162 htra proteinase do:precursor / heat shock protein htra (ec:3.4.21.-) (db:pir2.dat) (mp:4 min) S45229 S45229 Escherichia coli 562 -11533444 239790 htra heat shock protein htra (sr:escherichia coli (sub\_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0 min).) (le:69480) (re:70904) (di:direct) ECO82K D26562 g473819 Escherichia coli 562 -11533444 301630 htra heat shock protein htra (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:11959) (re:13383) (di:direct) ECU70214 U70214 g1552739 Escherichia coli 562 -11533444 233692 htra periplasmic serine protease do:heat shock (fn:enzyme; degradation of proteins, peptides,) (db:genpept-bct2) (ec:3.4.21.-) (de:escherichia coli k-12 mg1655 section 15 of 400 of the completegenome.) (nt:o474; 99 pct identical to htra\_ecoli sw: p09376;) (le:7391) (re:8815) (di:direct) AE000125 AE000125 g1786356 Escherichia coli 562 -11533444 5000690699 (de:(ecoli\_161) (pn:periplasmic serine protease do and heat shock protein) (gn:htra) (gtcfc:10.11) (ec:3.4.21.-) (htra\_ecoli) (keggfc:11.1) (rileyfc:3.2.3) (db:gtc-escherichia coli)) ECOLI\_161 ECOLI\_161 Escherichia coli 562 10086794

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831581	8518	30674	348	115

Description

6500729587 clpp:lopp:b0437 atp-dependent clp protease proteolytic subunit:endorpeptidase clp:caseinolytic protease:protease ti:heat shock protein f21.5 (gtcfc:10.11) (ec:3.4.21.92) (keggfc:14.1) (rileyfc:3.2.3) (db:gtc-escherichia coli) b0437 b0437 Escherichia coli 562 -11533445 64824 clpp:lopp (ec:3.4.21.92) (de:protein f21.5)) (db:swissprot) CLPP\_ECOLI P19245 ESCHERICHIA COLI 562 -11533445 162768 clpp:lopp atp-dependent clp proteinase:chain p:heat shock protein f21.5 (cl:atp-dependent clp proteinase chain p) (ec:3.4.21.-) (db:pir2.dat) B36575 B36575 Escherichia coli 562 -11533445 240214 (sr:e.coli (strain k12) dna) (db:genpept-bct1) (de:escherichia coli atp-dependent clp protease proteolytic component(clpp) gene, complete cds.) (nt:atp-dependent protease (clpp)) (le:378) (re:1001) (di:direct) ECOCLPPA J05534 g145556 Escherichia coli 562 -11533445 7500878868 clpp atp-dependent clp proteinase (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:36127) (re:36750) (di:direct) ECU82664 U82664 g1773121 Escherichia coli 562 -11533445 234009 clpp atp-dependent proteolytic subunit of clpa-clpp (fn:enzyme; degradation of proteins, peptides,) (db:genpept-bct2) (ec:3.4.21.92) (de:escherichia coli k-12 mg1655 section 40 of 400 of the completegenome.) (nt:o207; 100 pct identical to clpp\_ecoli sw: p19245) (le:1746) (re:2369) (di:direct) AE000150 AE000150 g1786641 Escherichia coli 562 -11533445 5000690700 (de:(ecoli\_421) (pn:atp-dependent proteolytic subunit of clpa- serine protease, heat shock protein f21) (gn:clpp) (gtcfc:10.11) (ec:3.4.21.92) (clpp\_ecoli) (keggfc:11.1) (rileyfc:3.2.3) (db:gtc-escherichia coli)) ECOLI\_421 ECOLI\_421 Escherichia coli 562 10007485

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831585	8519	30675	456	151
<u>Description</u>				
6500729588 clpx:lopc:b0438 atp-dependent clp protease atp-binding subunit clpx (gtcfc:10.11) (keggfc:14.2) (rileyfc:3.2.3) (db:gtc-escherichia coli) b0438 b0438 Escherichia coli 562 -11533446 162767 clpx:lopc atp-dependent clp proteinase:regulatory chain x (ec:3.4.21.-) (db:pir2.dat) A48709 A48709 Escherichia coli 562 -11533446 240215 clpx atp-dependent protease atpase subunit (fn:required for degradation of lambda o protein in) (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli atp-dependent protease atpase subunit (clpx) gene,complete cds.) (le:126) (re:1400) (di:direct) ECOCLPX L18867 g347729 Escherichia coli 562 -11533446 7500959678 clpx atp-dependent clp proteinase (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:36876) (re:38150) (di:direct) ECU82664 U82664 g1773122 Escherichia coli 562 -11533446 234010 clpx atp-dependent specificity component of clpp (fn:enzyme; degradation of proteins, peptides,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 40 of 400 of the completegenome.) (nt:o424; 100 pct identical to clpx_ecoli sw: p33138) (le:2495) (re:3769) (di:direct) AE000150 AE000150 g1786642 Escherichia coli 562 -11533446 5000690701 (de:(ecoli_422) (pn:atp-dependent subunit of clpp serine protease, determines specificity) (gn:clpx) (gtcfc:10.11) (ec:) (clpx_ecoli) (keggfc:11.2) (rileyfc:3.2.3) (db:gtc-escherichia coli)) ECOLI_422 ECOLI_422 Escherichia coli 562 10086614				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831591	8520	30676	183	60
<u>Description</u>				
Hypothetical protein				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831600	8521	30677	2082	694

Description

6500729589 clpa:lopd:b0882 atp-dependent clp protease atp-binding subunit  
clpa (gtcfc:10.11) (keggfc:14.2) (rileyfc:3.2.3) (db:gtc-escherichia coli)  
b0882 b0882 Escherichia coli 562 -11533447 64801 clpa:lopd  
(de:atp-dependent clp protease atp-binding subunit clpa) (db:swissprot)  
CLPA\_ECOLI P15716 ESCHERICHIA COLI 562 -11533447 7000684837 clpa:lopd  
atp-dependent clp proteinase:chain a:atp-dependent proteinase atp-binding  
protein (cl:atp-dependent clp proteinase chain a) (ec:3.4.21.-)  
(db:pir1.dat) (mp:19 min) SUECCA B64827 Escherichia coli 562 -11533447  
223241 clpa atp-dependent clp protease atp-binding subunit (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #212) (db:genpept-bct1)  
(de:escherichia coli genomic dna. (19.6 - 19.9 min).) (le:10201) (re:12477)  
(di:direct) D90725 D90725 g1651401 Escherichia coli 562 -11533447  
7500878851 clpa atp-binding component of serine protease (fn:enzyme;  
degradation of proteins, peptides,) (db:genpept-bct2) (de:escherichia coli  
k-12 mgl655 section 80 of 400 of the completegenome.) (nt:o758; 99 pct  
identical to clpa\_ecoli sw: p15716) (le:965) (re:3241) (di:direct) AE000190  
AE000190 g1787109 Escherichia coli 562 -11533447 5000690702 clpa  
atp-dependent clp protease atp-binding subunit (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #212) (db:genpept) (de:escherichia  
coli genomic dna. (19.7 - 20.0 min).) (nt:orf\_id:o213#7; similar to  
swissprot accession) (le:10201) (re:12477) (di:direct) D90725 D90725  
g1651401 Escherichia coli 562 -11533447

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831607	8522	30678	654	217

Description

6500729590 pepn:b0932 aminopeptidase n:alpha-aminoacylpeptide hydrolase (gtcfc:10.11) (ec:3.4.11.2) (keggfc:14.1) (rileyfc:3.2.3) (db:gtc-escherichia coli) b0932 b0932 Escherichia coli 562 -11533448  
7000688879 pepn membrane alanyl aminopeptidase::alpha-aminoacylpeptide hydrolase:aminopeptidase n:microsomal aminopeptidase (cl:microsomal aminopeptidase) (ec:3.4.11.2) (db:pir1.dat) (mp:21 min) DPECN C64833 Escherichia coli 562 -11533448 235387 pepn (sr:e.coli k12 (strain pc0031) dna, clone pmtm145 (1),(2)) (db:genpept-bct1) (de:e.coli k12 pepn gene encoding peptidase n, complete cds.) (nt:peptidase n) (le:465) (re:3077) (di:direct) ECOPEPN M15273 g147142 Escherichia coli 562 -11533448  
7500953304 pepn (sr:e.coli k12 (strain 9218) dna, clone pbm15) (db:genpept-bct1) (de:e.coli pepn gene encoding aminopeptidase n, complete cds.) (nt:aminopeptidase n) (le:1) (re:2613) (di:direct) ECOPEPNA M15676 g147144 Escherichia coli 562 -11533448 235386 pepn aminopeptidase n (fn:enzyme; degradation of proteins, peptides,) (db:genpept-bct2) (ec:3.4.11.2) (de:escherichia coli k-12 mg1655 section 85 of 400 of the completegenome.) (nt:o870; 100 pct identical to ampn\_ecoli sw: p04825) (le:7668) (re:10280) (di:direct) AE000195 AE000195 g1787163 Escherichia coli 562 -11533448 5000690703 pepn aminopeptidase n ec 3.4.11.2 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #219) (db:genpept) (de:escherichia coli genomic dna. (21.2 - 21.5 min).) (nt:orf\_id:o220#2; similar to swissprot accession) (le:7775) (re:10387) (di:direct) D90731 D90731 g4062498 Escherichia coli 562 -11533448

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831608	8523	30679	699	233

Description

6500729591 pept:b1127 peptidase t:aminotripeptidase:tripeptidase  
(gtcf:10.11) (ec:3.4.11.-) (keggfc:14.1) (rileyfc:3.2.3)  
(db:gtc-escherichia coli) b1127 b1127 Escherichia coli 562 -11533449 89032  
pept (ec:3.4.11.-) (de:peptidase t, (aminotripeptidase) (tripeptidase))  
(db:swissprot) PEPT\_ECOLI P29745 ESCHERICHIA COLI 562 -11533449 7000686114  
pept aminotripeptidase::peptidase t (ec:3.4.11.-) (db:pir2.dat) D64857  
D64857 Escherichia coli 562 -11533449 223375 pept peptidase t  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #239)  
(db:genpept-bct1) (de:escherichia coli genomic dna. (25.6 - 26.0 min).)  
(le:2078) (re:3304) (di:direct) D90748 D90748 g1651556 Escherichia coli 562  
-11533449 7500887828 pept putative peptidase t (fn:putative enzyme; not  
classified) (db:genpept-bct2) (ec:3.4.11.-) (de:escherichia coli k-12 mg1655  
section 103 of 400 of the completegenome.) (nt:o408; 100 pct identical to 42  
aa fragment) (le:155) (re:1381) (di:direct) AE000213 AE000213 g1787372  
Escherichia coli 562 -11533449 5000690704 pept peptidase t ec 3.4.11.-  
aminotripeptidase (sr:escherichia coli(strain:k12) dna, clone:kohara clone  
#239) (db:genpept) (de:escherichia coli genomic dna. (25.6 - 25.9 min).)  
(nt:orf\_id:o239#2; similar to swissprot accession) (le:2078) (re:3304)  
(di:direct) D90748 D90748 g1651556 Escherichia coli 562 -11533449

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831634	8524	30680	723	240
<u>Description</u>				
6500729592 dcp:b1538 dipeptidyl carboxypeptidase ii:peptidyl-dipeptidase:dipeptidyl carboxypeptidase (gtcfc:10.11) (ec:3.4.15.5) (keggfc:14.1) (rileyfc:3.2.3) (db:gtc-escherichia coli) b1538 b1538 Escherichia coli 562 -11533450 7000690870 dcp peptidyl-dipeptidase dcp::dipeptidyl carboxypeptidase ii (cl:peptidyl-dipeptidase dcp) (ec:3.4.15.5) (db:pir2.dat) E64908 E64908 Escherichia coli 562 -11533450 223905 dcp peptidyl-dipeptidase a ec 3.4.15.1 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #305(34.7-35.1 min.)). (nt:orf_id:o306#10; similar to (pir accession number) (le:14482) (re:16527) (di:complement) D90796 D90796 g1742521 Escherichia coli 562 -11533450 223918 dcp peptidyl-dipeptidase a ec 3.4.15.1 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #306(34.8-35.1 min.)). (nt:orf_id:o306#10; similar to (pir accession number) (le:7931) (re:9976) (di:complement) D90797 D90797 g1742535 Escherichia coli 562 -11533450 300637 dcp dipeptidyl carboxypeptidase ii (fn:enzyme; degradation of proteins, peptides,) (db:genpept-bct2) (ec:3.4.15.5) (de:escherichia coli k-12 mg1655 section 141 of 400 of the completegenome.) (nt:f681; 99 pct identical to dcp_ecoli sw: p24171; cg) (le:4150) (re:6195) (di:complement) AE000251 AE000251 g1787819 Escherichia coli 562 -11533450 5000690705 (de:(ecoli_1498) (pn:dipeptidyl carboxypeptidase) (gn:dcp) (gtcfc:10.11) (ec:3.4.15.5) (dcp_ecoli) (keggfc:11.1) (rileyfc:3.2.3) (db:gtc-escherichia coli)) ECOLI_1498 ECOLI_1498 Escherichia coli 562 10119686				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501831636	8525	30681	648	215

#### Description

6500729593 prc:tsp:b1830 tail-specific protease precursor:protease re:prc protein (gtcfc:10.11) (ec:3.4.21.-) (keggfc:14.1) (rileyfc:3.2.3) (db:gtc-escherichia coli) b1830 b1830 Escherichia coli 562 -11533451 90981 prc:tsp (ec:3.4.21.-) (de:protein) (db:swissprot) PRC\_ECOLI P23865 ESCHERICHIA COLI 562 -11533451 164675 prc:tsp carboxy-terminal proteinase:precursor:penicillin-binding protein 3 tail-specific proteinase tsp (ec:3.4.21.-) (db:pir2.dat) (mp:40 min) A41798 A41798 Escherichia coli 562 -11533451 224321 prc:tsp tail-specific protease precursor ec 3.4.21.- (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #335(40.9-41.3 min.)) (nt:orf\_id:o335#11; similar to (swissprot accession) (le:13932) (re:15980) (di:complement) D90826 D90826 g1736471 Escherichia coli 562 -11533451 300961 tsp tail-specific protease (sr:escherichia coli (sub\_strain w3110, strain k-12) (library: kohar) (db:genpept-bct1) (de:escherichia coli tail-specific protease (tsp) gene, complete cds.) (le:69) (re:2117) (di:direct) ECOTSP M75634 g148075 Escherichia coli 562 -11533451 236226 prc carboxy-terminal protease for penicillin-binding (fn:enzyme; degradation of proteins, peptides,) (db:genpept-bct2) (ec:3.4.21.-) (de:escherichia coli k-12 mg1655 section 167 of 400 of the completegenome.) (nt:f682; 99 pct identical to prc\_ecoli sw: p23865; cg) (le:4213) (re:6261) (di:complement) AE000277 AE000277 g1788134 Escherichia coli 562 -11533451 5000690706 (de:(ecoli\_1787) (pn:carboxy-terminal protease for penicillin-binding protein 3) (gn:prc) (gtcfc:10.11) (ec:3.4.21.-) (prc\_ecoli) (keggfc:11.1) (rileyfc:3.2.3) (db:gtc-escherichia coli)) ECOLI\_1787 ECOLI\_1787 Escherichia coli 562 10086628

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501831643	8526	30682	321	107

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831644	8527	30683	594	197

Description

6500729594 ptrb:tlp:b1845 protease ii:oligopeptidase b (gtcfc:10.11)  
(ec:3.4.21.83) (keggfc:14.1) (rileyfc:3.2.3) (db:gtc-escherichia coli) b1845  
b1845 Escherichia coli 562 -11533452 92305 ptrb:tlp (ec:3.4.21.83)  
(de:protease ii, (oligopeptidase b)) (db:swissprot) PTRB\_ECOLI P24555  
ESCHERICHIA COLI 562 -11533452 7000686231 ptrb:tlp oligopeptidase  
b::proteinase ii (cl:prolyl oligopeptidase) (ec:3.4.21.83) (db:pir2.dat)  
E64946 E64946 Escherichia coli 562 -11533452 224334 ptrb:tlp protease ii ec  
3.4.21.83 oligopeptidase b . (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #336(41.2-41.6 min.)) (nt:orf\_id:o336#12; similar to  
(swissprot accession) (le:13896) (re:15956) (di:complement) D90827 D90827  
g1736485 Escherichia coli 562 -11533452 300974 ptrb protease ii (fn:enzyme;  
degradation of proteins, peptides,) (db:genpept-bct2) (ec:3.4.21.83)  
(de:escherichia coli k-12 mgl655 section 168 of 400 of the completegenome.)  
(nt:f686; this 686 aa orf is 100 pct identical to) (le:6629) (re:8689)  
(di:complement) AE000278 AE000278 g1788150 Escherichia coli 562 -11533452  
5000690707 (de:(ecoli\_1802) (pn:protease ii) (gn:ptrb) (gtcfc:10.11)  
(ec:3.4.21.83) (ptrb\_ecoli) (keggfc:11.1) (rileyfc:3.2.3)  
(db:gtc-escherichia coli)) ECOLI\_1802 ECOLI\_1802 Escherichia coli 562  
10119870

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831646	8528	30684	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831665	8529	30685	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831675	8530	30686	363	120

Description

6500729595 eco:eti:b2209 tin precursor:ecotin precursor (gtcfc:10.11)  
(keggfc:14.2) (rileyfc:3.2.3) (db:gtc-escherichia coli) b2209 b2209  
Escherichia coli 562 -11533453 234221 eco:eti (de:ecotin precursor)  
(db:swissprot) ECOT\_ECOLI P23827 ESCHERICHIA COLI 562 -11533453 162983 eco  
ecotin precursor (db:pir2.dat) A38742 A38742 Escherichia coli 562 -11533453  
224676 eco:eti ecotin precursor. (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #373(49.5-49.9 min.)) (nt:orf\_id:o372#4; similar to (swissprot  
accession) (le:3424) (re:3912) (di:direct) D90850 D90850 g1736850  
Escherichia coli 562 -11533453 5000690708 eti ecotin (db:genpept-bct1)  
(de:e.coli eti gene for ecotin.) (le:284) (re:772) (di:direct) ECECOTIN  
X61951 g41328 Escherichia coli 562 -11533453 301316 ecotin (sr:e.coli  
(strain k-12) dna) (db:genpept-bct1) (de:e.coli ecotin gene, complete cds.)  
(le:274) (re:762) (di:direct) ECOEOA M60876 g145824 Escherichia coli 562  
-11533453 232742 eco ecotin:a serine protease inhibitor (fn:regulator;  
degradation of proteins, peptides,) (db:genpept-bct2) (de:escherichia coli  
k-12 mg1655 section 200 of 400 of the completegenome.) (nt:o162; 100 pct  
identical to ecot\_ecoli sw: p23827;) (le:225) (re:713) (di:direct) AE000310  
AE000310 g1788538 Escherichia coli 562 -11533453 69698 eco:eti (de:ecotin  
precursor) (db:swissprot) ECOT\_ECOLI P23827 ESCHERICHIA COLI 562 -11533453

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831677	8531	30687	744	247

#### Description

6500729596 clpb:htpm:b2592 clpb protein:heat shock protein f84.1  
 (gtcfc:10.11) (keggfc:14.2) (rileyfc:3.2.3) (db:gtc-escherichia coli) b2592  
 b2592 Escherichia coli 562 -11533454 64807 clpb:htpm (de:clpb protein (heat  
 shock protein f84.1)) (db:swissprot) CLPB\_ECOLI P03815 ESCHERICHIA COLI 562  
 -11533454 7000684838 clpb::3 atp-dependent clp proteinase:regulatory chain  
 b (cl:atp-dependent clp proteinase chain a) (ec:3.4.21.-) (db:pir1.dat)  
 (mp:56 min) D35905 C65037 Escherichia coli 562 -11533454 225166 clpb clpb  
 protein heat shock protein f84.1 . (sr:escherichia coli (strain:k12) dna,  
 clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
 kohara clone #437(58.6-59.0 min.)) (nt:similar to (swissprot accession  
 number p03815)) (le:9749) (re:12322) (di:complement) D90887 D90887 g1799995  
 Escherichia coli 562 -11533454 7500878852 clpb heat shock protein  
 (fn:putative enzyme; degradation of proteins,) (db:genpept-bct2)  
 (de:escherichia coli k-12 mg1655 section 235 of 400 of the completegenome.)  
 (nt:f857; 99 pct identical to clpb\_ecoli sw: p03815) (le:8962) (re:11535)  
 (di:complement) AE000345 AE000345 g1788943 Escherichia coli 562 -11533454  
 5000690709 (de:(ecoli\_2528) (pn:heat shock protein, probable atp-binding  
 subunit of serine protease, determines specificity; heat shock proteins f84)  
 (gn:clpb) (gtcfc:10.11) (ec:) (clpb\_ecoli) (keggfc:11.2) (rileyfc:3.2.3)  
 (db:gtc-escheric) ECOLI\_2528 ECOLI\_2528 Escherichia coli 562 10120280

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831690	8532	30688	204	67

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831696	8533	30689	186	61

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831698	8534	30690	1515	505

#### Description

GTC ORF with score 109 to: (fn:involved in heterokaryon incompatibility)  
 (sr:podospora anserina dna) (db:genpept-vrl) (de:podospora anserina beta  
 transducin-like protein (het-e1) gene,complete cds.) (nt:putative)  
 (le:810:3142) (re:3092:4929) ...



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831714	8535	30691	387	128

Description

6500729597 alpa:alp:b2624 prophage cp4-57 regulatory protein alpa (gtcfc:10.11) (keggfc:14.2) (rileyfc:3.2.3) (db:gtc-escherichia coli) b2624 b2624 Escherichia coli 562 -11533455 59217 alpa:alp (de:prophage cp4-57 regulatory protein alpa) (db:swissprot) ALPA\_ECOLI P33997 ESCHERICHIA COLI 562 -11533455 7000684562 alpa prophage cp4-57 regulatory protein alpa (db:pir2.dat) B65041 B65041 Escherichia coli 562 -11533455 239485 alpa alpa (fn:positive regulator of int transcription) (db:genpept-bct1) (de:escherichia coli k12 10sa stable rna (ssra) gene, partial sequence, and cryptic prophage cp4-57 slpa integrase (slpa) and alpatranscriptional regulator (alpa) genes, complete cds.) (le:2... ECOALPA U03737 g433350 Escherichia coli 562 -11533455 7500876774 alpa alpa (fn:positive regulator of int transcription) (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 57 minutes.) (le:7598) (re:7810) (di:direct) ECU36840 U36840 g1033119 Escherichia coli 562 -11533455 233765 alpa prophage cp4-57 regulatory protein alpa (fn:is, phage, tn; phage-related functions and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 238 of 400 of the completengenome.) (nt:o70; 100 pct identical to alpa\_ecoli sw: p33997) (le:1152) (re:1364) (di:direct) AE000348 AE000348 g1788977 Escherichia coli 562 -11533455 5000690710 (de:(ecoli\_2559) (pn:prophage cp4-57 regulatory protein alpa) (gn:alpa) (gtcfc:10.11) (ec:) (alpa\_ecoli) (keggfc:11.2) (rileyfc:3.2.3) (db:gtc-escherichia coli)) ECOLI\_2559 ECOLI\_2559 Escherichia coli 562 10001956

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831720	8536	30692	942	313
<u>Description</u>				
6500729598 pepp:b2908 proline aminopeptidase ii:xaa-pro aminopeptidase:x-pro aminopeptidase:aminopeptidase p ii:app-ii:aminoacylproline aminopeptidase (gtcf:10.11) (ec:3.4.11.9) (keggfc:14.1) (rileyfc:3.2.3) (db:gtc-escherichia coli) b2908 b2908 Escherichia coli 562 -11533456 124728 pepp x-pro aminopeptidase:ii:aminoacylproline aminopeptidase:aminopeptidase p:proline aminopeptidase ii (cl:aminopeptidase p) (ec:3.4.11.9) (db:pir1.dat) (mp:63 min) DPECP JX0067 Escherichia coli 562 -11533456 235632 (sr:e. coli (strain hb101) genomic dna) (db:genpept-bct1) (de:escherichia coli hb101 pepp gene for aminopeptidase p (app-ii), complete cds.) (nt:aminopeptidase p precursor) (le:369) (re:1694) (di:direct) ECOAPP2 D00398 g216529 Escherichia coli 562 -11533456 239122 pepp pepp proline amino peptidaseii (sr:escherichia coli (strain:k12 ca274) dna) (db:genpept-bct1) (de:escherichia coli pepp, ubih (visb) and visc genes.) (le:1087) (re:2412) (di:direct) ECOPUV D90281 g216627 Escherichia coli 562 -11533456 7500953305 pepp (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f441; third start codon) (le:7906) (re:9231) (di:complement) ECU28377 U28377 g882438 Escherichia coli 562 -11533456 233807 pepp proline aminopeptidase p ii (fn:enzyme; degradation of proteins, peptides,) (db:genpept-bct2) (ec:3.4.11.9) (de:escherichia coli k-12 mg1655 section 264 of 400 of the completegenome.) (nt:f441; 100 pct identical to ampp_ecoli sw:) (le:4445) (re:5770) (di:complement) AE000374 AE000374 g1789275 Escherichia coli 562 -11533456 5000690711 (de:(ecoli_2831) (pn:aminopeptidase p ii) (gn:pepp) (gtcf:10.11) (ec:3.4.11.9) (ampp_ecoli) (keggfc:11.1) (rileyfc:3.2.3) (db:gtc-escherichia coli)) ECOLI_2831 ECOLI_2831 Escherichia coli 562 10066195				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831744	8537	30693	921	306

#### Description

6500729599 soha:prlf:b3129 htra suppressor protein:protein prlf  
 (gtcfc:10.11) (keggfc:14.2) (rileyfc:3.2.3) (db:gtc-escherichia coli) b3129  
 b3129 Escherichia coli 562 -11533457 98946 soha:prlf (de:htra suppressor  
 protein (protein prlf)) (db:swissprot) SOHA\_ECOLI P15373 ESCHERICHIA COLI  
 562 -11533457 164670 soha:prlf suppressor protein soha:htra suppressor  
 protein (db:pir2.dat) A35137 A35137 Escherichia coli 562 -11533457 236009  
 (sr:e.coli (strain k12) dna) (db:genpept-bct1) (de:e.coli prlf protein gene,  
 complete cds.) (nt:prlf protein) (le:145) (re:480) (di:direct) ECOPRLF  
 M32358 g147351 Escherichia coli 562 -11533457 236368 (sr:e.coli (k12,  
 isolate w3110) cell line b178 dna, clones plb29(0,8) (db:genpept-bct1)  
 (de:e.coli htra suppressor protein (soha) gene, complete cds.) (nt:soha  
 protein) (le:378) (re:713) (di:direct) ECOSHA M30178 g147844 Escherichia  
 coli 562 -11533457 7500891848 soha (db:genpept-bct1) (de:escherichia coli  
 k-12 chromosomal region from 67.4 to 76.0 minutes.) (le:57755) (re:58090)  
 (di:direct) ECOUW67 U18997 g606069 Escherichia coli 562 -11533457 235555  
 soha putative protease:htra suppressor protein (fn:putative enzyme; not  
 classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 284  
 of 400 of the complete genome.) (nt:o111; 100 pct identical to soha\_ecoli sw:  
 p15373) (le:7400) (re:7735) (di:direct) AE000394 AE000394 g1789517  
 Escherichia coli 562 -11533457 5000690712 (de:(ecoli\_3053) (pn:htra  
 suppressor protein) (gn:soha) (gtcfc:10.11) (ec:) (soha\_ecoli) (keggfc:11.2)  
 (rileyfc:3.2.3) (db:gtc-escherichia coli)) ECOLI\_3053 ECOLI\_3053 Escherichia  
 coli 562 10040811

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831747	8538	30694	339	112

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831748	8539	30695	201	66

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831761	8540	30696	315	104

#### Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501831781	8541	30697	891	297

Description

6500729600 prlc:opda:b3498 oligopeptidase a (gtcfc:10.11) (ec:3.4.24.70)  
 (keggfc:14.1) (rileyfc:3.2.3) (db:gtc-escherichia coli) b3498 b3498  
 Escherichia coli 562 -11533458 87734 prlc:opda (ec:3.4.24.70)  
 (de:oligopeptidase a,) (db:swissprot) OPDA\_ECOLI P27298 ESCHERICHIA COLI 562  
 -11533458 164367 prlc oligopeptidase a::prlc protein  
 (cl:peptidyl-dipeptidase dcp) (ec:3.4.24.-) (db:pir2.dat) S47718 S47718  
 Escherichia coli 562 -11533458 7500887187 prlc (fn:protein export)  
 (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda)  
 (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.)  
 (nt:cg site no. 18031; heat shock regulated) (le:57399) (re:59441)  
 (di:complement) ECOUW76 U00039 g466635 Escherichia coli 562 -11533458  
 236734 prlc oligopeptidase a (fn:enzyme; degradation of proteins,  
 peptides,) (db:genpept-bct2) (ec:3.4.24.70) (de:escherichia coli k-12 mg1655  
 section 316 of 400 of the completegenome.) (nt:f680; 100 pct identical to  
 opda\_ecoli sw: p27298;) (le:2439) (re:4481) (di:complement) AE000426  
 AE000426 g1789913 Escherichia coli 562 -11533458 5000690713  
 (de:(ecoli\_3417) (pn:oligopeptidase a) (gn:prlc) (gtcfc:10.11)  
 (ec:3.4.24.70) (opda\_ecoli) (keggfc:11.1) (rileyfc:3.2.3)  
 (db:gtc-escherichia coli)) ECOLI\_3417 ECOLI\_3417 Escherichia coli 562  
 10029876

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501831814	8542	30698	963	320

Description

6500729601 pepq:b3847 xaa-pro dipeptidase:x-pro dipeptidase:proline  
 dipeptidase:prolidase:imidodipeptidase (gtcfc:10.11) (ec:3.4.13.9)  
 (keggfc:14.1) (rileyfc:3.2.3) (db:gtc-escherichia coli) b3847 b3847  
 Escherichia coli 562 -11533459 89028 pepq (ec:3.4.13.9) (de:dipeptidase)  
 (prolidase) (imidodipeptidase)) (db:swissprot) PEPQ\_ECOLI P21165 ESCHERICHIA  
 COLI 562 -11533459 7000686112 pepq x-pro  
 dipeptidase::iminodipeptidase:prolidase:proline dipeptidase (ec:3.4.13.9)  
 (db:pir2.dat) (mp:86 min) H65189 H65189 Escherichia coli 562 -11533459  
 7500887825 pepq proline dipeptidase (fn:enzyme; degradation of proteins,  
 peptides,) (db:genpept-bct2) (ec:3.4.13.9) (de:escherichia coli k-12 mg1655  
 section 350 of 400 of the completegenome.) (nt:o443; 99 pct identical amino  
 acid sequence and) (le:3902) (re:5233) (di:direct) AE000460 AE000460  
 g1790282 Escherichia coli 562 -11533459 5000690714 (de:(ecoli\_3752)  
 (pn:proline dipeptidase) (gn:pepq) (gtcfc:10.11) (ec:3.4.13.9) (pepq\_ecoli)  
 (keggfc:11.1) (rileyfc:3.2.3) (db:gtc-escherichia coli)) ECOLI\_3752  
 ECOLI\_3752 Escherichia coli 562 10031154

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831819	8543	30699	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831820	8544	30700	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831823	8545	30701	303	101

Description

6500729602 hflx:b4173 gtp-binding protein hflx (gtcfc:10.11) (keggfc:14.2) (rileyfc:3.2.3) (db:gtc-escherichia coli) b4173 b4173 Escherichia coli 562 -11533460 76914 hflx (de:gtp-binding protein hflx) (db:swissprot) HFLX\_ECOLI P25519 ESCHERICHIA COLI 562 -11533460 163147 hflx probable gtp-binding protein hflx (cl:gtp-binding protein hflx) (db:pir2.dat) S56398 S56398 Escherichia coli 562 -11533460 237378 hflx (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:putative gtpase required for high frequency) (le:91500) (re:92780) (di:direct) ECOUW93 U14003 g537014 Escherichia coli 562 -11533460 234641 hflx gtp -binding subunit of protease specific for (fn:enzyme; degradation of proteins, peptides,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 379 of 400 of the completegenome.) (nt:o426; 100 pct identical to hflx\_ecoli sw:) (le:8386) (re:9666) (di:direct) AE000489 AE000489 g1790615 Escherichia coli 562 -11533460 7500883240 hflx (sr:escherichia coli k12) (db:genpept-bct2) (de:e. coli hfla locus encoding the hflx, hflk and hflc genes, hfggene, complete cds; miaa gene, partial cds.) (nt:putative gtpase required for high frequency) (le:1122) (re:2402) (di:direct) ECOHFLA U00005 g436156 Escherichia coli 562 -11533460 5000690715 (de:(ecoli\_4056) (pn:gtp - binding subunit of protease specific for phage lambda cii repressor) (gn:hflx) (gtcfc:10.11) (ec:) (hflx\_ecoli) (keggfc:11.2) (rileyfc:3.2.3) (db:gtc-escherichia coli)) ECOLI\_4056 ECOLI\_4056 Escherichia coli 562 10019276

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831824	8546	30702	486	161

Description

GTC ORF with score 156 to: (fn:sugar transport) (sr:ricinus communis (strain carmencita) cdna to mrna) (db:genpept-pln1) (de:ricinus communis (clone pst9) sugar carrier protein (rcsta) mrna,complete cds.) (nt:putative) (le:102) (re:1670) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831828	8547	30703	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831829	8548	30704	408	135

Description

6500729603 hflk:hfla:b4174 hflk protein (gtcfc:10.11) (keggfc:14.2) (rileyfc:3.2.3) (db:gtc-escherichia coli) b4174 b4174 Escherichia coli 562 -11533461 76911 hflk:hfla (de:hflk protein) (db:swissprot) HFLK\_ECOLI P25662 ESCHERICHIA COLI 562 -11533461 164387 hflk probable integral membrane proteinase:hflk (ec:3.4.-.-) (db:pir2.dat) B43653 B43653 Escherichia coli 562 -11533461 237379 hflk (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 639; alternate gene name hfla; putative) (le:92866) (re:94125) (di:direct) ECOUW93 U14003 g537015 Escherichia coli 562 -11533461 234642 hflk protease specific for phage lambda cii (fn:enzyme; degradation of proteins, peptides,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 379 of 400 of the completegenome.) (nt:o419; 100 pct identical to hflk\_ecoli sw: p25662;) (le:9752) (re:11011) (di:direct) AE000489 AE000489 g1790616 Escherichia coli 562 -11533461 7500883238 hflk (sr:escherichia coli k12) (db:genpept-bct2) (de:e. coli hfla locus encoding the hflx, hflk and hflc genes, hfggene, complete cds; miaa gene, partial cds.) (nt:putative integral membrane protein required for) (le:2488) (re:3747) (di:direct) ECOHFLA U00005 g436157 Escherichia coli 562 -11533461 5000690716 (de:(ecoli\_4057) (pn:protease specific for phage lambda cii repressor) (gn:hflk) (gtcfc:10.11) (ec:) (hflk\_ecoli) (keggfc:11.2) (rileyfc:3.2.3) (db:gtc-escherichia coli)) ECOLI\_4057 ECOLI\_4057 Escherichia coli 562 10019273

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831834	8549	30705	303	101

Description

GTC ORF with score 224 to:

(gtcfc:1.1:1.11:1.5:1.6:1.7:3.5:4.3:5.13:5.3:5.9:9.3) (ec:1.1.1.-)  
(keggfc:1.5:1.6:1.7:1.11:3.5:4.3:5.3:5.9:5.13:9.3) (sgdgc:1.5.1:9.2.0)  
(db:gtc-saccharomyces cerevisiae) (gtcfc:carbohydrate ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831859	8550	30706	726	241
<u>Description</u>				
6500729604 pepa:xerb:carp:b4260 aminopeptidase a/l:aminopeptidase a/i (gtcfc:10.11) (ec:3.4.11.1) (keggfc:14.1) (rileyfc:3.2.3) (db:gtc-escherichia coli) b4260 b4260 Escherichia coli 562 -11533462 7500876827 pepa:xerb:carp (ec:3.4.11.1) (de:aminopeptidase a/i, (db:swissprot) AMPA_ECOLI P11648 ESCHERICHIA COLI 562 -11533462 124726 pepa:xerb leucyl aminopeptidase:a:aminopeptidase i:cytosol aminopeptidase a (cl:cytosol aminopeptidase) (ec:3.4.11.1) (db:pirl.dat) (mp:96.5 min) APECA S04462 Escherichia coli 562 -11533462 237773 pepa aminopeptidase a/1 (db:genpept-bct1) (ec:3.4.11.1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:alternate gene name xerb) (le:175275) (re:176786) (di:complement) ECOUW93 U14003 g537102 Escherichia coli 562 -11533462 240384 pepa/carp aminopeptidase a (db:genpept-bct1) (de:e.coli pepa/carp gene.) (le:371) (re:1882) (di:direct) ECPEPCAR X86443 g1054725 Escherichia coli 562 -11533462 5000690717 (db:genpept-bct1) (de:e. coli xerb gene for aminopeptidase a/i (ec 3.4.11.1).) (nt:aminopeptidase a/i (aa 1 - 503)) (le:60) (re:1571) (di:direct) ECXERB X15130 g43309 Escherichia coli 562 -11533462 237466 pepa aminopeptidase a/i (fn:enzyme; degradation of proteins, peptides,) (db:genpept-bct2) (ec:3.4.11.1) (de:escherichia coli k-12 mg1655 section 386 of 400 of the completegenome.) (nt:f503; 100 pct identical to ampa_ecoli sw: p11648;) (le:10289) (re:11800) (di:complement) AE000496 AE000496 g1790710 Escherichia coli 562 -11533462 59351 pepa:xerb:carp (ec:3.4.11.1) (de:aminopeptidase a/i,) (db:swissprot) AMPA_ECOLI P11648 ESCHERICHIA COLI 562 -11533462				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831860	8551	30707	516	171

Description

6500729605 rada:sms:b4389 sms protein:dna repair protein rada:dna repair protein sms (gtcfc:10.11) (keggfc:14.2) (rileyfc:3.2.3) (db:gtc-escherichia coli) b4389 b4389 Escherichia coli 562 -11533463 239743 rada:sms (de:dna repair protein rada (dna repair protein sms)) (db:swissprot) RADA\_ECOLI P24554 ESCHERICHIA COLI 562 -11533463 164633 sms dna repair protein sms (cl:dna repair protein sms) (db:pir2.dat) JC1417 JC1417 Escherichia coli 562 -11533463 238277 sms (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:316744) (re:318126) (di:direct) ECOUW93 U14003 g537229 Escherichia coli 562 -11533463 5000690718 sms (fn:unknown) (db:genpept-bct1) (de:e.coli sms gene.) (le:64) (re:1446) (di:direct) ECSMSG X63155 g581233 Escherichia coli 562 -11533463 237594 sms probable atp-dependent protease (fn:putative enzyme; degradation of proteins,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 399 of 400 of the completegenome.) (nt:o460; 100 pct identical amino acid sequence and) (le:1100) (re:2482) (di:direct) AE000509 AE000509 g1790850 Escherichia coli 562 -11533463 7500889337 rada rada (db:genpept-bct2) (de:escherichia coli rada gene, complete cds.) (nt:sms) (le:16) (re:1398) (di:direct) ECU59449 U59449 g1401238 Escherichia coli 562 -11533463 98711 rada:sms (de:dna repair protein rada (dna repair protein sms)) (db:swissprot) RADA\_ECOLI P24554 ESCHERICHIA COLI 562 -11533463

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831864	8552	30708	375	124

Description

6500729606 lytb:b0029 lytb protein (gtcfc:10.2) (keggfc:14.2) (rileyfc:2.0.0) (db:gtc-escherichia coli) b0029 b0029 Escherichia coli 562 -11533464 233566 lytb (de:lytb protein) (db:swissprot) LYTB\_ECOLI P22565 ESCHERICHIA COLI 562 -11533464 163273 lytb lytb protein (cl:penicillin tolerance protein) (db:pir2.dat) JE0403 JE0403 Escherichia coli 562 -11533464 5000691080 orf::2 (db:genpept-bct1) (de:e. coli lsp-dapb interval.) (le:597) (re:1547) (di:direct) ECLSPDAP X54945 g41933 Escherichia coli 562 -11533464 7500885221 orf (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (nt:hypothetical 34.8k protein(pir:je0403)) (le:25931) (re:26881) (di:direct) ECO110K D10483 g216456 Escherichia coli 562 -11533464 233330 lytb control of stringent response:involved in (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 3 of 400 of the completegenome.) (nt:o316; 100 pct identical to lytb\_ecoli sw: p22565) (le:5618) (re:6568) (di:direct) AE000113 AE000113 g1786212 Escherichia coli 562 -11533464 82775 lytb (de:lytb protein) (db:swissprot) LYTB\_ECOLI P22565 ESCHERICHIA COLI 562 -11533464



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831869	8553	30709	1002	333

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831877	8554	30710	1125	374

Description

6500729607 phob:b0399 phosphate regulon transcriptional regulatory protein  
phob (gtcfc:10.2:12.13) (keggfc:12.1) (rileyfc:2.0.0) (db:gtc-escherichia  
coli) b0399 b0399 Escherichia coli 562 -11533465 240016 phob (de:phosphate  
regulon transcriptional regulatory protein phob) (db:swissprot) PHOB\_ECOLI  
P08402 ESCHERICHIA COLI 562 -11533465 131467 phob transcription activator  
phob:transcription regulator of phosphate regulon:transcription regulator  
phob (cl:omp protein:response regulator homology) (db:pir1.dat) (mp:9 min)  
RGEFCB A24256 Escherichia coli 562 -11533465 5000691081 (db:genpept-bct1)  
(de:e. coli phob gene for positive regulator of phosphate regulon.) (nt:phob  
protein (aa 1-229)) (le:280) (re:969) (di:direct) ECPHOB X04026 g42388  
Escherichia coli 562 -11533465 7500888040 phob phosphate regulon  
transcriptional regulatory (db:genpept-bct1) (de:escherichia coli chromosome  
minutes 6-8.) (le:124732) (re:125421) (di:direct) ECU73857 U73857 g1657595  
Escherichia coli 562 -11533465 237802 phob positive response regulator for  
pho regulon (fn:regulator; global regulatory functions) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 36 of 400 of the completegenome.)  
(nt:o229; 100 pct identical to phob\_ecoli sw: p08402) (le:4628) (re:5317)  
(di:direct) AE000146 AE000146 g1786599 Escherichia coli 562 -11533465 89623  
phob (de:phosphate regulon transcriptional regulatory protein phob)  
(db:swissprot) PHOB\_ECOLI P08402 ESCHERICHIA COLI 562 -11533465

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831878	8555	30711	753	250

Description

6500729608 phor:nmpb:b0400 phosphate regulon sensor protein phor  
 (gtcfc:10.2:12.13) (ec:2.7.3.-) (keggfc:12.1) (rileyfc:2.0.0)  
 (db:gtc-escherichia coli) b0400 b0400 Escherichia coli 562 -11533466 240017  
 phor:nmpb (ec:2.7.3.-) (de:phosphate regulon sensor protein phor,)  
 (db:swissprot) PHOR\_ECOLI P08400 ESCHERICHIA COLI 562 -11533466 130853 phor  
 sensor kinase:phor:phosphate regulon sensor protein phor (cl:phosphate  
 regulon regulatory protein) (ec:2.7.3.-) (db:pir1.dat) (mp:9 min) RGE CFR  
 A25557 Escherichia coli 562 -11533466 5000691082 (db:genpept-bct1) (de:e.  
 coli phor gene.) (nt:phor gene product (aa 1-431)) (le:61) (re:1356)  
 (di:direct) ECPHORG X04704 g581188 Escherichia coli 562 -11533466  
 7500888060 phor phosphate regulon sensor protein phor (db:genpept-bct1)  
 (ec:2.7.3.-) (de:escherichia coli chromosome minutes 6-8.) (le:125479)  
 (re:126774) (di:direct) ECU73857 U73857 g1657596 Escherichia coli 562  
 -11533466 237806 phor positive and negative sensor protein for pho  
 (fn:enzyme; global regulatory functions) (db:genpept-bct2) (ec:2.7.3.-)  
 (de:escherichia coli k-12 mg1655 section 36 of 400 of the completegenome.)  
 (nt:o431; 100 pct identical to phor\_ecoli sw: p08400) (le:5375) (re:6670)  
 (di:direct) AE000146 AE000146 g1786600 Escherichia coli 562 -11533466 89646  
 phor:nmpb (ec:2.7.3.-) (de:phosphate regulon sensor protein phor,)  
 (db:swissprot) PHOR\_ECOLI P08400 ESCHERICHIA COLI 562 -11533466

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831902	8556	30712	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831903	8557	30713	588	195

Description

6500729609 lon:capr:deg:muc:lopa:b0439 lon protease:atp-dependent protease la (gtcfc:10.11:10.2) (ec:3.4.21.53) (keggfc:14.1) (rileyfc:2.0.0) (db:gtc-escherichia coli) b0439 b0439 Escherichia coli 562 -11533467 82321 lon:capr:deg:muc:lopa (ec:3.4.21.53) (de:atp-dependent protease la,) (db:swissprot) LON\_ECOLI P08177 ESCHERICHIA COLI 562 -11533467 7000685757 lon:capr:deg:muc:lopa endopeptidase la::atp-dependent serine proteinase la (cl:atp-dependent serine proteinase la) (ec:3.4.21.53) (db:pir1.dat) (mp:10 min) SUECLA G64773 Escherichia coli 562 -11533467 235001 lon dna-binding:atp-dependent protease la:heat (fn:enzyme; global regulatory functions) (db:genpept-bct2) (ec:3.4.21.53) (de:escherichia coli k-12 mg1655 section 40 of 400 of the completgenome.) (nt:o784; 100 pct identical to lon\_ecoli sw: p08177) (le:3957) (re:6311) (di:direct) AE000150 AE000150 g1786643 Escherichia coli 562 -11533467 7500885101 lon lon protease (fn:atp-dependant protease) (sr:escherichia coli dna) (db:genpept-bct2) (de:escherichia coli (clone plon+500) lon protease (lon) gene, completecds.) (nt:n-terminal amino acid sequence verified by) (le:8) (re:2362) (di:direct) ECOLONPRO L12349 g290454 Escherichia coli 562 -11533467 5000691083 (de:(ecoli\_423) (pn:dna-binding, atp-dependent protease la; heat shock k-protein) (gn:lon) (gtcfc:12.13) (ec:3.4.21.53) (lon\_ecoli) (keggfc:11.1) (rileyfc:2.0.0) (db:gtc-escherichia coli)) ECOLI\_423 ECOLI\_423 Escherichia coli 562 10024551

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831912	8558	30714	597	198

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831933	8559	30715	420	139

#### Description

6500729610 fur:b0683 ferric uptake regulation protein (gtcfc:10.2) (keggfc:14.2) (rileyfc:2.0.0) (db:gtc-escherichia coli) b0683 b0683 Escherichia coli 562 -11533468 7500881919 fur (de:ferric uptake regulation protein (ferric uptake regulator)) (db:swissprot) FUR\_ECOLI P06975 ESCHERICHIA COLI 562 -11533468 164467 fur ferric uptake transcription regulator:regulatory protein fur (cl:ferric uptake regulator) (db:pir2.dat) (mp:15.5 min) S07308 S07308 Escherichia coli 562 -11533468 223146 fur regulatory protein fur (sr:escherichia coli(strain:k12) dna, clone:kohara clone #172) (db:genpept-bct1) (de:escherichia coli genomic dna. (15.0 - 15.4 min).) (le:10027) (re:10473) (di:complement) D90707 D90707 g1651290 Escherichia coli 562 -11533468 232941 fur negative regulator (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 62 of 400 of the completegenome.) (nt:f148; 100 pct identical to fur\_ecoli sw: p06975) (le:2185) (re:2631) (di:complement) AE000172 AE000172 g1786899 Escherichia coli 562 -11533468 5000691084 fur fur protein (db:genpept-bct2) (de:escherichia coli fur gene.) (le:268) (re:714) (di:direct) ECFUR X02589 g41515 Escherichia coli 562 -11533468 7502851935 fur regulatory protein fur. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #172) (db:genpept) (de:escherichia coli genomic dna. (15.1 - 15.5 min).) (nt:orf\_id:ol72#8; similar to pir accession number) (le:10027) (re:10473) (di:complement) D90707 D90707 g1651290 Escherichia coli 562 -11533468 72543 fur (de:ferric uptake regulation protein) (db:swissprot) FUR\_ECOLI P06975 ESCHERICHIA COLI 562 -11533468

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831937	8560	30716	780	259

#### Description

6500729611 kdpe:b0694 kdp operon transcriptional regulatory protein kdpe (gtcfc:10.2:12.13) (keggfc:12.1) (rileyfc:2.0.0) (db:gtc-escherichia coli) b0694 b0694 Escherichia coli 562 -11533469 80594 kdpe (de:kdp operon transcriptional regulatory protein kdpe) (db:swissprot) KDPE\_ECOLI P21866 ESCHERICHIA COLI 562 -11533469 7000685674 kdpe transcription regulator kdpe:regulatory protein kdpe (cl:ompr protein:response regulator homology) (db:pir2.dat) E64804 E64804 Escherichia coli 562 -11533469 7500884569 kdpe regulator of kdp operon transcriptional (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 63 of 400 of the completegenome.) (nt:f225; 92 pct identical to kdpe\_ecoli sw: p21866) (le:328) (re:1005) (di:complement) AE000173 AE000173 g1786911 Escherichia coli 562 -11533469 5000691085 (de:(ecoli\_668) (pn:regulator of kdp operon:transcriptional effector) (gn:kdpe) (gtcfc:12.13) (ec:)(kdpe\_ecoli) (keggfc:11.2) (rileyfc:2.0.0) (db:gtc-escherichia coli)) ECOLI\_668 ECOLI\_668 Escherichia coli 562 10122959

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831938	8561	30717	846	281

Description

GTC ORF with score 428 to: (sr:y.lipolytica (strain nr1 y-1094) dna)  
(db:genpept-pln1) (de:y.lipolytica xpr2 gene encoding alkaline extracellular  
protease(aep), complete cds.) (nt:unidentified peptide) (le:<1) (re:936)  
(di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831956	8562	30718	1878	626

Description

6500729612 kdpd:b0695 sensor protein kdpd (gtcfc:10.2:12.13) (ec:2.7.3.-)  
(keggfc:12.1) (rileyfc:2.0.0) (db:gtc-escherichia coli) b0695 b0695  
Escherichia coli 562 -11533470 80593 kdpd (ec:2.7.3.-) (de:sensor protein  
kdpd,) (db:swissprot) KDPD\_ECOLI P21865 ESCHERICHIA COLI 562 -11533470  
164472 kdpd sensor protein kdpd (cl:sensor histidine kinase homology)  
(ec:2.7.3.-) (db:pir2.dat) B42372 B42372 Escherichia coli 562 -11533470  
223157 kdpd regulatory protein kdpd (sr:escherichia coli(strain:k12) dna,  
clone:kohara clone #173) (db:genpept-bct1) (de:escherichia coli genomic dna.  
(15.3 - 15.6 min).) (le:11352) (re:14036) (di:complement) D90708 D90708  
g1651302 Escherichia coli 562 -11533470 7500884560 (sr:e.coli (strain k12)  
dna) (db:genpept-bct1) (de:e.coli transmembrane protein (kdpd) and  
cytoplasmic protein (kdpe)genes, complete cds.) (nt:transmembrane protein  
(kdpd)) (le:141) (re:2825) (di:direct) ECOKDPDE M36066 g146551 Escherichia  
coli 562 -11533470 234927 kdpd sensor for high-affinity potassium transport  
(fn:enzyme; global regulatory functions) (db:genpept-bct2) (ec:2.7.3.-)  
(de:escherichia coli k-12 mgl655 section 63 of 400 of the completegenome.)  
(nt:f894; 100 pct identical to kdpd\_ecoli sw: p21865) (le:1002) (re:3686)  
(di:complement) AE000173 AE000173 g1786912 Escherichia coli 562 -11533470  
5000691086 kdpd regulatory protein kdpd. (sr:escherichia coli(strain:k12)  
dna, clone:kohara clone #173) (db:genpept) (de:escherichia coli genomic dna.  
(15.3 - 15.7 min).) (nt:orf\_id:o173#13; similar to pir accession number)  
(le:11352) (re:14036) (di:complement) D90708 D90708 g1651302 Escherichia  
coli 562 -11533470

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831969	8563	30719	597	198

Description

GTC ORF with score 601 to: (sr:aspergillus niger (strain:gn-3) dna)  
(db:genpept-pln1) (ec:3.2.1.20) (de:aspergillus niger agla gene for  
alpha-glucosidase, complete cds.) (le:1141:1896:2359:2584)  
(re:1835:2306:2529:4264) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831970	8564	30720	1194	398
<u>Description</u>				
6500729613 phoq:b1129 sensor protein phoq (gtcfc:10.2:12.13) (ec:2.7.3.-) (keggfc:12.1) (rileyfc:2.0.0) (db:gtc-escherichia coli) b1129 b1129 Escherichia coli 562 -11533471 89643 phoq (ec:2.7.3.-) (de:sensor protein phoq,) (db:swissprot) PHOQ_ECOLI P23837 ESCHERICHIA COLI 562 -11533471 130850 phoq sensor kinase phoq::sensor protein phoq (cl:envz protein:sensor histidine kinase homology) (ec:2.7.3.-) (db:pir1.dat) (mp:25 min) B41966 B41966 Escherichia coli 562 -11533471 223376 phoq virulence membrane protein phoq (sr:escherichia coli(strain:k12) dna, clone:kohara clone #239) (db:genpept-bct1) (de:escherichia coli genomic dna.(25.6 - 26.0 min).) (le:4550) (re:6010) (di:complement) D90748 D90748 g1651557 Escherichia coli 562 -11533471 7500888058 phoq phoq protein (sr:e.coli (strain k12) dna) (db:genpept-bct1) (de:e.coli phop and phoq genes, complete cds.) (nt:sensor protein) (le:1722) (re:3182) (di:direct) ECOPHOPQ D90393 g216609 Escherichia coli 562 -11533471 235480 phoq sensor protein phoq (fn:enzyme; global regulatory functions) (db:genpept-bct2) (ec:2.7.3.-) (de:escherichia coli k-12 mg1655 section 103 of 400 of the completegenome.) (nt:f486; 99 pct identical to phoq_ecoli sw: p23837) (le:2627) (re:4087) (di:complement) AE000213 AE000213 g1787374 Escherichia coli 562 -11533471 5000691087 phoq virulence membrane protein phoq. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #239) (db:genpept) (de:escherichia coli genomic dna. (25.6 - 25.9 min).) (nt:orf_id:o239#4; similar to pir accession number) (le:4550) (re:6010) (di:complement) D90748 D90748 g1651557 Escherichia coli 562 -11533471				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501831971	8565	30721	258	85

# Description

6500729614 phop:b1130 transcriptional regulatory protein phop  
(gtcf:10.2:12.13) (keggfc:12.1) (rileyfc:2.0.0) (db:gtc-escherichia coli)  
b1130 b1130 Escherichia coli 562 -11533472 89641 phop (de:transcriptional  
regulatory protein phop) (db:swissprot) PHOP\_ECOLI P23836 ESCHERICHIA COLI  
562 -11533472 131469 phop transcription regulator phop (cl:ompr  
protein:response regulator homology) (sr:strain k12, , strain k12)  
(sr:strain k12, ) (db:pir1.dat) (mp:25 min) A41965 A41965 Escherichia coli  
562 -11533472 223377 phop alkaline phosphatase regulatory protein  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #239)  
(db:genpept-bct1) (de:escherichia coli genomic dna.(25.6 - 26.0 min).)  
(le:6010) (re:6681) (di:complement) D90748 D90748 g1651558 Escherichia coli  
562 -11533472 223382 phop alkaline phosphatase regulatory protein  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #240)  
(db:genpept-bct1) (de:escherichia coli genomic dna.(25.6 - 26.0 min).)  
(le:327) (re:998) (di:complement) D90749 D90749 g1651564 Escherichia coli  
562 -11533472 235479 phop (sr:escherichia coli (strain k-12) (library:  
genomic library made wit) (db:genpept-bct1) (de:e.coli transcription factor  
(phop) gene, complete cds.) (le:163) (re:834) (di:direct) ECOPHOP M81433  
g147254 Escherichia coli 562 -11533472 7500888057 phop phop protein  
(sr:e.coli (strain k12) dna) (db:genpept-bct1) (de:e.coli phop and phoq  
genes, complete cds.) (nt:regulator protein) (le:1051) (re:1722) (di:direct)  
ECOPHOPQ D90393 g216608 Escherichia coli 562 -11533472 235478 phop  
transcriptional regulatory protein (fn:regulator; global regulatory  
functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 103 of  
400 of the completegenome.) (nt:f223; 100 pct identical to phop\_ecoli sw:  
p23836) (le:4087) (re:4758) (di:complement) AE000213 AE000213 g1787375  
Escherichia coli 562 -11533472 5000691088 phop transcriptional regulatory  
protein phop. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #239)  
(db:genpept) (de:escherichia coli genomic dna. (25.6 - 25.9 min).)  
(nt:orf\_id:o240#1; similar to swissprot accession) (le:6010) (re:6681)  
(di:complement) D90748 D90748 g1651558 Escherichia coli 562 -11533472  
7502851936 phop transcriptional regulatory protein phop. (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #240) (db:genpept) (de:escherichia  
coli genomic dna. (25.7 - 26.1 min).) (nt:orf\_id:o240#1; similar to  
swissprot accession) (le:327) (re:998) (di:complement) D90749 D90749  
g1651564 Escherichia coli 562 -11533472

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831974	8566	30722	408	135

Description

6500729615 fnr:nirr:b1334 fumarate and nitrate reduction regulatory protein (gtcfc:10.2) (keggfc:14.2) (rileyfc:2.0.0) (db:gtc-escherichia coli) b1334 b1334 Escherichia coli 562 -11533473 72213 fnr:nirr (de:fumarate and nitrate reduction regulatory protein) (db:swissprot) FNR\_ECOLI P03019 ESCHERICHIA COLI 562 -11533473 7000685312 fnr transcription regulator fnr:fumarate and nitrate reduction regulatory protein (cl:regulatory protein fnr:camp receptor protein cyclic nucleotide-binding domain homology) (db:pirl.dat) (mp:29 min) RGEFC A64883 Escherichia coli 562 -11533473 223600 fnr:nirr fumarate and nitrate reduction regulatory (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #260(29.8-30.2 min.)) (nt:orf\_id:o261#6; similar to (swissprot accession) (le:17247) (re:17999) (di:complement) D90771 D90771 g1742191 Escherichia coli 562 -11533473 300383 fnr:nirr fumarate and nitrate reduction regulatory (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #261(30.0-30.3 min.)) (nt:orf\_id:o261#6; similar to (swissprot accession) (le:7312) (re:8064) (di:complement) D90772 D90772 g1742202 Escherichia coli 562 -11533473 300373 fnr transcriptional regulation of aerobic:anaerobic (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 121 of 400 of the completegenome.) (nt:f250; 100 pct identical to fnr\_ecoli sw: p03019; cg) (le:6876) (re:7628) (di:complement) AE000231 AE000231 g1787595 Escherichia coli 562 -11533473 223610 fnr:nirr fumarate and nitrate reduction regulatory (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #261(30.0-30.3 min.)) (nt:orf\_id:o261#6; similar to (swissprot accession) (le:7312) (re:8064) (di:complement) D90772 D90772 g1742202 Escherichia coli 562 -11533473 5000691089 (de:(ecoli\_1294) (pn:regulatory gene for oxidoreductases and others; regulates aerobic osmotic balance, anaerobic respiration) (gn:fnr) (gtcfc:12.13) (ec:) (fnr\_ecoli) (keggfc:11.2) (rileyfc:2.0.0) (db:gtc-escherichia coli)) ECOLI\_1294 ECOLI\_1294 Escherichia coli 562 10014764



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831975	8567	30723	483	160

Description

6500729616 relb:b1564 relb protein (gtcfc:10.2) (keggfc:14.2)  
(rileyfc:2.0.0) (db:gtc-escherichia coli) b1564 b1564 Escherichia coli 562  
-11533474 300660 relb (de:relb protein) (db:swissprot) RELB\_ECOLI P07007  
ESCHERICHIA COLI 562 -11533474 131356 relb relb protein (cl:relb protein)  
(db:pir1.dat) (mp:34 min) BVECRB A22830 Escherichia coli 562 -11533474  
223941 relb relb protein (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #307(35.1-35.5 min.)) (nt:orf\_id:o308#20; similar to (pir  
accession number) (le:17627) (re:17866) (di:complement) D90798 D90798  
g1742559 Escherichia coli 562 -11533474 300670 relb relb protein  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #308(35.3-35.7  
min.)) (nt:orf\_id:o308#20; similar to (pir accession number) (le:7600)  
(re:7839) (di:complement) D90799 D90799 g1742570 Escherichia coli 562  
-11533474 300692 relb relb protein (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #309(35.4-35.7 min.)) (nt:orf\_id:o308#20; similar to (pir  
accession number) (le:4376) (re:4615) (di:complement) D90800 D90800 g1742593  
Escherichia coli 562 -11533474 5000691090 (db:genpept-bct1) (de:e. coli  
relb gene region.) (nt:relb protein (aa 1-79)) (le:494) (re:733) (di:direct)  
ECRELB X02405 g42700 Escherichia coli 562 -11533474 238041 relb negative  
regulator of translation (fn:regulator; global regulatory functions)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 143 of 400 of the  
completegenome.) (nt:f79; 100 pct identical to relb\_ecoli sw: p07007; cg)  
(le:3385) (re:3624) (di:complement) AE000253 AE000253 g1787847 Escherichia  
coli 562 -11533474 93885 relb (de:relb protein) (db:swissprot) RELB\_ECOLI  
P07007 ESCHERICHIA COLI 562 -11533474 223951 relb relb protein  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #308(35.3-35.7  
min.)) (nt:orf\_id:o308#20; similar to (pir accession number) (le:7600)  
(re:7839) (di:complement) D90799 D90799 g1742570 Escherichia coli 562  
-11533474 223973 relb relb protein (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #309(35.4-35.7 min.)) (nt:orf\_id:o308#20; similar to (pir  
accession number) (le:4376) (re:4615) (di:complement) D90800 D90800 g1742593  
Escherichia coli 562 -11533474

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501831977	8568	30724	354	117

Description

6500729617 era:rbaa:b2566 gtp-binding protein:gtp-binding protein era (gtcfc:10.2) (keggfc:14.2) (rileyfc:2.0.0) (db:gtc-escherichia coli) b2566 b2566 Escherichia coli 562 -11533475 70479 era:rbaa (de:gtp-binding protein era) (db:swissprot) ERA\_ECOLI P06616 ESCHERICHIA COLI 562 -11533475 143114 era gtp-binding protein era (cl:ras transforming protein:translation elongation factor tu homology) (db:pir1.dat) RGE CGT S44713 Escherichia coli 562 -11533475 234891 era (sr:escherichia coli dna) (db:genpept-bct1) (de:e. coli rnc (partial cds) and era genes (complete cds) encodingribonuclease iii and a ras-like protein (era).) (le:34) (re:939) (di:direct) ECOERA M14658 g416295 Escherichia coli 562 -11533475 239520 rbaa gtp binding protein (sr:escherichia coli (strain k12) (library: kohara) dna, clone 7g4) (db:genpept-bct1) (de:escherichia coli ribonuclease iii and other genes, complete cds.) (le:9949) (re:10854) (di:complement) ECOK12RIII D64044 g987641 Escherichia coli 562 -11533475 7500881107 era gtp-binding protein (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 55 minutes.) (nt:cg site no. 29010) (le:13725) (re:14630) (di:complement) ECU36841 U36841 g1033155 Escherichia coli 562 -11533475 234256 era gtp-binding protein (fn:factor; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 233 of 400 of the completegenome.) (nt:f301; 100 pct identical to era\_ecoli sw: p06616; cg) (le:2241) (re:3146) (di:complement) AE000343 AE000343 g1788919 Escherichia coli 562 -11533475 5000691091 (de:(ecoli\_2506) (pn:gtp-binding protein) (gn:era) (gtcfc:12.13) (ec:) (era\_ecoli) (keggfc:11.2) (rileyfc:2.0.0) (db:gtc-escherichia coli)) ECOLI\_2506 ECOLI\_2506 Escherichia coli 562 10013058

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831980	8569	30725	204	67
<u>Description</u>				
6500729618 rpoe:sige:b2573 rna polymerase sigma-e factor:sigma-24 (gtcfc:10.2) (keggfc:14.2) (rileyfc:2.0.0) (db:gtc-escherichia coli) b2573 b2573 Escherichia coli 562 -11533476 96272 rpoe:sige (de:rna polymerase sigma-e factor (sigma-24)) (db:swissprot) RPOE_ECOLI P34086 ESCHERICHIA COLI 562 -11533476 164576 rpoe rna polymerase sigma-e factor sigma-24 (cl:transcription initiation factor sigma e) (db:pir2.dat) I60227 I60227 Escherichia coli 562 -11533476 239524 rpoe rna polymerase:sigma-e factor:heat shock and (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 233 of 400 of the completengenome.) (nt:f191; 100 pct identical to rpoe_ecoli sw: p34086) (le:9197) (re:9772) (di:complement) AE000343 AE000343 g1788926 Escherichia coli 562 -11533476 7500890648 rpoe rpoe (fn:heat shock sigma factor) (db:genpept-bct2) (de:escherichia coli heat shock sigma factor (rpoe) gene, and rsea,rseb and rsec genes, complete cds.) (le:334) (re:909) (di:direct) ECU37089 U37089 g1045628 Escherichia coli 562 -11533476 5000691092 (de:(ecoli_2513) (pn:rna polymerase, sigma-e factor; heat shock and oxidative stress) (gn:rpoe) (gtcfc:12.13) (ec:) (rpoe_ecoli) (keggfc:11.2) (rileyfc:2.0.0) (db:gtc-escherichia coli)) ECOLI_2513 ECOLI_2513 Escherichia coli 562 10038215				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831991	8570	30726	186	61

Description

6500729619 csra:zfia:b2696 csra:carbon storage regulator (gtcfc:10.2) (keggfc:14.2) (rileyfc:2.0.0) (db:gtc-escherichia coli) b2696 b2696 Escherichia coli 562 -11533477 66694 csra:zfia (de:carbon storage regulator) (db:swissprot) CSRA\_ECOLI P31803 ESCHERICHIA COLI 562 -11533477 163138 csra glycogen biosynthesis inhibitor csra:carbon storage regulator csra (cl:glycogen biosynthesis inhibitor) (db:pir2.dat) B40608 B40608 Escherichia coli 562 -11533477 225248 csra carbon storage regulator. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #446(60.5-60.9 min.)) (nt:similar to (swissprot accession number p31803)) (le:7867) (re:8052) (di:complement) D90892 D90892 g1800082 Escherichia coli 562 -11533477 4000707010 zfia zfia protein (fn:modulator of interaction between letd protein) (sr:escherichia coli (isolate:kp4714) dna, clone\_lib:kohar) (db:genpept-bct1) (de:escherichia coli dna for zfia protein and alanyl t-rna synthetase,complete cds,trna-arg and trna-ser.) (le:473) (re:658... ECOALAS3 D44453 g2281030 Escherichia coli 562 -11533477 7500879503 csra carbon storage regulator (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli carbon storage regulator (csra) gene, completecds, alas gene, 3' end, and serv promoter region.) (le:271) (re:456) (di:direct) ECOCSRASER L07596 g304882 Escherichia coli 562 -11533477 234069 csra carbon storage regulator:controls glycogen (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 243 of 400 of the completegenome.) (nt:f61; 100 pct identical to csra\_ecoli sw: p31803) (le:9437) (re:9622) (di:complement) AE000353 AE000353 g1789047 Escherichia coli 562 -11533477 5000691093 (de:(ecoli\_2624) (pn:carbon storage regulator; affects g;ycogen synthesis, gluconeogenesis, cell size and surface properties) (gn:csra) (gtcfc:12.13) (ec:) (csra\_ecoli) (keggfc:11.2) (rileyfc:2.0.0) (db:gtc-escherichia coli)) ECOLI\_2624 ECOLI\_2624 Escherichia coli 562 10009312

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501831996	8571	30727	540	179

Description

GTC ORF with score 93 to: (fn:putative lectin-like protein involved in) (sr:saccharomyces cerevisiae (sub\_species:pastorianus, strain:kms004) (db:genpept) (de:saccharomyces cerevisiae gene for flocculin, partial cds.) (le:<1) (re:2550) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832006	8572	30728	345	114

Description

6500729620 rpos:katf:appr:sigs:otsx:nur:b2741 rna polymerase sigma subunit  
rpos:rna polymerase sigma factor rpos:sigma-38 (gtcfc:10.2) (keggfc:14.2)  
(rileyfc:2.0.0) (db:gtc-escherichia coli) b2741 b2741 Escherichia coli 562  
-11533478 96302 rpos:katf:appr:sigs:otsx:nur (de:rna polymerase sigma  
factor rpos (sigma-38)) (db:swissprot) RPOS\_ECOLI P13445 ESCHERICHIA COLI  
562 -11533478 7000686464 rpos:katf transcription initiation factor sigma  
katf:transcription initiation factor sigma-18 (cl:transcription initiation  
factor sigma katf:transcription initiation factor sigma katf homology)  
(db:pir1.dat) (mp:59.0 min) RNECKF A65055 Escherichia coli 562 -11533478  
7500890671 rpos rna polymerase sigma subunit rpos sigma-38 (fn:controls a  
regulon of genes required for) (db:genpept-bct1) (de:escherichia coli k-12  
genome; approximately 61 to 62 minutes.) (nt:cg site no. 18208; alternate  
gene names katf, appr,) (le:38864) (re:39856) (di:complement) ECU29579  
U29579 g882634 Escherichia coli 562 -11533478 239315 rpos rna  
polymerase:sigma s sigma38 factor (fn:enzyme; global regulatory functions)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 248 of 400 of the  
completegenome.) (nt:f330; 99 pct identical to rpos\_ecoli sw: p13445; cg)  
(le:1533) (re:2525) (di:complement) AE000358 AE000358 g1789098 Escherichia  
coli 562 -11533478 5000691094 (de:(ecoli\_2670) (pn:rna polymerase, sigma  
s:sigma38 subunit; synthesis of many growth phase related proteins)  
(gn:rpos) (gtcfc:12.13) (ec:) (rpos\_ecoli) (keggfc:11.2) (rileyfc:2.0.0)  
(db:gtc-escherichia coli)) ECOLI\_2670 ECOLI\_2670 Escherichia coli 562  
10038245

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832008	8573	30729	1401	466

Description

6500729621 bara:b2786 sensor protein bara (gtcfc:10.2:12.13) (ec:2.7.3.-) (keggfc:14.1) (rileyfc:2.0.0) (db:gtc-escherichia coli) b2786 b2786 Escherichia coli 562 -11533479 61404 bara (ec:2.7.3.-) (de:sensor protein bara,) (db:swissprot) BARA\_ECOLI P26607 ESCHERICHIA COLI 562 -11533479 164597 bara sensor-regulator protein bara (cl:sensor-regulator protein bara:response regulator homology) (ec:2.7.3.-) (db:pir2.dat) (mp:60 min) S20550 S20550 Escherichia coli 562 -11533479 7500877670 bara sensor-regulator protein (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli bara gene for sensor-regulator protein.) (le:114) (re:2870) (di:direct) ECOBARA D10888 g216535 Escherichia coli 562 -11533479 233883 bara sensor-regulator:activates ompR by (fn:enzyme; global regulatory functions) (db:genpept-bct2) (ec:2.7.3.-) (de:escherichia coli k-12 mg1655 section 252 of 400 of the completegenome.) (nt:o918; 100 pct identical to the 918 aa bara\_ecoli) (le:5307) (re:8063) (di:direct) AE000362 AE000362 g1789149 Escherichia coli 562 -11533479 5000691095 (de:(ecoli\_2717) (pn:sensor-regulator, probably activates ompR by phosphorylation) (gn:bara) (gtcfc:12.13) (ec:2.7.3.-) (bara\_ecoli) (keggfc:11.1) (rileyfc:2.0.0) (db:gtc-escherichia coli)) ECOLI\_2717 ECOLI\_2717 Escherichia coli 562 10004113

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832030	8574	30730	471	156

Description

6500729622 rpod:alt:b3067 rna polymerase sigma-70 factor:rna polymerase sigma factor rpod:sigma-70 (gtcfc:10.2) (keggfc:14.2) (rileyfc:2.0.0) (db:gtc-escherichia coli) b3067 b3067 Escherichia coli 562 -11533480 96326 rpod:alt (de:rna polymerase sigma factor rpod (sigma-70)) (db:swissprot) RPSD\_ECOLI P00579 ESCHERICHIA COLI 562 -11533480 7000686467 rpod transcription initiation factor sigma 70:dna-directed rna polymerase sigma chain:major sigma factor:transcriptase sigma chain (cl:transcription initiation factor sigma 70:transcription initiation factor sigma katf homology:transcription initiation factor sigma region 1 homology) (db:pirl.dat) (mp:67 min) RNECS A65095 Escherichia coli 562 -11533480 7500890683 rpod (fn:rna polymerase, sigma-70 subunit) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 68 minutes.) (nt:cg site no. 231; alternate gene name alt) (le:17842) (re:19683) (di:direct) ECU28379 U28379 g882590 Escherichia coli 562 -11533480 239272 rpod rna polymerase:sigma 70 factor:regulation of (fn:factor; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 278 of 400 of the completegenome.) (nt:o613; 99 pct identical to rp70\_ecoli sw: p00579; cg) (le:6718) (re:8559) (di:direct) AE000388 AE000388 g1789448 Escherichia coli 562 -11533480 5000691096 (de:(ecoli\_2990) (pn:rna polymerase, sigma:70 subunit; regulation of proteins induced at high temperatures) (gn:rpod) (gtcfc:12.13) (ec:) (rpsd\_ecoli) (keggfc:11.2) (rileyfc:2.0.0) (db:gtc-escherichia coli)) ECOLI\_2990 ECOLI\_2990 Escherichia coli 562 10038269

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832031	8575	30731	396	131

Description

6500729623 rpon:glnf:ntra:b3202 sigma-n:rna polymerase sigma-54 factor (gtcfc:10.2) (keggfc:14.2) (rileyfc:2.0.0) (db:gtc-escherichia coli) b3202 b3202 Escherichia coli 562 -11533481 238604 rpon:glnf:ntra (de:rna polymerase sigma-54 factor) (db:swissprot) RP54\_ECOLI P24255 ESCHERICHIA COLI 562 -11533481 164614 rpon transcription initiation factor sigma-54:rna polymerase sigma-54 factor sigma-n:rpon (cl:pseudomonas transcription initiation factor sigma) (db:pir2.dat) (mp:70 min) A35695 I57054 Escherichia coli 562 -11533481 238256 rpon sigma-n sigma-54 (fn:transcription factor) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (le:125468) (re:126901) (di:direct) ECOUW67 U18997 g606141 Escherichia coli 562 -11533481 5000691097 rpon sigma factor (db:genpept-bct1) (de:e.coli(k12) rpon gene for sigma factor 54.) (le:93) (re:1526) (di:direct) ECSIG540 Z27094 g414885 Escherichia coli 562 -11533481 7500890507 rpon sigma-n sigma-54 (fn:transcription factor) (db:genpept-bct1) (de:escherichia coli rpon operon and adjoining regions includingorf185, orf241, sigma-54 (rpon), orf95, iiantr (ptsn), orf284, andnpr (npr) genes, complete cds.) (le:1478) (re:2911) (di:direct) ECU12684 U12684 g551338 Escherichia coli 562 -11533481 236440 rpon rna polymerase:sigma 54 or 60 factor:nitrogen (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 289 of 400 of the completegenome.) (nt:o477; 100 pct identical amino acid sequence and) (le:15990) (re:17423) (di:direct) AE000399 AE000399 g1789594 Escherichia coli 562 -11533481 95963 rpon:glnf:ntra (de:rna polymerase sigma-54 factor) (db:swissprot) RP54\_ECOLI P24255 ESCHERICHIA COLI 562 -11533481

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832046	8576	30732	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832049	8577	30733	210	69

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832057	8578	30734	1551	516

Description

GTC ORF with score 202 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone\_lib:mizukam) (db:genpept-pln1) (de:schizosaccharomyces pombe 38 kb genomic dna, clone c1241.) (nt:similar to s.cerevisiae hypothetical 229.9kd) (le:11010:11253:11494) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832073	8579	30735	342	113

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832090	8580	30736	1641	546

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832100	8581	30737	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832113	8582	30738	1587	529

Description

6500729624 arch:b3210 aerobic respiration control sensor protein arch  
 (gtcfc:10.2:12.13) (ec:2.7.3.-) (keggfc:12.1) (rileyfc:2.0.0)  
 (db:gtc-escherichia coli) b3210 b3210 Escherichia coli 562 -11533482 59990  
 arch (ec:2.7.3.-) (de:aerobic respiration control sensor protein arch,)  
 (db:swissprot) ARCB\_ECOLI P22763 ESCHERICHIA COLI 562 -11533482 7000684604  
 arch aerobic respiration control sensor protein arch (cl:aerobic respiration  
 control sensor protein arch:response regulator homology) (ec:2.7.3.-)  
 (db:pir1.dat) (mp:69.5 min) RGE CAR D65112 Escherichia coli 562 -11533482  
 7500877077 arch protein kinase (db:genpept-bct1) (de:escherichia coli k-12  
 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 29063)  
 (le:131440) (re:133770) (di:complement) ECOUW67 U18997 g606149 Escherichia  
 coli 562 -11533482 236448 arch aerobic respiration sensor-response protein  
 (fn:enzyme; global regulatory functions) (db:genpept-bct2) (ec:2.7.3.-)  
 (de:escherichia coli k-12 mg1655 section 290 of 400 of the completegenome.)  
 (nt:f776; cg site no. 29063; 100 pct identical) (le:4219) (re:6549)  
 (di:complement) AE000400 AE000400 g1789603 Escherichia coli 562 -11533482  
 5000691098 (de:(ecoli\_3133) (pn:aerobic respiration sensor-response  
 protein; histidine protein kinase) (gn:arch) (gtcfc:12.13) (ec:2.7.3.-)  
 (arch\_ecoli) (keggfc:11.1) (rileyfc:2.0.0) (db:gtc-escherichia coli))  
 ECOLI\_3133 ECOLI\_3133 Escherichia coli 562 10002723

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832120	8583	30739	246	81

Description

6500729625 ssfb:b3228 stringent starvation protein b (gtcfc:10.2)  
(keggfc:14.2) (rileyfc:2.0.0) (db:gtc-escherichia coli) b3228 b3228  
Escherichia coli 562 -11533483 99578 ssfb (de:stringent starvation protein  
b) (db:swissprot) SSPB\_ECOLI P25663 ESCHERICHIA COLI 562 -11533483 164644  
ssfb stringent starvation protein b:ssfb (cl:stringent starvation protein  
ssfb) (db:pir2.dat) JS0666 JS0666 Escherichia coli 562 -11533483 236466  
ssfb stringent starvation protein (sr:escherichia coli (sub\_strain w3110,  
strain k-12) (library: kohar) (db:genpept-bct1) (de:escherichia coli  
stringent starvation protein b (ssfb) gene,complete cds.) (le:1) (re:498)  
(di:direct) ECOSSPB M69028 g147872 Escherichia coli 562 -11533483  
7500892143 ssfb stringent starvation protein b (db:genpept-bct1)  
(de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.)  
(le:157024) (re:157521) (di:complement) ECOUW67 U18997 g606167 Escherichia  
coli 562 -11533483 236032 ssfb stringent starvation protein b  
(fn:regulator; global regulatory functions) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 292 of 400 of the completegenome.)  
(nt:f165; 100 pct identical amino acid sequence and) (le:3666) (re:4163)  
(di:complement) AE000402 AE000402 g1789623 Escherichia coli 562 -11533483  
5000691099 (de:(ecoli\_3151) (pn:stringent starvation protein b) (gn:ssfb)  
(gtcfc:12.13) (ec:) (ssfb\_ecoli) (keggfc:11.2) (rileyfc:2.0.0)  
(db:gtc-escherichia coli)) ECOLI\_3151 ECOLI\_3151 Escherichia coli 562  
10041435

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832122	8584	30740	201	66

Description

GTC ORF with score 124 to: (sr:arabidopsis thaliana (strain columbia)  
(clone: kab1) cdna to mrna) (db:genpept-pln1) (de:arabidopsis thaliana  
(clone kab1) k+ channel beta subunit proteinmrna, complete cds.) (le:68)  
(re:1054) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832123	8585	30741	621	206

Description

6500729626 sspa:ssp:pog:b3229 stringent starvation protein:stringent  
starvation protein a (gtcfc:10.2) (keggfc:14.2) (rileyfc:2.0.0)  
(db:gtc-escherichia coli) b3229 b3229 Escherichia coli 562 -11533484 131639  
sspa::ssp stringent starvation protein (cl:stringent starvation protein)  
(db:pir1.dat) (mp:69.5 min) RGECS A26422 Escherichia coli 562 -11533484  
238298 sspa stringent starvation protein (db:genpept-bct1) (de:escherichia  
coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (le:157527)  
(re:158165) (di:complement) ECOUW67 U18997 g606168 Escherichia coli 562  
-11533484 7500953669 (db:genpept-bct1) (de:e. coli ssp gene for stringent  
starvation protein.) (nt:ssp (aa1-212)) (le:555) (re:1193) (di:direct)  
ECSSPG X05088 g42998 Escherichia coli 562 -11533484 236467 sspa regulator  
of transcription:stringent starvation (fn:regulator; global regulatory  
functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 292 of  
400 of the completegenome.) (nt:f212; 100 pct identical amino acid sequence  
and) (le:4169) (re:4807) (di:complement) AE000402 AE000402 g1789624  
Escherichia coli 562 -11533484 5000691100 (de:(ecoli\_3152) (pn:stringent  
starvation protein a) (gn:sspa) (gtcfc:12.13) (ec:) (sspa\_ecoli)  
(keggfc:11.2) (rileyfc:2.0.0) (db:gtc-escherichia coli)) ECOLI\_3152  
ECOLI\_3152 Escherichia coli 562 10068166

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832127	8586	30742	402	133
<u>Description</u>				
6500729627 crp:cap:csm:b3357 cyclic amp receptor protein:catabolite gene activator:camp receptor protein:camp-regulatory protein (gtcfc:10.2) (keggfc:14.2) (rileyfc:2.0.0) (db:gtc-escherichia coli) b3357 b3357 Escherichia coli 562 -11533485 66479 crp:cap:csm (de:protein)) (db:swissprot) CRP_ECOLI P03020 ESCHERICHIA COLI 562 -11533485 7502851937 crp:cap:csm (de:protein)) (db:swissprot) CRP_ECOLI P03020 SHIGELLA FLEXNERI 623 -11533485 131437 crp camp receptor protein:catabolite gene activator protein cap (cl:regulatory protein fnr:camp receptor protein cyclic nucleotide-binding domain homology) (db:pir1.dat) (mp:74 min) QRECC A93416 Escherichia coli 562 -11533485 234044 (sr:escherichia coli k12 dna) (db:genpept-bct1) (de:e.coli crp gene coding for cyclic amp receptor protein.) (nt:camp receptor protein (crp)) (le:369) (re:1001) (di:direct) ECOCRP J01598 g145594 Escherichia coli 562 -11533485 236590 crp cyclic amp receptor protein (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 906; alternate names cap, csm) (le:266867) (re:267499) (di:direct) ECOUW67 U18997 g606291 Escherichia coli 562 -11533485 260605 (sr:s.flexneri (strain 2b, atcc 12022) dna, clone psf281) (db:genpept-bct1) (de:shigella flexneri 2b crp gene encoding catabolite gene activatorprotein, complete cds.) (nt:catabolite gene activator protein) (le:1) (re:633) (di:direct) SHFCRP M13772 g152731 Shigella flexneri 623 -11533485 7500879411 crp cyclic amp receptor protein (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 301 of 400 of the completegenome.) (nt:o210; cg site no. 906; alternate names cap, csm) (le:8621) (re:9253) (di:direct) AE000411 AE000411 g1789756 Escherichia coli 562 -11533485 66478 crp:cap:csm (de:protein)) (db:swissprot) CRP_ECOLI P03020 ESCHERICHIA COLI 562 -11533485 7502851938 crp:cap:csm (de:protein)) (db:swissprot) CRP_ECOLI P03020 SHIGELLA FLEXNERI 623 -11533485 5000691101 (de:(ecoli_3275) (pn:cyclic amp receptor protein) (gn:crp) (gtcfc:12.13) (ec:) (crp_ecoli) (keggfc:11.2) (rileyfc:2.0.0) (db:gtc-escherichia coli)) ECOLI_3275 ECOLI_3275 Escherichia coli 562 10009099				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832173	8587	30743	606	202
<u>Description</u>				
6500729628 envz:ompb:pera:tpo:b3404 osmolarity sensor protein envz (gtcfc:12.11:12.13) (ec:2.7.3.-) (keggfc:12.1) (rileyfc:2.0.0) (db:gtc-escherichia coli) b3404 b3404 Escherichia coli 562 -11533486 70250 envz:ompb:pera:tpo (ec:2.7.3.-) (de:osmolarity sensor protein envz,) (db:swissprot) ENVZ_ECOLI P02933 ESCHERICHIA COLI 562 -11533486 130847 envz histidine kinase osmosensor envz (cl:envz protein:sensor histidine kinase homology) (ec:2.7.3.-) (db:pir1.dat) (mp:75 min) MMECZB B25024 Escherichia coli 562 -11533486 236637 envz (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli ompb operon: ompr and envz genes coding for proteinsrequired for osmolarity-sensitive biosynthetic regulation of theouter membrane matrix proteins.) (nt:envz protein; (envz)) (le:967) (re:2319) (di... ECOOMP B J01656 g147006 Escherichia coli 562 -11533486 7500881069 envz (fn:production of outer membrane proteins;) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 807; alternate names ompb, pera, tpo) (le:315264) (re:316616) (di:complement) ECOUW67 U18997 g606338 Escherichia coli 562 -11533486 235276 envz protein histidine kinase/phosphatase sensor for (fn:enzyme; global regulatory functions) (db:genpept-bct2) (ec:2.7.3.-) (de:escherichia coli k-12 mg1655 section 306 of 400 of the completegenome.) (nt:f450; cg site no. 807; alternate names ompb,) (le:1773) (re:3125) (di:complement) AE000416 AE000416 g1789808 Escherichia coli 562 -11533486 5000691102 (de:(ecoli_3322) (pn:protein histidine kinase) (gn:envz) (gtcfc:12.13) (ec:2.7.3.-) (envz_ecoli) (keggfc:11.1) (rileyfc:2.0.0) (db:gtc-escherichia coli) ECOLI_3322 ECOLI_3322 Escherichia coli 562 10012828				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832184	8588	30744	1131	376

Description

6500729629 ompr:ompb:kmt:b3405 ompr:transcriptional regulatory protein ompr (gtcfc:10.2:12.13) (keggfc:12.1) (rileyfc:2.0.0) (db:gtc-escherichia coli) b3405 b3405 Escherichia coli 562 -11533487 87691 ompr:ompb:kmt (de:transcriptional regulatory protein ompr) (db:swissprot) OMPR\_ECOLI P03025 ESCHERICHIA COLI 562 -11533487 7000686040 ompr osmosensor response regulator ompr (cl:ompr protein:response regulator homology) (db:pirl.dat) (mp:75 min) RGEOR H65135 Escherichia coli 562 -11533487 236638 ompr (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli ompb operon: ompr and envz genes coding for proteinsrequired for osmolarity-sensitive biosynthetic regulation of theouter membrane matrix proteins.) (nt:ompr protein) (le:251) (re:970) (di:direct) ECOOMPB J01656 g453287 Escherichia coli 562 -11533487 263344 ompr (fn:positive regulatory gene for ompc and ompf) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 434; alternate name ompb) (le:316613) (re:317332) (di:complement) ECOUW67 U18997 g606339 Escherichia coli 562 -11533487 7500887178 ompr (fn:positive transcriptional regulator) (db:genpept-bct1) (de:s.typhi ompb operon gene.) (le:199) (re:918) (di:direct) STOMP X77305 g602089 Salmonella typhi 601 -11533487 235275 ompr response regulator sensor:envz affecting (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 306 of 400 of the completgenome.) (nt:f239; cg site no. 434; alternate name ompb; 100 pct) (le:3122) (re:3841) (di:complement) AE000416 AE000416 g1789809 Escherichia coli 562 -11533487 5000691103 (de:(ecoli\_3323) (pn:response regulator:sensor, envz affecting transcription of ompc and ompf, outer membrane protein synthesis) (gn:ompr) (gtcfc:12.13) (ec:) (ompr\_ecoli) (keggfc:11.2) (rileyfc:2.0.0) (db:gtc-escherichia coli)) ECOLI\_3323 ECOLI\_3323 Escherichia coli 562 10029834

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832185	8589	30745	276	91

#### Description

6500729630 phou:nmpa:b3724 peripheral membrane protein u:phosphate transport system regulatory protein (gtcfc:12.4:11.3) (keggfc:14.2) (rileyfc:2.0.0) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of anions (cl\_so4\_po4\_etc\_):cell envelope-surface proteins--glycoproteins--and structures) b3724 b3724 Escherichia coli 562 -11533488 7500888061 phou:nmpa (de:phosphate transport system regulatory protein) (db:swissprot) PHOU\_ECOLI P07656 ESCHERICHIA COLI 562 -11533488 131355 phou peripheral membrane protein u (cl:phou protein) (db:pir1.dat) (mp:84 min) BVECPU D23311 Escherichia coli 562 -11533488 237810 phou peripheral membrane protein u (sr:e.coli strain k-12 dna, clones pan92 (1), psn518 (2), and pan12) (db:genpept-bct1) (de:e.coli phosphate-repressible periplasmic phosphate-binding protein(phos), peripheral membrane proteins (pstc, pstb and phou) and integral membrane protein (psta) ... ECOPHOS K01992 g147260 Escherichia coli 562 -11533488 5000691104 (db:genpept-bct1) (de:e. coli dna for psta-phou region involved in phosphate transport and regulation of the phosphate regulon.) (nt:phou gene product (aa 1-241)) (le:2845) (re:3570) (di:direct) ECPHOWTU X02723 g42399 Escherichia coli 562 -11533488 235485 phou negative regulator for pho regulon and putative (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 339 of 400 of the complete genome.) (nt:f241; 99 pct identical amino acid sequence and) (le:8237) (re:8962) (di:complement) AE000449 AE000449 g1790161 Escherichia coli 562 -11533488 89654 phou:nmpa (de:phosphate transport system regulatory protein) (db:swissprot) PHOU\_ECOLI P07656 ESCHERICHIA COLI 562 -11533488

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832187	8590	30746	186	62

#### Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832201	8591	30747	474	157

Description

6500729631 cpxa:ecfb:ssd:eup:b3911 cpxa:sensor protein cpxa  
(gtcf:10.2:12.13) (ec:2.7.3.-) (keggfc:12.1) (rileyfc:2.0.0)  
(db:gtc-escherichia coli) b3911 b3911 Escherichia coli 562 -11533489 66220  
cpxa:ecfb:ssd:eup (ec:2.7.3.-) (de:sensor protein cpxa,) (db:swissprot)  
CPXA\_ECOLI P08336 ESCHERICHIA COLI 562 -11533489 153381 cpxa chemotaxis  
protein cpxa (cl:envz protein:sensor histidine kinase homology) (ec:2.7.3.-)  
(db:pir2.dat) (mp:88 min) S40855 S40855 Escherichia coli 562 -11533489  
7500879350 cpxa (fn:chemosensory transducer) (sr:escherichia coli  
(sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e.  
coli chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 908)  
(le:65235) (re:66608) (di:complement) ECOUW87 L19201 g305015 Escherichia  
coli 562 -11533489 237129 cpxa probable sensor protein histidine protein  
(fn:putative regulator; global regulatory) (db:genpept-bct2) (ec:2.7.3.-)  
(de:escherichia coli k-12 mg1655 section 356 of 400 of the completegenome.)  
(nt:f457; 100 pct identical to cpxa\_ecoli sw: p08336;) (le:879) (re:2252)  
(di:complement) AE000466 AE000466 g1790346 Escherichia coli 562 -11533489  
5000691105 (de:(ecoli\_3810) (pn:probable inner membrane sensor  
protein:histidine protein kinase, acting on arca, energy coupling factor,  
f-pilin forma) (gn:cpxa) (gtcf:12.13) (ec:2.7.3.-) (cpxa\_ecoli)  
(keggfc:11.1) (rileyfc:2.0.0) (db:gtc) ECOLI\_3810 ECOLI\_3810 Escherichia  
coli 562 10008851

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832217	8592	30748	1512	503

Description

GTC ORF with score 178 to: (sr:thale cress) (db:genpept-pln1)  
(de:arabidopsis thaliana chromosome 1 yac yup8h12 complete sequence.)  
(nt:similar to hypothetical protein pid|e327464)  
(le:38138:38800:39341:39665) (re:38509:39255:39619:39967) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832230	8593	30749	1473	490
<u>Description</u>				
6500729632 cytr:b3934 transcriptional repressor cytr (gtcfc:10.2) (keggfc:14.2) (rileyfc:2.0.0) (db:gtc-escherichia coli) b3934 b3934 Escherichia coli 562 -11533490 237151 cytr (de:transcriptional repressor cytr) (db:swissprot) CYTR_ECOLI P06964 ESCHERICHIA COLI 562 -11533490 130807 cytr cyt transcription repressor cytr (cl:lac repressor) (db:pir1.dat) (mp:88.8 min) RPECCT A24963 Escherichia coli 562 -11533490 5000691106 (db:genpept-bct1) (de:e. coli cytr gene coding for cyt repressor.) (nt:put. cyt repressor (aa 1-341)) (le:301) (re:1326) (di:direct) ECCYTR X03683 g581060 Escherichia coli 562 -11533490 7500879949 cytr (fn:regulation of deo operon) (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 887) (le:85064) (re:86089) (di:complement) ECOUW87 L19201 g305037 Escherichia coli 562 -11533490 232629 cytr regulator for deo operon:udp:cdd:tsx:nupc (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 357 of 400 of the completegenome.) (nt:f341; 100 pct identical to cytr_ecoli sw: p06964;) (le:10557) (re:11582) (di:complement) AE000467 AE000467 g1790369 Escherichia coli 562 -11533490 67753 cytr (de:transcriptional repressor cytr) (db:swissprot) CYTR_ECOLI P06964 ESCHERICHIA COLI 562 -11533490				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832246	8594	30750	420	139

Description

6500729633 oxyr:momr:mor:b3961 hydrogen peroxide-inducible genes activator:morphology and auto-aggregation control protein (gtcfc:10.2) (keggfc:14.2) (rileyfc:2.0.0) (db:gtc-escherichia coli) b3961 b3961 Escherichia coli 562 -11533491 237653 oxyr:momr:mor (de:aggregation control protein)) (db:swissprot) OXYR\_ECOLI P11721 ESCHERICHIA COLI 562 -11533491 7000686066 oxyr:momr hydrogen peroxide-inducible genes activator:regulatory protein momr (cl:regulatory protein ilvy) (db:pir1.dat) (mp:89.6 min) RGE COX D65203 Escherichia coli 562 -11533491 237652 (db:genpept-bct1) (de:escherichia coli oxyr gene for a 34kd positive regulatory proteininvolved in response to oxidative stress.) (nt:oxyr gene product 34kd protein (aa 1-305)) (le:203) (re:1120) (di:direct) ECOXYR X16531 g42212 Escherichia coli 562 -11533491 5000691107 oxyr regulatory protein (db:genpept-bct1) (de:e.coli oxyr gene for regulatory protein.) (le:203) (re:1120) (di:direct) ECOXYRGEN X52666 g42214 Escherichia coli 562 -11533491 237179 oxyr activator:hydrogen peroxide-inducible genes (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 360 of 400 of the completegenome.) (nt:o305; 100 pct identical to oxyr\_ecoli sw: p11721;) (le:5376) (re:6293) (di:direct) AE000470 AE000470 g1790399 Escherichia coli 562 -11533491 7500887444 oxyr (fn:positive regulator of hydrogen) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:alternate gene names mor, momr) (le:23731) (re:24648) (di:direct) ECOUW89 U00006 g396308 Escherichia coli 562 -11533491 88030 oxyr:momr:mor (de:aggregation control protein)) (db:swissprot) OXYR\_ECOLI P11721 ESCHERICHIA COLI 562 -11533491

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832254	8595	30751	792	264

Description

GTC ORF with score 1224 to: (fn:putative regulatory subunit of holoenzyme) (db:genpept-pln1) (de:ajellomyces capsulatus nad(+)-isocitrate dehydrogenase subunit i(idh1) mrna, nuclear gene encoding mitochondrial protein, completeds.) (nt:precursor form;...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832259	8596	30752	420	140

Description

GTC ORF with score 473 to: (sr:neurospora crassa strain=74-or23-1va) (db:genpept-pln1) (de:neurospora crassa two-component histidine kinase (nik-1) gene, 5'region and partial cds.) (nt:two-component histidine kinase) (le:1619:2488:3404:3732) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832262	8597	30753	2586	861

Description

6500729634 lexa:extra:spr:tsl:umua:b4043 lexa:lexa repressor (gtcfc:10.2) (ec:3.4.21.88) (keggfc:14.1) (rileyfc:2.0.0) (db:gtc-escherichia coli) b4043 b4043 Escherichia coli 562 -11533492 81975 lexa:extra:spr:tsl:umua (ec:3.4.21.88) (de:lexa repressor,) (db:swissprot) LEXA\_ECOLI P03033 ESCHERICHIA COLI 562 -11533492 131420 lexa lexa repressor (cl:lexa repressor) (db:pir1.dat) (mp:92 min) ILEC A90808 Escherichia coli 562 -11533492 237249 (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli lexa gene coding for sos function regulatory protein.) (nt:sos function regulatory protein (lexa)) (le:102) (re:710) (di:direct) ECOLEXA J01643 g146608 Escherichia coli 562 -11533492 234973 lexa regulator for sos lexa regulon (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 367 of 400 of the completgenome.) (nt:o202b; cg site no. 558) (le:9210) (re:9818) (di:direct) AE000477 AE000477 g1790476 Escherichia coli 562 -11533492 7500884971 lexa (fn:regulatory gene for sos regulon) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 558) (le:122357) (re:122965) (di:direct) ECOUW89 U00006 g396378 Escherichia coli 562 -11533492 5000691108 (de:(ecoli\_3929) (pn:regulator for sos: regulon) (gn:lexa) (gtcfc:12.13) (ec:3.4.21.88) (lexa\_ecoli) (keggfc:11.1) (rileyfc:2.0.0) (db:gtc-escherichia coli)) ECOLI\_3929 ECOLI\_3929 Escherichia coli 562 10024209

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832269	8598	30754	291	96

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832288	8599	30755	717	239

Description

6500729635 soxs:b4062 regulatory protein soxs (gtcfc:10.2) (keggfc:14.2) (rileyfc:2.0.0) (db:gtc-escherichia coli) b4062 b4062 Escherichia coli 562 -11533493 164638 soxs regulatory protein soxs (db:pir2.dat) (mp:92.2 min) JS0578 JS0578 Escherichia coli 562 -11533493 237268 soxs (sr:e.coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli soxr and soxs protein (soxr, soxs) genes, complete cds.) (le:164) (re:487) (di:complement) ECOSOXRS M60111 g147848 Escherichia coli 562 -11533493 238279 soxs (db:genpept-bct1) (de:e.coli soxs and soxr regulatory genes for superoxide strengthresponse.) (le:341) (re:664) (di:complement) ECOSXSR X59593 g42975 Escherichia coli 562 -11533493 236011 soxs regulation of superoxide response regulon (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 369 of 400 of the completegenome.) (nt:f107; 100 pct identical amino acid sequence and) (le:8039) (re:8362) (di:complement) AE000479 AE000479 g1790497 Escherichia coli 562 -11533493 7500960446 soxs (fn:involved in regulation of superoxide response) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:142300) (re:142623) (di:complement) ECOUW89 U00006 g396397 Escherichia coli 562 -11533493 5000691109 (de:(ecoli\_3948) (pn:regulation of superoxide response regulon) (gn:soxs) (gtcfc:12.13) (ec:) (soxs\_ecoli) (keggfc:11.2) (rileyfc:2.0.0) (db:gtc-escherichia coli)) ECOLI\_3948 ECOLI\_3948 Escherichia coli 562 10087409

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832293	8600	30756	249	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832303	8601	30757	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832310	8602	30758	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832320	8603	30759	477	158

Description

6500729636 soxr:b4063 soxr protein (gtcfc:10.2) (keggfc:14.2) (rileyfc:2.0.0) (db:gtc-escherichia coli) b4063 b4063 Escherichia coli 562 -11533494 238280 soxr:marc (de:soxr protein) (db:swissprot) SOXR\_ECOLI P22538 ESCHERICHIA COLI 562 -11533494 164637 soxr soxr protein (db:pir2.dat) (mp:92.2 min) JS0577 JS0577 Escherichia coli 562 -11533494 237269 soxr (sr:e.coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli soxr and soxs protein (soxr, soxs) genes, complete cds.) (nt:putative) (le:573) (re:1037) (di:direct) ECOSOXRS M60111 g147849 Escherichia coli 562 -11533494 5000691110 soxr (db:genpept-bct1) (de:e.coli soxs and soxr regulatory genes for superoxide strengthresponse.) (le:750) (re:1214) (di:direct) ECOSOXSR X59593 g42976 Escherichia coli 562 -11533494 236012 soxr redox-sensing activator of soxs (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 369 of 400 of the completegenome.) (nt:o154; 100 pct identical amino acid sequence and) (le:8448) (re:8912) (di:direct) AE000479 AE000479 g1790498 Escherichia coli 562 -11533494 7500891890 soxr (fn:involved in regulation of superoxide response) (sr:escherichia coli (sub\_strain mgl655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:142709) (re:143173) (di:direct) ECOUW89 U00006 g396398 Escherichia coli 562 -11533494 99062 soxr (de:soxr protein) (db:swissprot) SOXR\_ECOLI P22538 ESCHERICHIA COLI 562 -11533494

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832324	8604	30760	756	251

Description

6500729637 creb:b4398 transcriptional regulatory protein creb  
(gtcf:10.2:12.13) (keggfc:12.1) (rileyfc:2.0.0) (db:gtc-escherichia coli)  
b4398 b4398 Escherichia coli 562 -11533495 66391 creb (de:transcriptional  
regulatory protein creb) (db:swissprot) CREB\_ECOLI P08368 ESCHERICHIA COLI  
562 -11533495 131472 creb transcription regulator creb (cl:ompr  
protein:response regulator homology) (db:pir1.dat) (mp:100 min) QQECFJ  
B25038 Escherichia coli 562 -11533495 237603 (sr:escherichia coli (strain  
klf125/kl181) dna) (db:genpept-bct1) (de:e.coli (clone pthr34) phom operon,  
containing phom gene (positveregulation for pho regulon) and three  
unidentified genes.) (nt:28 kd protein) (le:1066) (re:1755) (di:direct)  
ECOPHOM M13608 g147250 Escherichia coli 562 -11533495 7500879394 creb  
(fn:involved in catabolic regulation) (db:genpept-bct1) (de:escherichia coli  
k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:326840) (re:327529)  
(di:direct) ECOUW93 U14003 g537238 Escherichia coli 562 -11533495 235475  
creb catabolic regulation response regulator (fn:regulator; global  
regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655  
section 400 of 400 of the completegenome.) (nt:o229; 100 pct identical amino  
acid sequence and) (le:664) (re:1353) (di:direct) AE000510 AE000510 g1790860  
Escherichia coli 562 -11533495 5000691111 (de:(ecoli\_4280) (pn:catabolic  
regulation response regulator) (gn:creb) (gtcf:12.13) (ec:) (creb\_ecoli)  
(keggfc:11.2) (rileyfc:2.0.0) (db:gtc-escherichia coli)) ECOLI\_4280  
ECOLI\_4280 Escherichia coli 562 10009013

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832325	8605	30761	414	137

#### Description

6500729638 crec:phom:b4399 sensor protein crec (gtcfc:10.2:12.13) (ec:2.7.3.-) (keggfc:12.1) (rileyfc:2.0.0) (db:gtc-escherichia coli) b4399 b4399 Escherichia coli 562 -11533496 153378 crec:phom sensor protein crec::pho regulon positive regulatory protein crec (cl:envz protein:sensor histidine kinase homology) (ec:2.7.3.-) (db:pir1.dat) (mp:100 min) RGECFM S56623 Escherichia coli 562 -11533496 7500953620 crec (fn:positive regulatory gene for pho regulon) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:alternate gene name phom; cg site no. 395) (le:327529) (re:328953) (di:direct) ECOUW93 U14003 g537239 Escherichia coli 562 -11533496 237604 crec catabolite repression sensor kinase for phob (fn:enzyme; global regulatory functions) (db:genpept-bct2) (ec:2.7.3.-) (de:escherichia coli k-12 mg1655 section 400 of 400 of the completegenome.) (nt:o474; 99 pct identical amino acid sequence and) (le:1353) (re:2777) (di:direct) AE000510 AE000510 g1790861 Escherichia coli 562 -11533496 5000691112 (de:(ecoli\_4281) (pn:catabolite repression sensor autophosphorylates and phosphorylates phob; alternative sensor for pho regulon) (gn:crec) (gtcfc:12.13) (ec:2.7.3.-) (crec\_ecoli) (keggfc:11.1) (rileyfc:2.0.0) (db:gtc-escherichi) ECOLI\_4281 ECOLI\_4281 Escherichia coli 562 10080961

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832330	8606	30762	852	283

#### Description

GTC ORF with score 199 to: (sr:information) (db:genpept) (de:homo sapiens bac clone rg054d04 from 7q31, complete sequence.) (nt:similar to calcium-independent phospholipase a2;) (le:79671:86454:95029) (re:79945:86649:95223) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832332	8607	30763	252	83

#### Description

GTC ORF with score 107 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome 1 bac f8k4 sequence, completesequence.) (nt:contains similarity to gb|u51898 ca2+-independent) (le:33258:33792:34028:34442) (re:33695:33939:34126:34647) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832343	8608	30764	588	195

#### Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832349	8609	30765	1554	517

Description

6500729639 arca:dye:fexa:sfra:seg:msp:cpxc:b4401 aerobic respiration control protein arca:dye resistance protein (gtcfc:10.2:12.13) (keggfc:12.1) (rileyfc:2.0.0) (db:gtc-escherichia coli) b4401 b4401 Escherichia coli 562 -11533497 59984 arca:dye:fexa:sfra:seg:msp:cpxc (de:aerobic respiration control protein arca (dye resistance protein)) (db:swissprot) ARCA\_ECOLI P03026 ESCHERICHIA COLI 562 -11533497 131466 arca:dye:fexa:msp:seg:sfra dye resistance protein:aerobic respiration control protein arca:protein dye negative regulator in aerobic pathways (cl:ompr protein:response regulator homology) (db:pir1.dat) (mp:100 min) JYECR A03561 Escherichia coli 562 -11533497 237606 dye (sr:e.coli k12 dna, clone prb52) (db:genpept-bct1) (de:e.coli dye gene coding for dye protein, complete cds.) (le:98) (re:814) (di:direct) ECODYE M10044 g145818 Escherichia coli 562 -11533497 7500877072 dye (fn:negative regulator of genes in aerobic) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:alternate gene names arca, fexa, msp, seg, sfr; cg) (le:330423) (re:331139) (di:complement) ECOUW93 U14003 g537241 Escherichia coli 562 -11533497 234215 arca negative response regulator of genes in aerobic (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 400 of 400 of the completegenome.) (nt:f238; 100 pct identical to arca\_ecoli sw: p03026;) (le:4247) (re:4963) (di:complement) AE000510 AE000510 g1790863 Escherichia coli 562 -11533497 5000691113 (de:(ecoli\_4283) (pn:negative response regulator of genes in aerobic pathways,:sensors, arch and cpxa) (gn:arca) (gtcfc:12.13) (ec:) (arca\_ecoli) (keggfc:11.2) (rileyfc:2.0.0) (db:gtc-escherichia coli)) ECOLI\_4283 ECOLI\_4283 Escherichia coli 562 10002717

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832353	8610	30766	1467	488

Description

6500729640 hepa:b0059 probable atp-dependent helicase hepa (gtcfc:10.2) (keggfc:14.2) (rileyfc:3.1.9) (db:gtc-escherichia coli) b0059 b0059 Escherichia coli 562 -11533498 7000685520 hepa probable atp-dependent helicase hepa (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) (mp:2 min) C64727 C64727 Escherichia coli 562 -11533498 7500954377 hepa probable atp-dependent rna helicase (fn:putative enzyme; rna synthesis, modification,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 6 of 400 of the completegenome.) (nt:f968; 96 pct identical to hepa\_ecoli sw: p23852) (le:3152) (re:6058) (di:complement) AE000116 AE000116 g1786245 Escherichia coli 562 -11533498 76797 hepa\_ecoli (de:probable atp-dependent helicase hepa.) P23852 P23852 Escherichia coli 562 -11533498 5000690719 (de:(ecoli\_59) (pn:probable rna helicase) (gn:hepa) (gtcfc:10.2) (ec:) (hepa\_ecoli) (keggfc:11.2) (rileyfc:3.1.9) (db:gtc-escherichia coli)) ECOLI\_59 ECOLI\_59 Escherichia coli 562 10122636

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832360	8611	30767	1146	381

Description

6500729641 pcnb:b0143 poly:a polymerase (gtcfc:10.2) (ec:2.7.7.19)  
 (keggfc:14.1) (rileyfc:3.1.9) (db:gtc-escherichia coli) b0143 b0143  
 Escherichia coli 562 -11533499 7000691888 pcnb polynucleotide  
 adenylyltransferase::nucleic acid-binding protein pcnb:plasmid copy number  
 control protein (ec:2.7.7.19) (db:pir2.dat) G64737 G64737 Escherichia coli  
 562 -11533499 7500960415 pcnb poly a polymerase i (fn:enzyme; rna  
 synthesis, modification, dna) (db:genpept-bct2) (ec:2.7.7.19)  
 (de:escherichia coli k-12 mg1655 section 13 of 400 of the completegenome.)  
 (nt:f454; 98 pct identical to 436 residues) (le:8101) (re:9465)  
 (di:complement) AE000123 AE000123 g1786336 Escherichia coli 562 -11533499  
 5000690720 (de:(ecoli\_143) (pn:poly:a polymerase i) (gn:pcnb) (gtcfc:10.2)  
 (ec:2.7.7.19) (pcnb\_ecoli) (keggfc:11.1) (rileyfc:3.1.9) (db:gtc-escherichia  
 coli)) ECOLI\_143 ECOLI\_143 Escherichia coli 562 10122679

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832371	8612	30768	342	114

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832375	8613	30769	426	142

Description

6500729642 nusb:ssyb:b0416 n utilization substance protein b:nusb protein (gtcfc:10.2) (keggfc:14.2) (rileyfc:3.1.9) (db:gtc-escherichia coli) b0416 b0416 Escherichia coli 562 -11533500 235259 nusb:ssyb (de:n utilization substance protein b (nusb protein)) (db:swissprot) NUSB\_ECOLI P04381 ESCHERICHIA COLI 562 -11533500 164175 nusb:ssyb:gronb transcription termination factor nusb:n utilization substance protein b (cl:nusb protein) (db:pir1.dat) (mp:10 min) FJECB I51822 Escherichia coli 562 -11533500 233540 nusb:ssyb (db:genpept-bct1) (de:e.coli genes nusb (ssyb) and 3 orfs.) (le:2526) (re:2945) (di:direct) ECNUSB X64395 g581148 Escherichia coli 562 -11533500 5000690721 (db:genpept-bct1) (de:e. coli nusb gene (n utilization substance).) (nt:nusb protein) (le:117) (re:536) (di:direct) ECNUSB1 X00681 g581149 Escherichia coli 562 -11533500 240193 nusb (sr:e.coli dna) (db:genpept-bct1) (de:e.coli nusb gene, complete cds and open reading frame a.) (le:398) (re:817) (di:direct) ECONUSAA M26839 g146976 Escherichia coli 562 -11533500 7500887013 nusb n utilization substance protein b (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:14587) (re:15006) (di:direct) ECU82664 U82664 g1773100 Escherichia coli 562 -11533500 233539 nusb transcription termination:1 factor (fn:factor; rna synthesis, modification, dna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 38 of 400 of the completegenome.) (nt:ol39; 100 pct identical to nusb\_ecoli sw: p04381;) (le:2211) (re:2630) (di:direct) AE000148 AE000148 g1786618 Escherichia coli 562 -11533500 87239 nusb:ssyb (de:n utilization substance protein b (nusb protein)) (db:swissprot) NUSB\_ECOLI P04381 ESCHERICHIA COLI 562 -11533500

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832376	8614	30770	393	130

Description

6500729643 rhle:b0797 putative atp-dependent rna helicase:putative  
atp-dependent rna helicase rhle (gtcfc:10.2) (keggfc:14.2) (rileyfc:3.1.9)  
(db:gtc-escherichia coli) b0797 b0797 Escherichia coli 562 -11533501 94276  
rhle (de:putative atp-dependent rna helicase rhle) (db:swissprot) RHLE\_ECOLI  
P25888 ESCHERICHIA COLI 562 -11533501 7000686320 rhle probable  
atp-dependent rna helicase rhle (cl:unassigned dead/h box helicases:dead/h  
box helicase homology) (db:pir2.dat) E64816 E64816 Escherichia coli 562  
-11533501 223207 rhle putative atp-dependent rna helicase rhle  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #204)  
(db:genpept-bct1) (de:escherichia coli genomic dna. (17.8 - 18.1 min).)  
(le:2174) (re:3538) (di:direct) D90717 D90717 g1651360 Escherichia coli 562  
-11533501 7500889740 rhle atp-dependent rna helicase (db:genpept-bct1)  
(de:escherichia coli putative atp-dependent rna helicase (rhle), putative dna  
helicase (ding), ybia, ybib, and ybic genes, completecds.) (nt:dead box  
protein; swissprot accession number) (le:540) (re:1904) (di:direct) ECORHLEA  
L02123 g560801 Escherichia coli 562 -11533501 235787 rhle putative  
atp-dependent rna helicase (fn:putative enzyme; not classified)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 72 of 400 of the  
completegenome.) (nt:o454; 99 pct identical to rhle\_ecoli sw: p25888)  
(le:139) (re:1503) (di:direct) AE000182 AE000182 g1787016 Escherichia coli  
562 -11533501 5000690722 rhle putative atp-dependent rna helicase rhle.  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #203) (db:genpept)  
(de:escherichia coli genomic dna. (17.6 - 18.0 min).) (nt:orf\_id:o204#3;  
similar to swissprot accession) (le:16845) (re:18209) (di:direct) D90716  
D90716 g4062355 Escherichia coli 562 -11533501 7502851939 rhle putative  
atp-dependent rna helicase rhle. (sr:escherichia coli(strain:k12) dna,  
clone:kohara clone #204) (db:genpept) (de:escherichia coli genomic dna.  
(17.9 - 18.2 min).) (nt:orf\_id:o204#3; similar to swissprot accession)  
(le:2174) (re:3538) (di:direct) D90717 D90717 g1651360 Escherichia coli 562  
-11533501

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832381	8615	30771	327	108

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832391	8616	30772	1584	528

Description

6500729644 dbpa:b1343 atp-dependent rna helicase dbpa (gtcfc:10.2)  
(keggfc:14.2) (rileyfc:3.1.9) (db:gtc-escherichia coli) b1343 b1343  
Escherichia coli 562 -11533502 67941 dbpa (de:atp-dependent rna helicase  
dbpa) (db:swissprot) DBPA\_ECOLI P21693 ESCHERICHIA COLI 562 -11533502  
7000684987 dbpa atp-dependent rna helicase dbpa (cl:unassigned dead/h box  
helicases:dead/h box helicase homology) (db:pir2.dat) (mp:29.6 min) B64884  
B64884 Escherichia coli 562 -11533502 223619 dbpa atp-dependent rna  
helicase dbpa. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara  
lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#262(30.3-30.5 min.)) (nt:orf\_id:o262#3; similar to (swissprot accession)  
(le:5310) (re:6683) (di:direct) D90773 D90773 g1742212 Escherichia coli 562  
-11533502 300392 dbpa atp-dependent rna helicase (fn:enzyme; rna synthesis,  
modification, dna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655  
section 122 of 400 of the completegenome.) (nt:o457; 100 pct identical to  
dbpa\_ecoli sw: p21693;) (le:4881) (re:6254) (di:direct) AE000232 AE000232  
g1787605 Escherichia coli 562 -11533502 5000690723 (de:(ecoli\_1303)  
(pn:atp-dependent rna helicase) (gn:dbpa) (gtcfc:10.2) (ec:) (dbpa\_ecoli)  
(keggfc:11.2) (rileyfc:3.1.9) (db:gtc-escherichia coli)) ECOLI\_1303  
ECOLI\_1303 Escherichia coli 562 10010534

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832398	8617	30773	231	77

Description

6500729645 baes:b2078 sensor protein baes (gtcfc:10.2:12.13) (ec:2.7.3.-) (keggfc:12.1) (rileyfc:3.1.9) (db:gtc-escherichia coli) b2078 b2078 Escherichia coli 562 -11533503 61373 baes (ec:2.7.3.-) (de:sensor protein baes,) (db:swissprot) BAES\_ECOLI P30847 ESCHERICHIA COLI 562 -11533503 7000684685 baes sensory kinase baes::signal transduction protein (cl:sensor histidine kinase homology) (ec:2.7.3.-) (db:pir2.dat) E64974 E64974 Escherichia coli 562 -11533503 224617 baes sensor protein baes ec 2.7.3.-. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #357(46.5-46.8 min.)) (nt:orf\_id:o357#3; similar to (swissprot accession) (le:5628) (re:7031) (di:direct) D90846 D90846 g1736787 Escherichia coli 562 -11533503 301268 baes sensor protein baes ec 2.7.3.-. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #358(46.6-46.9 min.)) (nt:orf\_id:o357#3; similar to (swissprot accession) (le:273) (re:1676) (di:direct) D90847 D90847 g1736799 Escherichia coli 562 -11533503 301257 baes sensor protein for baer (fn:enzyme; rna synthesis, modification, dna) (db:genpept-bct2) (ec:2.7.3.-) (de:escherichia coli k-12 mg1655 section 187 of 400 of the completegenome.) (nt:o467; 98 pct identical (1 gap) to baes\_ecoli) (le:16269) (re:17672) (di:direct) AE000297 AE000297 g1788393 Escherichia coli 562 -11533503 224628 baes sensor protein baes ec 2.7.3.-. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #358(46.6-46.9 min.)) (nt:orf\_id:o357#3; similar to (swissprot accession) (le:273) (re:1676) (di:direct) D90847 D90847 g1736799 Escherichia coli 562 -11533503 5000690724 (de:(ecoli\_2026) (pn:member of 2-component regulatory system, sensor protein) (gn:baes) (gtcfc:10.2) (ec:2.7.3.-) (baes\_ecoli) (keggfc:11.1) (rileyfc:3.1.9) (db:gtc-escherichia coli)) ECOLI\_2026 ECOLI\_2026 Escherichia coli 562 10119993

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832411	8618	30774	849	282

Description

6500729646 baer:b2079 transcriptional regulatory protein baer  
(gtcf:10.2:12.13) (keggfc:12.1) (rileyfc:3.1.9) (db:gtc-escherichia coli)  
b2079 b2079 Escherichia coli 562 -11533504 61372 baer (de:transcriptional  
regulatory protein baer) (db:swissprot) BAER\_ECOLI P30846 ESCHERICHIA COLI  
562 -11533504 164510 baer response-regulator baer protein:signal  
transduction protein:transcriptional regulatory protein baer (cl:ompr  
protein:response regulator homology) (db:pir2.dat) JX0283 JX0283 Escherichia  
coli 562 -11533504 224618 baer response-regulator baer protein  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #357(46.5-46.8  
min.)) (nt:orf\_id:o357#4; similar to (pir accession number) (le:7028)  
(re:7750) (di:direct) D90846 D90846 g1736788 Escherichia coli 562 -11533504  
301269 baer response-regulator baer protein (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #358(46.6-46.9 min.))  
(nt:orf\_id:o357#4; similar to (pir accession number) (le:1673) (re:2395)  
(di:direct) D90847 D90847 g1736800 Escherichia coli 562 -11533504 301258  
baer baer (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1)  
(de:e.coli gene for baer and baes, complete cds.) (le:1671) (re:2393)  
(di:direct) ECOBAESR D14054 g216533 Escherichia coli 562 -11533504 233882  
baer transcriptional response regulatory protein (fn:regulator; rna  
synthesis, modification, dna) (db:genpept-bct2) (de:escherichia coli k-12  
mg1655 section 187 of 400 of the completegenome.) (nt:o240; 100 pct  
identical to baer\_ecoli sw: p30846;) (le:17669) (re:18391) (di:direct)  
AE000297 AE000297 g1788394 Escherichia coli 562 -11533504 224629 baer  
response-regulator baer protein (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #358(46.6-46.9 min.)) (nt:orf\_id:o357#4; similar to (pir  
accession number) (le:1673) (re:2395) (di:direct) D90847 D90847 g1736800  
Escherichia coli 562 -11533504 5000690725 (de:(ecoli\_2027)  
(pn:transcriptional regulatory protein, member of 2-component system)  
(gn:baer) (gtcf:10.2) (ec:) (baer\_ecoli) (keggfc:11.2) (rileyfc:3.1.9)  
(db:gtc-escherichia coli)) ECOLI\_2027 ECOLI\_2027 Escherichia coli 562  
10004081

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832426	8619	30775	450	149

Description

6500729647 evga:b2369 putative positive transcription regulator evga (gtcfc:10.2:12.13) (keggfc:12.1) (rileyfc:3.1.9) (db:gtc-escherichia coli) b2369 b2369 Escherichia coli 562 -11533505 70761 evga (de:putative positive transcription regulator evga) (db:swissprot) EVGA\_ECOLI P30854 ESCHERICHIA COLI 562 -11533505 163001 evga probable positive transcription regulator evga (cl:response regulator homology) (db:pir2.dat) JU0220 JU0220 Escherichia coli 562 -11533505 224927 evga evga protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #412(53.4-53.8 min.)) (nt:similar to (pir accession number ju0220)) (le:7523) (re:8137) (di:direct) D90867 D90867 g1799780 Escherichia coli 562 -11533505 234263 evga evga protein (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli evga gene.) (le:445) (re:1059) (di:direct) ECOEVGA D11142 g216551 Escherichia coli 562 -11533505 7500881210 evga evga (fn:regulatory protein of two component regulatory) (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli genes for sensor protein evgs and regulatory protein evga of two component regulatory system, complete cds.) (le:445) (re:1059) (di:... ECOEVGS D14008 g216553 Escherichia coli 562 -11533505 234262 evga putative positive transcription regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 215 of 400 of the complete genome.) (nt:o204; 100 pct identical to evga\_ecoli sw: p30854) (le:3201) (re:3815) (di:direct) AE000325 AE000325 g1788712 Escherichia coli 562 -11533505 5000690726 (de:(ecoli\_2317) (pn:putative positive transcription regulator evga) (gn:evga) (gtcfc:10.2) (ec:) (evga\_ecoli) (keggfc:11.2) (rileyfc:3.1.9) (db:gtc-escherichia coli)) ECOLI\_2317 ECOLI\_2317 Escherichia coli 562 10013336

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832427	8620	30776	297	98

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832429	8621	30777	1467	488

Description

6500729648 evgs:b2370 putative sensor protein evgs precursor  
 (gtcfc:10.2:12.13) (ec:2.7.3.-) (keggfc:12.1) (rileyfc:3.1.9)  
 (db:gtc-escherichia coli) b2370 b2370 Escherichia coli 562 -11533506 70762  
 evgs (ec:2.7.3.-) (de:putative sensor protein evgs precursor,)  
 (db:swissprot) EVGS\_ECOLI P30855 ESCHERICHIA COLI 562 -11533506 7000685198  
 evgs sensor protein evgs:precursor (cl:evgs protein:response regulator  
 homology) (ec:2.7.3.-) (db:pir2.dat) G65010 G65010 Escherichia coli 562  
 -11533506 224928 evgs putative sensor protein evgs precursor ec  
 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
 (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #412(53.4-53.8  
 min.)) (nt:similar to (swissprot accession number p30855)) (le:8142)  
 (re:11735) (di:direct) D90867 D90867 g1799781 Escherichia coli 562 -11533506  
 7500881211 evgs putative sensor for regulator evga (fn:putative regulator;  
 not classified) (db:genpept-bct2) (ec:2.7.3.-) (de:escherichia coli k-12  
 mgl655 section 215 of 400 of the completegenome.) (nt:ol197; 98 pct  
 identical to evgs\_ecoli sw: p30855) (le:3820) (re:7413) (di:direct) AE000325  
 AE000325 g1788713 Escherichia coli 562 -11533506 5000690727  
 (de:(ecoli\_2318) (pn:putative sensor protein evgs precursor) (gn:evgs)  
 (gtcfc:10.2) (ec:2.7.3.-) (evgs\_ecoli) (keggfc:11.1) (rileyfc:3.1.9)  
 (db:gtc-escherichia coli) ECOLI\_2318 ECOLI\_2318 Escherichia coli 562  
 10120152

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832430	8622	30778	258	85

Description

GTC ORF with score 110 to: (sr:thale cress) (db:genpept-pln1)  
 (de:arabidopsis thaliana dna chromosome 4, bac clone f4d11 (essaiiproject).)  
 (nt:similarity to protein kinase tmk1, arabidopsis) (le:33819:34133:34431)  
 (re:34034:34294:34578) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832443	8623	30779	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832451	8624	30780	939	312

Description

6500729649 dead:mssb:b3162 dead:atp-dependent rna helicase dead (gtcfc:10.2) (keggfc:14.2) (rileyfc:3.1.9) (db:gtc-escherichia coli) b3162 b3162 Escherichia coli 562 -11533507 7000690869 dead probable atp-dependent rna helicase dead (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) F65106 F65106 Escherichia coli 562 -11533507 7500954378 dead (fn:encodes a presumed atp-dependent rna helicase) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:two frameshifts relative to ecodead) (le:86723) (re:88663) (di:complement) ECOUW67 U18997 g606102 Escherichia coli 562 -11533507 236401 dead inducible atp-independent rna helicase (fn:enzyme; rna synthesis, modification, dna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 287 of 400 of the completegenome.) (nt:f646; alternate gene name csda) (le:2594) (re:4534) (di:complement) AE000397 AE000397 g1789553 Escherichia coli 562 -11533507 5000690728 (de:(ecoli\_3086) (pn:atp-dependent rna helicase dead) (gn:dead) (gtcfc:10.2) (ec:) (dead\_ecoli) (keggfc:11.2) (rileyfc:3.1.9) (db:gtc-escherichia coli)) ECOLI\_3086 ECOLI\_3086 Escherichia coli 562 10123984

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832459	8625	30781	1056	351

Description

6500729650 nusa:b3169 n utilization substance protein a:nusa protein:l factor (gtcfc:10.2) (keggfc:14.2) (rileyfc:3.1.9) (db:gtc-escherichia coli) b3169 b3169 Escherichia coli 562 -11533508 87227 nusa (de:n utilization substance protein a (nusa protein) (l factor)) (db:swissprot) NUSA\_ECOLI P03003 ESCHERICHIA COLI 562 -11533508 7000686018 nusa transcription termination-antitermination factor nusa (cl:escherichia coli transcription factor nusa:transcription termination factor nusa homology) (db:pir1.dat) (mp:69 min) FJEC E65107 Escherichia coli 562 -11533508 7500887007 nusa l factor (fn:transcription terminator) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 441) (le:96791) (re:98278) (di:complement) ECOUW67 U18997 g606109 Escherichia coli 562 -11533508 236408 nusa transcription pausing:l factor (fn:factor; rna synthesis, modification, dna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 287 of 400 of the completegenome.) (nt:f495; cg site no. 441; 100 pct identical amino) (le:12662) (re:14149) (di:complement) AE000397 AE000397 g1789560 Escherichia coli 562 -11533508 5000690729 (de:(ecoli\_3093) (pn:transcription pausing; l factor) (gn:nusa) (gtcfc:10.2) (ec:) (nusa\_ecoli) (keggfc:11.2) (rileyfc:3.1.9) (db:gtc-escherichia coli)) ECOLI\_3093 ECOLI\_3093 Escherichia coli 562 10029378

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832469	8626	30782	228	75

Description

6500729651 greb:b3406 transcription elongation factor greb:transcript cleavage fac (gtcfc:10.2) (keggfc:14.2) (rileyfc:3.1.9) (db:gtc-escherichia coli) b3406 b3406 Escherichia coli 562 -11533509 7000691923 greb transcription elongation factor greb (cl:transcription elongation factor greb) (db:pir2.dat) A65136 A65136 Escherichia coli 562 -11533509 7500960470 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf\_o170) (le:317524) (re:318036) (di:direct) ECOUW67 U18997 g606340 Escherichia coli 562 -11533509 236639 greb transcription elongation factor and transcript (fn:regulator; rna synthesis, modification, dna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 306 of 400 of the completegenome.) (nt:o170; 100 pct identical to 158 amino acids) (le:4033) (re:4545) (di:direct) AE000416 AE000416 g1789810 Escherichia coli 562 -11533509 5000690730 (de:(ecoli\_3324) (pn:transcription elongation factor and transcript cleavage) (gn:greb) (gtcfc:10.2) (ec:) (greb\_ecoli) (keggfc:11.2) (rileyfc:3.1.9) (db:gtc-escherichia coli)) ECOLI\_3324 ECOLI\_3324 Escherichia coli 562 10124024

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832470	8627	30783	684	227

Description

6500729652 spou:b3651 spou protein (gtcfc:10.2) (keggfc:14.2) (rileyfc:3.1.9) (db:gtc-escherichia coli) b3651 b3651 Escherichia coli 562 -11533510 99301 trmh:spou (ec:2.1.1.34) (de:methyltransferase) (db:swissprot) TRMH\_ECOLI P19396 ESCHERICHIA COLI 562 -11533510 163261 spou spou protein:hypothetical 25k protein spot 3 region (db:pir2.dat) (mp:82 min) JV0043 JV0043 Escherichia coli 562 -11533510 236889 spou (sr:e. coli (strain k-12) dna, clone pgal) (db:genpept-bct1) (de:e. coli spot gene encoding (p)ppgpp 3'-pyrophosphohydrolase, omega(rpoz) protein genes, complete cds.) (le:2476) (re:3165) (di:direct) ECOSPOT M24503 g147866 Escherichia coli 562 -11533510 7500891992 spou (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:13907) (re:14596) (di:direct) ECOUW82 L10328 g290501 Escherichia coli 562 -11533510 236026 spou putative rna methylase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 332 of 400 of the completegenome.) (nt:o229; 100 pct identical amino acid sequence and) (le:5906) (re:6595) (di:direct) AE000442 AE000442 g1790083 Escherichia coli 562 -11533510 5000690731 (de:(ecoli\_3571) (pn:putative rrna methylase) (gn:spou) (gtcfc:10.2) (ec:) (spou\_ecoli) (keggfc:11.2) (rileyfc:3.1.9) (db:gtc-escherichia coli)) ECOLI\_3571 ECOLI\_3571 Escherichia coli 562 10041160

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832481	8628	30784	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832499	8629	30785	471	156

Description

6500729653 rhlb:mmra:b3780 rhlb:putative atp-dependent rna helicase rhlb (gtcfc:10.2) (keggfc:14.2) (rileyfc:3.1.9) (db:gtc-escherichia coli) b3780 b3780 Escherichia coli 562 -11533511 7000691906 rhlb:rhlb:nmra rhlb protein:probable atp-dependent rna helicase (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) G65181 G65181 Escherichia coli 562 -11533511 7500954379 rhlb putative atp-dependent rna helicase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 344 of 400 of the completegenome.) (nt:f421; 99 pct identical amino acid sequence and) (le:6450) (re:7715) (di:complement) AE000454 AE000454 g1790214 Escherichia coli 562 -11533511 5000690732 (de:(ecoli\_3690) (pn:putative atp-dependent rna helicase) (gn:rhlb) (gtcfc:10.2) (ec:) (rhlb\_ecoli) (keggfc:11.2) (rileyfc:3.1.9) (db:gtc-escherichia coli)) ECOLI\_3690 ECOLI\_3690 Escherichia coli 562 10124092

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832508	8630	30786	507	168

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832532	8631	30787	1398	466

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832533	8632	30788	447	148

Description

6500729654 rho1:b3782 rho operon leader peptide (gtcfc:10.2) (keggfc:14.2) (rileyfc:3.1.9) (db:gtc-escherichia coli) b3782 b3782 Escherichia coli 562 -11533512 82421 rho1 (de:rho operon leader peptide) (db:swissprot) LPRH\_ECOLI P37324 ESCHERICHIA COLI 562 -11533512 164399 rho1 probable rho leader peptide (cl:unassigned leader peptides) (db:pir2.dat) A05111 A05111 Escherichia coli 562 -11533512 235796 (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli rho gene coding for transcription termination factor.) (nt:rho operon leader peptide) (le:282) (re:383) (di:direct) ECORHO J01673 g147606 Escherichia coli 562 -11533512 7500885132 rho leader peptide (sr:escherichia coli (sub\_strain sk3983, strain k-12) dna) (db:genpept-bct1) (de:e.coli (clone pbhk10) thioredoxin (trxa) and termination factor(rho) genes, complete cds.) (le:719) (re:820) (di:direct) ECORHOB K02845 g147612 Escherichia coli 562 -11533512 235792 rho1 rho operon leader peptide (fn:leader; rna synthesis, modification, dna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 344 of 400 of the completengenome.) (nt:o33; 100 pct identical to lprh\_ecoli sw: p37324) (le:8316) (re:8417) (di:direct) AE000454 AE000454 g1790216 Escherichia coli 562 -11533512 5000690733 (de:(ecoli\_3692) (pn:rho operon leader peptide) (gn:rho1) (gtcfc:10.2) (ec:) (lprh\_ecoli) (keggfc:11.2) (rileyfc:3.1.9) (db:gtc-escherichia coli)) ECOLI\_3692 ECOLI\_3692 Escherichia coli 562 10024645

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832538	8633	30789	342	113

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832540	8634	30790	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832543	8635	30791	255	85

Description

6500729655 rho:nita:psua:rnc:b3783 transcription termination factor:transcription termination factor rho (gtcfc:10.2) (keggfc:14.2) (rileyfc:3.1.9) (db:gtc-escherichia coli) b3783 b3783 Escherichia coli 562 -11533513 94309 rho:nita:psua:rnc:tsu:sbaa (de:transcription termination factor rho) (db:swissprot) RHO\_ECOLI P03002 ESCHERICHIA COLI 562 -11533513 131286 rho transcription termination factor rho (cl:transcription termination factor rho) (db:pir1.dat) (mp:85 min) TWECR A03530 Escherichia coli 562 -11533513 237011 rho (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli rho gene coding for transcription termination factor.) (nt:transcription termination factor) (le:468) (re:1727) (di:direct) ECORHO J01673 g147607 Escherichia coli 562 -11533513 7500889757 rho::cgsc no. 288 transcription termination factor rho (db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (nt:protein spot sequence confirms start) (le:19545) (re:20804) (di:direct) ECOUW85 M87049 g148186 Escherichia coli 562 -11533513 235793 rho transcription termination factor rho:polarity (fn:factor; rna synthesis, modification, dna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 344 of 400 of the completengenome.) (nt:o419; 100 pct identical to rho\_ecoli sw: p03002) (le:8502) (re:9761) (di:direct) AE000454 AE000454 g1790217 Escherichia coli 562 -11533513 5000690734 (de:(ecoli\_3693) (pn:transcription termination factor rho; polarity suppressor) (gn:rho) (gtcfc:10.2) (ec:) (rho\_ecoli) (keggfc:11.2) (rileyfc:3.1.9) (db:gtc-escherichia coli)) ECOLI\_3693 ECOLI\_3693 Escherichia coli 562 10036289

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832544	8636	30792	549	182

Description

6500729656 nusg:b3982 transcription antitermination protein nusg (gtcfc:10.2) (keggfc:14.2) (rileyfc:3.1.9) (db:gtc-escherichia coli) b3982 b3982 Escherichia coli 562 -11533514 87243 nusg (de:transcription antitermination protein nusg) (db:swissprot) NUSG\_ECOLI P16921 ESCHERICHIA COLI 562 -11533514 131282 nusg transcription antitermination factor nusg:transcription elongation factor nusg (cl:transcription antitermination factor nusg) (db:pirl.dat) (mp:90 min) TWECNG B35139 Escherichia coli 562 -11533514 237192 (sr:e.coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli sece-nusg operon encoding sece and nusg proteins, completecds, tufb rplk genes, partial cds.) (nt:nusg protein) (le:625) (re:1170) (di:direct) ECOSCE M30610 g147801 Escherichia coli 562 -11533514 235964 nusg component in transcription antitermination (fn:putative factor; rna synthesis, modification,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 362 of 400 of the completegenome.) (nt:o181; 100 pct identical amino acid sequence and) (le:2707) (re:3252) (di:direct) AE000472 AE000472 g1790414 Escherichia coli 562 -11533514 7500887016 nusg (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e.coli chromosomal region from 89.2 to 92.8 minutes.) (le:42985) (re:43530) (di:direct) ECOUW89 U00006 g396321 Escherichia coli 562 -11533514 5000690735 (de:(ecoli\_3872) (pn:component in transcription antitermination) (gn:nusg) (gtcfc:10.2) (ec:) (nusg\_ecoli) (keggfc:11.2) (rileyfc:3.1.9) (db:gtc-escherichia coli)) ECOLI\_3872 ECOLI\_3872 Escherichia coli 562 10029394

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832547	8637	30793	288	95

Description

6500729657 bass:pmrb:b4112 sensor protein bass/pmrb (gtcfc:10.2:12.13) (ec:2.7.3.-) (keggfc:12.1) (rileyfc:3.1.9) (db:gtc-escherichia coli) b4112 b4112 Escherichia coli 562 -11533515 61416 bass:pmrb (ec:2.7.3.-) (de:sensor protein bass/pmrb,) (db:swissprot) BASS\_ECOLI P30844 ESCHERICHIA COLI 562 -11533515 164599 bass sensor protein bass/pmrb::sensory kinase bass:signal transduction protein (cl:sensor histidine kinase homology) (ec:2.7.3.-) (db:pir2.dat) JX0285 JX0285 Escherichia coli 562 -11533515 237320 bass bass (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli gene for basr and bass, complete cds.) (le:1389) (re:2480) (di:direct) ECOBASRS D14055 g216539 Escherichia coli 562 -11533515 7500877676 bass (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:23010) (re:24101) (di:complement) ECOUW93 U14003 g536956 Escherichia coli 562 -11533515 233886 bass sensor protein for basr (fn:enzyme; rna synthesis, modification, dna) (db:genpept-bct2) (ec:2.7.3.-) (de:escherichia coli k-12 mg1655 section 373 of 400 of the completgenome.) (nt:f363; 100 pct identical amino acid sequence and) (le:6980) (re:8071) (di:complement) AE000483 AE000483 g1790551 Escherichia coli 562 -11533515 5000690736 (de:(ecoli\_3998) (pn:member of 2-component regulatory system, sensor protein for basr) (gn:bass) (gtcfc:10.2) (ec:2.7.3.-) (bass\_ecoli) (keggfc:11.1) (rileyfc:3.1.9) (db:gtc-escherichia coli)) ECOLI\_3998 ECOLI\_3998 Escherichia coli 562 10004125



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832548	8638	30794	1194	397

Description

6500729658 basr:pmra:b4113 transcriptional regulatory protein basr/pmra (gtcfc:10.2:12.13) (keggfc:12.1) (rileyfc:3.1.9) (db:gtc-escherichia coli) b4113 b4113 Escherichia coli 562 -11533516 7000689440 basr transcription regulator basr/pmra:response-regulator protein basr:signal transduction protein (cl:ompr protein:response regulator homology) (db:pir2.dat) H65220 H65220 Escherichia coli 562 -11533516 237321 basr (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:24111) (re:24779) (di:complement) ECOUW93 U14003 g536957 Escherichia coli 562 -11533516 7500955497 basr transcriptional regulatory protein:member of (fn:regulator; rna synthesis, modification, dna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 373 of 400 of the completgenome.) (nt:f222; 99 pct identical amino acid sequence and) (le:8081) (re:8749) (di:complement) AE000483 AE000483 g1790552 Escherichia coli 562 -11533516 162776 basr transcriptional regulatory protein basr/pmra:response-regulator protein basr:signal transduction protein (cl:ompr protein:response regulator homology) (db:pir) H65220 H65220 Escherichia coli 562 -11533516 5000690737 (de:(ecoli\_3999) (pn:transcriptional regulatory protein, member of 2-component regulatory system,) (gn:basr) (gtcfc:10.2) (ec:) (basr\_ecoli) (keggfc:11.2) (rileyfc:3.1.9) (db:gtc-escherichia coli)) ECOLI\_3999 ECOLI\_3999 Escherichia coli 562 10086617

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832553	8639	30795	360	119

Description

6500729659 msra:pms:b4219 peptide methionine sulfoxide reductase:peptide met:o reductase (gtcfc:10.2) (keggfc:14.2) (rileyfc:3.1.9) (db:gtc-escherichia coli) b4219 b4219 Escherichia coli 562 -11533517 164251 msra protein-methionine-s-oxide reductase::peptide methionine sulfoxide reductase (cl:peptide methionine sulfoxide reductase) (ec:1.8.4.6) (db:pir2.dat) S56444 S56444 Escherichia coli 562 -11533517 237424 peptide methionine sulfoxide reductase (sr:escherichia coli (strain b) dna) (db:genpept-bct1) (de:escherichia coli peptide methionine sulfoxide reductase gene,complete cds.) (le:241) (re:879) (di:direct) ECOPMSR M89992 g147305 Escherichia coli 562 -11533517 7500960435 pmsr peptide methionine sulfoxide reductase (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:alternate gene name msra) (le:132369) (re:133007) (di:complement) ECOUW93 U14003 g537060 Escherichia coli 562 -11533517 235506 msra peptide methionine sulfoxide reductase (fn:enzyme; proteins - translation and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 383 of 400 of the completegenome.) (nt:f212; 100 pct identical amino acid sequence and) (le:3986) (re:4624) (di:complement) AE000493 AE000493 g1790665 Escherichia coli 562 -11533517 5000690738 (de:(ecoli\_4102) (pn:methionine sulfoxide reductase) (gn:msra) (gtcfc:10.2) (ec:) (pmsr\_ecoli) (keggfc:11.2) (rileyfc:3.1.9) (db:gtc-escherichia coli)) ECOLI\_4102 ECOLI\_4102 Escherichia coli 562 10087246

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832571	8640	30796	540	179

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832573	8641	30797	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832578	8642	30798	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832593	8643	30799	798	265
<u>Description</u>				
6500729660 rpst:b0023 30s ribosomal protein s20 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b0023 b0023 Escherichia coli 562 -11533518 128843 rpst ribosomal protein s20 (cl:escherichia coli ribosomal protein s20) (db:pir1.dat) (mp:0 min) R3EC20 A30425 Escherichia coli 562 -11533518 235914 rpst ribosomal protein s20 (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (le:20478) (re:20741) (di:complement) ECO110K D10483 g285763 Escherichia coli 562 -11533518 238176 rpst ribosomal protein s20 (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli gene rpst encoding ribosomal protein s20, anddistal region with is1 and an orf encoding a 28kd polypeptide.) (le:273) (re:536) (di:direct) ECORPST J01683 g457114 Escherichia coli 562 -11533518 7500953519 ribosomal protein s20 (db:genpept-bct1) (de:e. coli gene rpst for ribosomal protein s20 and distal region withis1 and orf for 28kd polypeptide.) (le:273) (re:536) (di:direct) ECRPSTB X04382 g581224 Escherichia coli 562 -11533518 233561 rpst 30s ribosomal subunit protein s20 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 3 of 400 of the completegenome.) (nt:f87; 100 pct identical rs20_ecoli sw: p02378 but) (le:156) (re:419) (di:complement) AE000113 AE000113 g1786206 Escherichia coli 562 -11533518 5000690739 (de:(ecoli_23) (pn:30s ribosomal subunit protein s20) (gn:rpst) (gtcfc:10.3) (ec:) (rs20_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI_23 ECOLI_23 Escherichia coli 562 10067231				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832595	8644	30800	300	99

Description

6500729661 rpsb:b0169 30s ribosomal protein s2 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b0169 b0169 Escherichia coli 562 -11533519 128635 rpsb ribosomal protein s2 (cl:escherichia coli ribosomal protein s2) (db:pir1.dat) (mp:4 min) R3EC2 A02696 Escherichia coli 562 -11533519 238160 rpsb ribosomal protein s2 (sr:escherichia coli (sub\_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0 min).) (le:78468) (re:79193) (di:direct) ECO82K D26562 g473824 Escherichia coli 562 -11533519 239797 rpsb ribosomal protein s2 (db:genpept-bct1) (de:e. coli genes tsf and rpsb, encoding elongation factor ts andribosomal protein s2.) (le:284) (re:1009) (di:direct) ECRPSB V00343 g42842 Escherichia coli 562 -11533519 301635 rpsb ribosomal protein s2 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:20949) (re:21674) (di:direct) ECU70214 U70214 g1552746 Escherichia coli 562 -11533519 233697 rpsb 30s ribosomal subunit protein s2 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 16 of 400 of the completegenome.) (nt:o241; 100 pct identical to rs2\_ecoli sw: p02351 but) (le:6240) (re:6965) (di:direct) AE000126 AE000126 g1786365 Escherichia coli 562 -11533519 5000690740 rpsb ribosomal protein s2 (db:genpept) (de:e. coli genes tsf and rpsb, encoding elongation factor ts andribosomal protein s2.) (le:284) (re:1009) (di:direct) ECRPSB V00343 g42842 Escherichia coli 562 -11533519

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832607	8645	30801	831	276

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832616	8646	30802	270	89

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832618	8647	30803	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832629	8648	30804	555	184

Description

6500729662 rpsa:ssyf:b0911 30s ribosomal protein s1 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b0911 b0911 Escherichia coli 562 -11533520 97137 rpsa:ssyf (de:30s ribosomal protein s1) (db:swissprot) RS1\_ECOLI P02349 ESCHERICHIA COLI 562 -11533520 7000686497 rpsa:ssyf ribosomal protein s1 (cl:escherichia coli ribosomal protein s1) (db:pir1.dat) (mp:21 min) R3EC1 F64830 Escherichia coli 562 -11533520 223275 rpsa 30s ribosomal protein s1 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #217) (db:genpept-bct1) (de:escherichia coli genomic dna. (20.4 - 20.8 min).) (le:10155) (re:11828) (di:direct) D90729 D90729 g1651439 Escherichia coli 562 -11533520 7500890983 rpsa 30s ribosomal subunit protein s1 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 83 of 400 of the completegenome.) (nt:o557; 99 pct identical to rs1\_ecoli sw: p02349) (le:5324) (re:6997) (di:direct) AE000193 AE000193 g1787140 Escherichia coli 562 -11533520 5000690741 rpsa 30s ribosomal protein s1. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #217) (db:genpept) (de:escherichia coli genomic dna. (20.5 - 20.9 min).) (nt:orf\_id:o217#8; similar to swissprot accession) (le:10155) (re:11828) (di:direct) D90729 D90729 g1651439 Escherichia coli 562 -11533520

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832632	8649	30805	423	141

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832634	8650	30806	627	208

Description

6500729663 rpmf:b1089 50s ribosomal protein l32 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b1089 b1089 Escherichia coli 562 -11533521 129174 rpmf ribosomal protein l32 (cl:escherichia coli ribosomal protein l32) (db:pir1.dat) (mp:24 min) RSEC32 JV0048 Escherichia coli 562 -11533521 223353 rpmf ribosomal protein l32 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #234) (db:genpept-bct1) (de:escherichia coli genomic dna. (24.4 - 24.7 min).) (le:14321) (re:14494) (di:direct) D90744 D90744 g1651531 Escherichia coli 562 -11533521 7500953553 rpmf ribosomal protein l32 (sr:e.coli dna, clone pay2-5) (db:genpept-bct1) (de:e.coli g30k protein and ribosomal protein l32 (rpmf) genes,complete cds.) (le:868) (re:1041) (di:direct) ECORPMFA M29698 g147712 Escherichia coli 562 -11533521 235877 rpmf 50s ribosomal subunit protein l32 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 99 of 400 of the completegenome.) (nt:o57; 100 pct identical to rl32\_ecoli sw: p02435 but) (le:9052) (re:9225) (di:direct) AE000209 AE000209 g1787330 Escherichia coli 562 -11533521 7500953554 rpmf 50s ribosomal protein l32 (db:genpept-bct2) (de:salmonella typhimurium (g30k) gene, partial cds; and 50s ribosomalprotein l32 (rpmf), plsx (plsx), 3-oxoacyl-acyl carrier proteinsynthase iii (fabh), malonyl coa-acyl carrier protein transacylase(fabd), and 3-oxoacyl-acyl carrier ... AF044668 AF044668 g3282800 Salmonella typhimurium 602 -11533521 5000690742 rpmf ribosomal protein l32. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #234) (db:genpept) (de:escherichia coli genomic dna. (24.5 - 24.8 min).) (nt:orf\_id:o235#7; similar to pir accession number) (le:14321) (re:14494) (di:direct) D90744 D90744 g1651531 Escherichia coli 562 -11533521

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832636	8651	30807	588	195

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501832647	8652	30808	387	128

Description

6500729664 rpsv:b1480 30s ribosomal protein s22 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b1480 b1480 Escherichia coli 562 -11533522 97177 rpsv (de:very hypothetical 30s ribosomal protein s22) (db:swissprot) RS22\_ECOLI P28690 ESCHERICHIA COLI 562 -11533522 7000686503 rpsv ribosomal protein s22 (db:pir2.dat) C64901 C64901 Escherichia coli 562 -11533522 7500890999 rpsv ribosomal protein s22 (sr:escherichia coli (sub\_strain w3110, strain k-12) (library: kohar) (db:genpept-bct1) (de:escherichia coli rpsv gene for ribosomal protein s22.) (le:1289) (re:1426) (di:direct) ECORPSVW D13179 g216642 Escherichia coli 562 -11533522 235922 rpsv 30s ribosomal subunit protein s22 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 135 of 400 of the completegenome.) (nt:f45; 100 pct identical to rs22\_ecoli sw: p28690; cg) (le:3062) (re:3199) (di:complement) AE000245 AE000245 g1787755 Escherichia coli 562 -11533522 5000690743 (de:(ecoli\_1440) (pn:30s ribosomal subunit protein s22) (gn:rpsv) (gtcfc:10.3) (ec:) (rs22\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_1440 ECOLI\_1440 Escherichia coli 562 10039091

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501832648	8653	30809	246	81

Description

6500729665 rplt:pdza:b1716 50s ribosomal subunit protein 120:50s ribosomal protein 120 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b1716 b1716 Escherichia coli 562 -11533523 7000688951 rplt:pdza ribosomal protein 120 (cl:escherichia coli ribosomal protein 120) (db:pir1.dat) (mp:38 min) R5EC20 D64930 Escherichia coli 562 -11533523 7500953541 rplt 50s ribosomal subunit protein 120:and (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 156 of 400 of the completegenome.) (nt:f118; 100 pct identical to rl20\_ecoli sw: p02421;) (le:9876) (re:10232) (di:complement) AE000266 AE000266 g1788009 Escherichia coli 562 -11533523 5000690744 (de:(ecoli\_1673) (pn:50s ribosomal subunit protein 120, and regulator) (gn:rplt) (gtcfc:10.3) (ec:) (rl20\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_1673 ECOLI\_1673 Escherichia coli 562 10123432

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832651	8654	30810	210	69

Description

GTC ORF with score 114 to: (db:genpept-bct2) (de:pseudomonas fluorescens cyclohexanone monooxygenase homolog gene,partial cds; lactone-specific esterase (estf1) gene, complete cds;and alkane-1 monooxygenase homolog gene, partial cds.) (nt:orf1) (le:<1)...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832652	8655	30811	756	251

Description

6500729666 rpmi:b1717 50s ribosomal subunit protein l35:50s ribosomal protein l35:ribosomal protein a (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b1717 b1717 Escherichia coli 562 -11533524  
7000688956 rpmi ribosomal protein l35:ribosomal protein a:ribosomal protein x1 (cl:escherichia coli ribosomal protein l35) (db:pir1.dat) (mp:38 min) R5EC35 E64930 Escherichia coli 562 -11533524 224163 rpmi ribosomal protein l35 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #322(38.4-38.8 min.)) (nt:orf\_id:o322#17; similar to (pir accession number) (le:16547) (re:16744) (di:complement) D90813 D90813 g1742796 Escherichia coli 562 -11533524 224175 rpmi ribosomal protein l35 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #323(38.6-39.0 min.)) (nt:orf\_id:o322#17; similar to (pir accession number) (le:9387) (re:9584) (di:complement) D90814 D90814 g1742809 Escherichia coli 562 -11533524  
300832 rpmi 50s ribosomal subunit protein a (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 156 of 400 of the completegenome.) (nt:f65; 98 pct identical to pir: r5ec35; cg site) (le:10285) (re:10482) (di:complement) AE000266 AE000266 g1788010 Escherichia coli 562 -11533524 5000690745 (de:(ecoli\_1674) (pn:50s ribosomal subunit protein a) (gn:rpmi) (gtcfc:10.3) (ec:) (rl35\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_1674 ECOLI\_1674 Escherichia coli 562 10119787

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832653	8656	30812	210	69

Description

Hypothetical protein





<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832677	8657	30813	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832684	8658	30814	432	143

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832693	8659	30815	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832696	8660	30816	198	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832699	8661	30817	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832702	8662	30818	327	108

Description

6500729667 rply:b2185 50s ribosomal protein 125 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b2185 b2185 Escherichia coli 562 -11533525 95034 rply (de:50s ribosomal protein 125) (db:swissprot) RL25\_ECOLI P02426 ESCHERICHIA COLI 562 -11533525 129129 rply ribosomal protein 125 (cl:escherichia coli ribosomal protein 125) (db:pir1.dat) (mp:48 min) R5EC25 S16002 Escherichia coli 562 -11533525 7500890120 rply ribosomal protein 125 (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:escherichia coli rply gene for ribosomal protein 125.) (le:382) (re:666) (di:direct) ECORPLY D13326 g216640 Escherichia coli 562 -11533525 235873 rply 50s ribosomal subunit protein 125 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 198 of 400 of the completegenome.) (nt:o94; 100 pct identical to rl25\_ecoli sw: p02426) (le:4144) (re:4428) (di:direct) AE000308 AE000308 g1788512 Escherichia coli 562 -11533525 5000690746 (de:(ecoli\_2134) (pn:50s ribosomal subunit protein 125) (gn:rply) (gtcfc:10.3) (ec:) (rl25\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_2134 ECOLI\_2134 Escherichia coli 562 10037005

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832707	8663	30819	324	107

Description

GTC ORF with score 94 to: (sr:baker's yeast) (db:genpept-pln1) (de:s.cerevisiae g1301, g1304, g1307, g1315, g1330, g1334, gcn1, spo8,cox13, partial emp24 and partial cdc55 genes.) (nt:a component of endoplasmic reticulum (er) derived) (le:<1) (re:508) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832719	8664	30820	642	213

Description

6500729668 rpls:b2606 50s ribosomal subunit protein l19:50s ribosomal protein l19 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b2606 b2606 Escherichia coli 562 -11533526 129079 rpls ribosomal protein l19 (cl:escherichia coli ribosomal protein l19) (db:pir1.dat) (mp:57 min) R5EC19 S07951 Escherichia coli 562 -11533526 225181 rpls ribosomal protein l19 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #438(58.9-59.3 min.)) (nt:similar to (pir accession number s07951)) (le:7070) (re:7417) (di:complement) D90888 D90888 g1800011 Escherichia coli 562 -11533526 7500953540 (db:genpept-bct1) (de:e. coli trmd operon and nearby regions.) (nt:ribosomal protein l19 (rpls gene) (aa 1-115)) (le:3426) (re:3773) (di:direct) ECTRMD X01818 g43145 Escherichia coli 562 -11533526 238406 rpls 50s ribosomal subunit protein l19 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 236 of 400 of the completgenome.) (nt:f115; 100 pct identical to rl19\_ecoli sw: p02420;) (le:9975) (re:10322) (di:complement) AE000346 AE000346 g1788958 Escherichia coli 562 -11533526 5000690747 (de:(ecoli\_2542) (pn:50s ribosomal subunit protein l19) (gn:rpls) (gtcfc:10.3) (ec:) (rl19\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_2542 ECOLI\_2542 Escherichia coli 562 10067310

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832722	8665	30821	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832724	8666	30822	474	157

Description

6500729669 rps:b2609 30s ribosomal subunit protein s16:30s ribosomal protein s16 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b2609 b2609 Escherichia coli 562 -11533527 7500890919 rpsp (de:30s ribosomal protein s16) (db:swissprot) RS16\_ECOLI P02372 ESCHERICHIA COLI 562 -11533527 128796 rpsp ribosomal protein s16:dna-binding protein:434-specific (cl:escherichia coli ribosomal protein s16) (db:pir1.dat) (mp:57 min) R3EC16 S07948 Escherichia coli 562 -11533527 5000690748 (db:genpept-bct1) (de:e. coli trmd operon and nearby regions.) (nt:ribosomal protein s16 (rps p gene) (aa 1-82)) (le:1771) (re:2019) (di:direct) ECTRMD X01818 g43143 Escherichia coli 562 -11533527 238404 rpsp 30s ribosomal subunit protein s16 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 236 of 400 of the completegenome.) (nt:f82; 100 pct identical to rs16\_ecoli sw: p02372; cg) (le:11729) (re:11977) (di:complement) AE000346 AE000346 g1788961 Escherichia coli 562 -11533527 97055 rpsp (de:30s ribosomal protein s16) (db:swissprot) RS16\_ECOLI P02372 ESCHERICHIA COLI 562 -11533527

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832730	8667	30823	231	76

Description

6500729670 rpsu:b3065 30s ribosomal subunit protein s21:30s ribosomal protein s21 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3065 b3065 Escherichia coli 562 -11533528 128844 rpsu ribosomal protein s21 (cl:escherichia coli ribosomal protein s21) (db:pir1.dat) (mp:67 min) R3EC21 A02749 Escherichia coli 562 -11533528 128845 rpsu ribosomal protein s21 (cl:escherichia coli ribosomal protein s21) (db:pir1.dat) R3EB21 A23985 Salmonella typhimurium 602 -11533528 238178 rpsu ribosomal protein s21 (sr:escherichia coli k12 and hb101 dna) (db:genpept-bct1) (de:e.coli rpsu-dnag-rpod operon with genes coding for ribosomalprotein s21, dna primase and rna polymerase sigma-subunit.) (le:715) (re:930) (di:direct) ECORPSRPO J01687 g147754 Escherichia coli 562 -11533528 239270 (db:genpept-bct1) (de:e. coli gene rpsu coding for protein s21 of the small subunit ofthe ribosome and fragment (5'-end) of dnag.) (nt:coding sequence) (le:715) (re:930) (di:direct) ECRPSU V00346 g42868 Escherichia coli 562 -11533528 264511 rpsu 30s ribosomal subunit protein s21 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 68 minutes.) (nt:cg site no. 211) (le:15576) (re:15791) (di:direct) ECU28379 U28379 g882588 Escherichia coli 562 -11533528 7500953520 (sr:salmonella typhimurium dna) (db:genpept-bct1) (de:s.typhimurium rpsu-dnag-rpod operon, complete cds.) (nt:rpsu protein) (le:359) (re:574) (di:direct) STYUGDOP M14427 g154404 Salmonella typhimurium 602 -11533528 235911 rpsu 30s ribosomal subunit protein s21 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 278 of 400 of the completegenome.) (nt:o71; 100 pct identical to rs21\_ecoli sw: p02379; cg) (le:4452) (re:4667) (di:direct) AE000388 AE000388 g1789446 Escherichia coli 562 -11533528 5000690749 (de:(ecoli\_2988) (pn:30s ribosomal subunit protein s21) (gn:rpsu) (gtcfc:10.3) (ec:) (rs21\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_2988 ECOLI\_2988 Escherichia coli 562 10067232

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832739	8668	30824	621	206

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832757	8669	30825	1089	362

Description

6500729671 rpso:secc:b3165 30s ribosomal subunit protein s15:30s ribosomal protein s15 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3165 b3165 Escherichia coli 562 -11533529 128790 rpso ribosomal protein s15 (cl:escherichia coli ribosomal protein s15:eubacterial ribosomal protein s15 homology) (db:pir1.dat) (mp:69 min) R3EC15 B26118 Escherichia coli 562 -11533529 235907 rpso ribosomal protein s15 (sr:escherichia coli (strain jch5/jc553) (clone: pbp280.) dna) (db:genpept-bct1) (de:e.coli rpso and pnp genes encoding ribosomal protein s15 and polynucleotide phosphorylase, complete cds.) (le:148) (re:417) (di:direct) ECORPSOP J02638 g147745 Escherichia coli 562 -11533529 236404 (sr:e.coli dna, clone phel) (db:genpept-bct1) (de:e.coli ribosomal protein s15 (rpso), complete cds, and polynucleotide phosphorylase gene (pnp), 5' end.) (nt:ribosomal protein s15) (le:148) (re:417) (di:direct) ECRPSPNP M14425 g147748 Escherichia coli 562 -11533529 238173 rpso 30s ribosomal subunit protein s15 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 217; alternate name secc) (le:92167) (re:92436) (di:complement) ECOUW67 U18997 g606105 Escherichia coli 562 -11533529 238174 (db:genpept-bct1) (de:e. coli rps0 gene for ribosomal protein s15.) (nt:ribosomal protein s15) (le:145) (re:414) (di:direct) ECRPSO X01073 g42860 Escherichia coli 562 -11533529 7500953513 (db:genpept-bct1) (de:e.coli rpso gene for ribosomal protein s15 and pnp gene fragment for polynucleotide phosphorylase (ec 2.7.7.8).) (nt:ribosomal protein s15) (le:148) (re:417) (di:direct) ECRPSOP X00761 g42862 Escherichia coli 562 -11533529 235904 rpso 30s ribosomal subunit protein s15 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 287 of 400 of the complete genome.) (nt:f89; cg site no. 217; alternate name secc; 100 pct) (le:8038) (re:8307) (di:complement) AE000397 AE000397 g1789556 Escherichia coli 562 -11533529 5000690750 (de:(ecoli\_3089) (pn:30s ribosomal subunit protein s15) (gn:rpso) (gtcfc:10.3) (ec:) (rs15\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3089 ECOLI\_3089 Escherichia coli 562 10067213

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832759	8670	30826	801	267

Description

6500729672 rpma:b3185 50s ribosomal subunit protein 127:50s ribosomal protein 127 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3185 b3185 Escherichia coli 562 -11533530 129134 rpma ribosomal protein 127 (cl:escherichia coli ribosomal protein 127:eubacterial ribosomal protein 127 homology) (db:pir1.dat) (mp:69 min) R5EC27 JS0767 Escherichia coli 562 -11533530 236422 rpma ribosomal protein 127 (sr:escherichia coli (sub\_strain w3110, strain k-12) (library;lambd) (db:genpept-bct1) (de:e.coli genes for ribosomal protein l21 and l27, complete cds.) (le:1352) (re:1609) (di:direct) ECORPLRPM D13267 g216637 Escherichia coli 562 -11533530 7500953545 rpma 50s ribosomal subunit protein 127 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 241) (le:113614) (re:113871) (di:complement) ECOUW67 U18997 g606123 Escherichia coli 562 -11533530 235871 rpma 50s ribosomal subunit protein 127 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 289 of 400 of the completegenome.) (nt:f85; cg site no. 241; 100 pct identical amino) (le:4135) (re:4392) (di:complement) AE000399 AE000399 g1789576 Escherichia coli 562 -11533530 5000690751 (de:(ecoli\_3107) (pn:50s ribosomal subunit protein 127) (gn:rpma) (gtcfc:10.3) (ec:) (rl27\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3107 ECOLI\_3107 Escherichia coli 562 10067328

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832760	8671	30827	1416	471

Description

6500729673 rplu:b3186 50s ribosomal subunit protein l21:50s ribosomal protein l21 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3186 b3186 Escherichia coli 562 -11533531 94957 rplu (de:50s ribosomal protein l21) (db:swissprot) RL21\_ECOLI P02422 ESCHERICHIA COLI 562 -11533531 129096 rplu ribosomal protein l21 (cl:escherichia coli ribosomal protein l21) (db:pir1.dat) (mp:69 min) R5EC21 JS0766 Escherichia coli 562 -11533531 236423 rplu ribosomal protein l21 (sr:escherichia coli (sub\_strain w3110, strain k-12) (library;lambd) (db:genpept-bct1) (de:e.coli genes for ribosomal protein l21 and l27, complete cds.) (le:1020) (re:1331) (di:direct) ECORPLRPM D13267 g216636 Escherichia coli 562 -11533531 7500890053 rplu 50s ribosomal subunit protein l21 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 246) (le:113892) (re:114203) (di:complement) ECOUW67 U18997 g606124 Escherichia coli 562 -11533531 235870 rplu 50s ribosomal subunit protein l21 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 289 of 400 of the completegenome.) (nt:f103; cg site no. 246; 100 pct identical amino) (le:4413) (re:4724) (di:complement) AE000399 AE000399 g1789577 Escherichia coli 562 -11533531 5000690752 (de:(ecoli\_3108) (pn:50s ribosomal subunit protein l21) (gn:rplu) (gtcfc:10.3) (ec:) (rl21\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3108 ECOLI\_3108 Escherichia coli 562 10036931

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832772	8672	30828	225	75

#### Description

6500729674 rpsi:b3230 30s ribosomal subunit protein s9:30s ribosomal protein s9 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3230 b3230 Escherichia coli 562 -11533532 7000688946 rpsi ribosomal protein s9:30s ribosomal subunit protein s9 (cl:escherichia coli ribosomal protein s9) (db:pir1.dat) (mp:70 min) R3EC9 H65114 Escherichia coli 562 -11533532 238170 rpsi 30s ribosomal subunit protein s9 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 17596) (le:158560) (re:158952) (di:complement) ECOUW67 U18997 g606169 Escherichia coli 562 -11533532 7500953505 (db:genpept-bct1) (de:e. coli genes rpsi and rplm for ribosomal proteins s9 and l13.) (nt:s9 (rpsi) (1-130)) (le:659) (re:1051) (di:direct) ECRPSI X02130 g535073 Escherichia coli 562 -11533532 236468 rpsi 30s ribosomal subunit protein s9 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 292 of 400 of the completegenome.) (nt:fl130; cg site no. 17596; 100 pct identical) (le:5202) (re:5594) (di:complement) AE000402 AE000402 g1789625 Escherichia coli 562 -11533532 5000690753 (de:(ecoli\_3153) (pn:30s ribosomal subunit protein s9) (gn:rpsi) (gtcfc:10.3) (ec:) (rs9\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3153 ECOLI\_3153 Escherichia coli 562 10123996

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832774	8673	30829	702	234

#### Description

6500729675 rplm:b3231 50s ribosomal subunit protein l13:50s ribosomal protein l13 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3231 b3231 Escherichia coli 562 -11533533 7500889929 rplm (de:50s ribosomal protein l13) (db:swissprot) RL13\_ECOLI P02410 ESCHERICHIA COLI 562 -11533533 129025 rplm ribosomal protein l13 (cl:escherichia coli ribosomal protein l13) (db:pir1.dat) (mp:70 min) R5EC13 A02787 Escherichia coli 562 -11533533 238169 rplm 50s ribosomal subunit protein l13 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 253) (le:158968) (re:159396) (di:complement) ECOUW67 U18997 g606170 Escherichia coli 562 -11533533 5000690754 (db:genpept-bct1) (de:e. coli genes rpsi and rplm for ribosomal proteins s9 and l13.) (nt:l13 (rplm) (aa 1-129)) (le:216) (re:644) (di:direct) ECRPSI X02130 g42855 Escherichia coli 562 -11533533 236469 rplm 50s ribosomal subunit protein l13 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 292 of 400 of the completegenome.) (nt:fl142; cg site no. 253; 100 pct identical amino) (le:5610) (re:6038) (di:complement) AE000402 AE000402 g1789626 Escherichia coli 562 -11533533 94774 rplm (de:50s ribosomal protein l13) (db:swissprot) RL13\_ECOLI P02410 ESCHERICHIA COLI 562 -11533533

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832785	8674	30830	351	116

Description

6500729676 rplq:b3294 50s ribosomal subunit protein 117:50s ribosomal protein 117 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3294 b3294 Escherichia coli 562 -11533534 7500889991 rplq (de:50s ribosomal protein 117) (db:swissprot) RL17\_ECOLI P02416 ESCHERICHIA COLI 562 -11533534 129067 rplq ribosomal protein 117 (cl:escherichia coli ribosomal protein 117) (db:pir1.dat) (mp:73 min) R5EC17 B22884 Escherichia coli 562 -11533534 236527 rplq (sr:escherichia coli dna, clones phr14 and phr15 (2)) (db:genpept-bct1) (de:e.coli alpha ribosomal protein operon (rpoa, rplq, and rpsd) genes coding for rna polymerase alpha subunit and ribosomal proteins 117 and s4.) (nt:ribosomal protein 117) (le:1240... ECORPOA J01685 g147716 Escherichia coli 562 -11533534 238122 rplq 50s ribosomal subunit protein 117 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 249) (le:220364) (re:220747) (di:complement) ECOUW67 U18997 g606228 Escherichia coli 562 -11533534 238134 (db:genpept-bct1) (de:e. coli alpha ribosomal protein operon for ribosomal proteins s13,s11, s4,l17 and rna polymerase alpha-subunit.) (nt:ribosomal protein 117 (aa 1-127)) (le:2692) (re:3075) (di:direct) ECRPA X02543 g42800 Escherichia coli 562 -11533534 5000690755 (db:genpept-bct1) (de:e.coli rpoa-rplq dna for rna-polymerase alpha subunit and ribosomal component 117.) (nt:ribosomal component 117) (le:1041) (re:1424) (di:direct) ECRPOA X00766 g42808 Escherichia coli 562 -11533534 235880 rplq 50s ribosomal subunit protein 117 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 297 of 400 of the complete genome.) (nt:f127; cg site no. 249; 100 pct identical amino) (le:7686) (re:8069) (di:complement) AE000407 AE000407 g1789689 Escherichia coli 562 -11533534 94851 rplq (de:50s ribosomal protein 117) (db:swissprot) RL17\_ECOLI P02416 ESCHERICHIA COLI 562 -11533534

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832787	8675	30831	828	275

Description

6500729677 rpsd:rama:b3296 30s ribosomal subunit protein s4:30s ribosomal protein s4 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3296 b3296 Escherichia coli 562 -11533535 128658 rpsd ribosomal protein s4 (cl:escherichia coli ribosomal protein s4) (db:pir1.dat) (mp:73 min) R3EC4 C23807 Escherichia coli 562 -11533535 238120 rpsd 30s ribosomal subunit protein s4 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (le:221803) (re:222423) (di:complement) ECOUW67 U18997 g606231 Escherichia coli 562 -11533535 7500953497 (db:genpept-bct1) (de:e. coli alpha ribosomal protein operon for ribosomal proteins s13,s11, s4,l17 and rna polymerase alpha-subunit.) (nt:ribosomal protein s4 (aa 1-206)) (le:1016) (re:1636) (di:direct) ECRPA X02543 g42798 Escherichia coli 562 -11533535 236529 rpsd 30s ribosomal subunit protein s4 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 297 of 400 of the completegenome.) (nt:f206; 100 pct identical amino acid sequence and) (le:9125) (re:9745) (di:complement) AE000407 AE000407 g1789691 Escherichia coli 562 -11533535 5000690756 (de:(ecoli\_3214) (pn:30s ribosomal subunit protein s4) (gn:rpsd) (gtcfc:10.3) (ec:) (rs4\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3214 ECOLI\_3214 Escherichia coli 562 10067169

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832794	8676	30832	450	149

Description

6500729678 rpsk:b3297 30s ribosomal subunit protein s11:30s ribosomal protein s11 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3297 b3297 Escherichia coli 562 -11533536 128726 rpsk ribosomal protein s11 (cl:escherichia coli ribosomal protein s11) (db:pir1.dat) (mp:73 min) R3EC11 B23807 Escherichia coli 562 -11533536 238119 rpsk 30s ribosomal subunit protein s11 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (le:222457) (re:222846) (di:complement) ECOUW67 U18997 g606232 Escherichia coli 562 -11533536 7500953506 (db:genpept-bct1) (de:e. coli alpha ribosomal protein operon for ribosomal proteins s13,s11, s4,l17 and rna polymerase alpha-subunit.) (nt:ribosomal protein s11 (aa 1-129)) (le:593) (re:982) (di:direct) ECRPA X02543 g42797 Escherichia coli 562 -11533536 236530 rpsk 30s ribosomal subunit protein s11 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 297 of 400 of the completegenome.) (nt:f129; 100 pct identical amino acid sequence and) (le:9779) (re:10168) (di:complement) AE000407 AE000407 g1789692 Escherichia coli 562 -11533536 5000690757 (de:(ecoli\_3215) (pn:30s ribosomal subunit protein s11) (gn:rpsk) (gtcfc:10.3) (ec:) (rs11\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3215 ECOLI\_3215 Escherichia coli 562 10067187

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832800	8677	30833	516	171

Description

6500729679 rpsm:b3298 30s ribosomal subunit protein s13:30s ribosomal protein s13 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3298 b3298 Escherichia coli 562 -11533537 128755 rpsm ribosomal protein s13 (cl:escherichia coli ribosomal protein s13) (db:pir1.dat) (mp:73 min) R3EC13 A23807 Escherichia coli 562 -11533537 238118 rpsm 30s ribosomal subunit protein s13 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 219) (le:222863) (re:223219) (di:complement) ECOUW67 U18997 g606230 Escherichia coli 562 -11533537 7500953509 (db:genpept-bct1) (de:e. coli alpha ribosomal protein operon for ribosomal proteins s13,s11, s4,l17 and rna polymerase alpha-subunit.) (nt:ribosomal protein s13 (aa 1-118)) (le:220) (re:576) (di:direct) ECRPA X02543 g581217 Escherichia coli 562 -11533537 236531 rpsm 30s ribosomal subunit protein s13 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 297 of 400 of the completegenome.) (nt:f118; cg site no. 219) (le:10185) (re:10541) (di:complement) AE000407 AE000407 g1789693 Escherichia coli 562 -11533537 5000690758 (de:(ecoli\_3216) (pn:30s ribosomal subunit protein s13) (gn:rpsm) (gtcfc:10.3) (ec:) (rs13\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3216 ECOLI\_3216 Escherichia coli 562 10067198

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832801	8678	30834	333	110

Description

GTC ORF with score 273 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid t13h5, complete sequence.) (nt:homology with squid retinal-binding protein (pir) (le:18431:18727:19238:19414) (re:18617:19012:19364:19670) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832802	8679	30835	1011	337

Description

6500729680 rpmj:b3299 50s ribosomal subunit protein 136:50s ribosomal protein 136:ribosomal protein b (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3299 b3299 Escherichia coli 562 -11533538  
7500890242 rpmj (de:50s ribosomal protein 136 (ribosomal protein b)) (db:swissprot) RL36\_ECOLI P21194 ESCHERICHIA COLI 562 -11533538 129194 rpmj ribosomal protein 136:ribosomal protein x (cl:escherichia coli ribosomal protein 136) (db:pir1.dat) (mp:73 min) R5EC36 S14057 Escherichia coli 562 -11533538 236532 (sr:escherichia coli (clone library: lambda-fus-3.) dna) (db:genpept-bct1) (de:e.coli alpha operon ribosomal protein s13 (rpsm) gene, 5' end and promoter region.) (nt:orf; putative) (le:388) (re:504) (di:direct) ECORPLP2 M12432 g1128970 Escherichia coli 562 -11533538 238293 rpmj 50s ribosomal subunit protein 136 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 17599) (le:223366) (re:223482) (di:complement) ECOUW67 U18997 g606233 Escherichia coli 562 -11533538 5000690759 (db:genpept-bct1) (de:escherichia coli spc ribosomal protein operon.) (nt:unidentified reading frame x (aa 1-38)) (le:5657) (re:5773) (di:direct) ECSPC X01563 g42990 Escherichia coli 562 -11533538 235868 rpmj 50s ribosomal subunit protein 136 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 298 of 400 of the complete genome.) (nt:f38; cg site no. 17599; 100 pct identical amino) (le:145) (re:261) (di:complement) AE000408 AE000408 g1789695 Escherichia coli 562 -11533538 95236 rpmj (de:50s ribosomal protein 136 (ribosomal protein b)) (db:swissprot) RL36\_ECOLI P21194 ESCHERICHIA COLI 562 -11533538

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832810	8680	30836	282	93

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832835	8681	30837	501	166

Description

6500729681 rplo:b3301 50s ribosomal subunit protein 115:50s ribosomal protein 115 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3301 b3301 Escherichia coli 562 -11533539 7500889965 rplo (de:50s ribosomal protein 115) (db:swissprot) RL15\_ECOLI P02413 ESCHERICHIA COLI 562 -11533539 129051 rplo ribosomal protein 115 (cl:escherichia coli ribosomal protein 115) (db:pir1.dat) (mp:73 min) R5EC15 A02794 Escherichia coli 562 -11533539 5000690760 (db:genpept-bct1) (de:escherichia coli spc ribosomal protein operon.) (nt:115 (rp10) (aa 1-144)) (le:3852) (re:4286) (di:direct) ECSPC X01563 g42988 Escherichia coli 562 -11533539 238291 rplo 50s ribosomal subunit protein 115 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 298 of 400 of the completegenome.) (nt:f144; cg site no. 251; 99 pct identical amino) (le:1632) (re:2066) (di:complement) AE000408 AE000408 g1789697 Escherichia coli 562 -11533539 94814 rplo (de:50s ribosomal protein 115) (db:swissprot) RL15\_ECOLI P02413 ESCHERICHIA COLI 562 -11533539

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832837	8682	30838	411	136

Description

6500729682 rpmd:b3302 50s ribosomal subunit protein 130:50s ribosomal protein 130 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3302 b3302 Escherichia coli 562 -11533540 7000688953 rpmd ribosomal protein 130 (cl:escherichia coli ribosomal protein 130) (db:pir1.dat) (mp:73 min) R5EC30 A65123 Escherichia coli 562 -11533540 238290 rpmd 50s ribosomal subunit protein 130 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 238) (le:225291) (re:225470) (di:complement) ECOUW67 U18997 g606236 Escherichia coli 562 -11533540 7500953547 (db:genpept-bct1) (de:escherichia coli spc ribosomal protein operon.) (nt:130 (rpmd) (aa 1-59)) (le:3669) (re:3848) (di:direct) ECSPC X01563 g42987 Escherichia coli 562 -11533540 236535 rpmd 50s ribosomal subunit protein 130 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 298 of 400 of the completegenome.) (nt:f59; cg site no. 238; 100 pct identical amino) (le:2070) (re:2249) (di:complement) AE000408 AE000408 g1789698 Escherichia coli 562 -11533540 5000690761 (de:(ecoli\_3220) (pn:50s ribosomal subunit protein 130) (gn:rpmd) (gtcfc:10.3) (ec:) (rl30\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3220 ECOLI\_3220 Escherichia coli 562 10124007

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832844	8683	30839	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832845	8684	30840	231	76

Description

6500729683 rpse:spc:b3303 30s ribosomal subunit protein s5:30s ribosomal protein s5 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3303 b3303 Escherichia coli 562 -11533541 7000688942 rpse ribosomal protein s5 (cl:escherichia coli ribosomal protein s5) (db:pir1.dat) (mp:73 min) R3EC5 B65123 Escherichia coli 562 -11533541 238289 rpse 30s ribosomal subunit protein s5 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 226; alternate names eps, spca, spc) (le:225474) (re:225977) (di:complement) ECOUW67 U18997 g606237 Escherichia coli 562 -11533541 7500953499 (db:genpept-bct1) (de:escherichia coli spc ribosomal protein operon.) (nt:s5 (rpse) (aa 1-167)) (le:3162) (re:3665) (di:direct) ECSPC X01563 g42986 Escherichia coli 562 -11533541 236536 rpse 30s ribosomal subunit protein s5 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 298 of 400 of the completegenome.) (nt:f167; cg site no. 226; alternate names eps,) (le:2253) (re:2756) (di:complement) AE000408 AE000408 g1789699 Escherichia coli 562 -11533541 5000690762 (de:(ecoli\_3221) (pn:30s ribosomal subunit protein s5) (gn:rpse) (gtcfc:10.3) (ec:) (rs5\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3221 ECOLI\_3221 Escherichia coli 562 10124008

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832858	8685	30841	189	62

Description

GTC ORF with score 117 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana dna chromosome 4, bac clone f4d11 (essaiiproject).) (nt:similarity to mus308 gene, drosophila melanogaster;) (le:38015:38256:38642) (re:38131:38396:38750) ...



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832860	8686	30842	510	169

Description

6500729684 rplr:b3304 50s ribosomal subunit protein 118:50s ribosomal protein 118 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3304 b3304 Escherichia coli 562 -11533542 7500889999 rplr (de:50s ribosomal protein 118) (db:swissprot) RL18\_ECOLI P02419 ESCHERICHIA COLI 562 -11533542 129073 rplr ribosomal protein 118 (cl:escherichia coli ribosomal protein 118) (db:pir1.dat) (mp:73 min) R5EC18 A02803 Escherichia coli 562 -11533542 238288 rplr 50s ribosomal subunit protein 118 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 248) (le:225992) (re:226345) (di:complement) ECOUW67 U18997 g606238 Escherichia coli 562 -11533542 5000690763 (db:genpept-bct1) (de:escherichia coli spc ribosomal protein operon.) (nt:l18 (rplr) (aa 1-117)) (le:2794) (re:3147) (di:direct) ECSPC X01563 g42985 Escherichia coli 562 -11533542 236537 rplr 50s ribosomal subunit protein 118 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 298 of 400 of the completegenome.) (nt:f117; cg site no. 248; 100 pct identical amino) (le:2771) (re:3124) (di:complement) AE000408 AE000408 g1789700 Escherichia coli 562 -11533542 94864 rplr (de:50s ribosomal protein 118) (db:swissprot) RL18\_ECOLI P02419 ESCHERICHIA COLI 562 -11533542

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832862	8687	30843	477	158

Description

6500729685 rplf:b3305 50s ribosomal subunit protein 16:50s ribosomal protein 16 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3305 b3305 Escherichia coli 562 -11533543 7000688950 rplf ribosomal protein 16 (cl:escherichia coli ribosomal protein 16) (db:pir1.dat) (mp:73 min) R5EC6 D65123 Escherichia coli 562 -11533543 7500953528 rplf 50s ribosomal subunit protein 16 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 258) (le:226355) (re:226888) (di:complement) ECOUW67 U18997 g606239 Escherichia coli 562 -11533543 236538 rplf 50s ribosomal subunit protein 16 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 298 of 400 of the completegenome.) (nt:f177; cg site no. 258) (le:3134) (re:3667) (di:complement) AE000408 AE000408 g1789701 Escherichia coli 562 -11533543 5000690764 (de:(ecoli\_3223) (pn:50s ribosomal subunit protein 16) (gn:rplf) (gtcfc:10.3) (ec:) (rl6\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3223 ECOLI\_3223 Escherichia coli 562 10124009

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832864	8688	30844	258	85

Description

GTC ORF with score 145 to: (sr:thale cress) (db:genpept-pln1)  
 (de:arabidopsis thaliana dna chromosome 4, bac clone f4d11 (essaiiproject).)  
 (nt:similarity to mus308 gene, drosophila melanogaster;)  
 (le:38015:38256:38642) (re:38131:38396:38750) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832865	8689	30845	546	181

Description

6500729686 rpsh:b3306 30s ribosomal subunit protein s8:30s ribosomal protein  
 s8 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)  
 b3306 b3306 Escherichia coli 562 -11533544 7000688945 rpsh ribosomal  
 protein s8 (cl:escherichia coli ribosomal protein s8) (db:pir1.dat) (mp:73  
 min) R3EC8 E65123 Escherichia coli 562 -11533544 7500953503 rpsh 30s  
 ribosomal subunit protein s8 (db:genpept-bct1) (de:escherichia coli k-12  
 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 223)  
 (le:226901) (re:227293) (di:complement) ECOUW67 U18997 g606240 Escherichia  
 coli 562 -11533544 236539 rpsh 30s ribosomal subunit protein s8:and  
 regulator (fn:structural component; ribosomal proteins -) (db:genpept-bct2)  
 (de:escherichia coli k-12 mg1655 section 298 of 400 of the completegenome.)  
 (nt:f130; cg site no. 223; 100 pct identical amino) (le:3680) (re:4072)  
 (di:complement) AE000408 AE000408 g1789702 Escherichia coli 562 -11533544  
 5000690765 (de:(ecoli\_3224) (pn:30s ribosomal subunit protein s8, and  
 regulator) (gn:rpsh) (gtcfc:10.3) (ec:) (rs8\_ecoli) (keggfc:11.2)  
 (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3224 ECOLI\_3224 Escherichia  
 coli 562 10124010

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832880	8690	30846	588	195

Description

6500729687 rpsn:b3307 30s ribosomal subunit protein s14:30s ribosomal protein s14 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3307 b3307 Escherichia coli 562 -11533545 7000688948 rpsn ribosomal protein s14 (cl:escherichia coli ribosomal protein s14) (db:pir1.dat) (mp:73 min) R3EC14 F65123 Escherichia coli 562 -11533545 7500953511 rpsn 30s ribosomal subunit protein s14 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 218) (le:227327) (re:227632) (di:complement) ECOUW67 U18997 g606241 Escherichia coli 562 -11533545 236540 rpsn 30s ribosomal subunit protein s14 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 298 of 400 of the completegenome.) (nt:f101; cg site no. 218; 100 pct identical amino) (le:4106) (re:4411) (di:complement) AE000408 AE000408 g1789703 Escherichia coli 562 -11533545 5000690766 (de:(ecoli\_3225) (pn:30s ribosomal subunit protein s14) (gn:rpsn) (gtcfc:10.3) (ec:) (rs14\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3225 ECOLI\_3225 Escherichia coli 562 10124011

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832903	8691	30847	249	82

Description

GTC ORF with score 301 to: (or:Neurospora crassa) (sr:neurospora crassa (strain oak ridge, individual/isolate 74-0r23-1a) (db:genpept-pln1) (de:neurospora crassa ribosomal protein gene, complete cds.) (le:869:1109:1408) (re:1015:1309:1500) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832936	8692	30848	510	169

Description

6500729688 rple:b3308 50s ribosomal subunit protein 15:50s ribosomal protein 15 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3308 b3308 Escherichia coli 562 -11533546 7000688949 rple ribosomal protein 15 (cl:escherichia coli ribosomal protein 15) (db:pir1.dat) (mp:73 min) R5EC5 G65123 Escherichia coli 562 -11533546 238284 rple 50s ribosomal subunit protein 15 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 259) (le:227647) (re:228186) (di:complement) ECOUW67 U18997 g606242 Escherichia coli 562 -11533546 7500953525 (db:genpept-bct1) (de:escherichia coli spc ribosomal protein operon.) (nt:15 (rple) (aa 1-179)) (le:951) (re:1490) (di:direct) ECSPC X01563 g42981 Escherichia coli 562 -11533546 236541 rple 50s ribosomal subunit protein 15 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 298 of 400 of the completegenome.) (nt:f179; cg site no. 259; 100 pct identical amino) (le:4426) (re:4965) (di:complement) AE000408 AE000408 g1789704 Escherichia coli 562 -11533546 5000690767 (de:(ecoli\_3226) (pn:50s ribosomal subunit protein 15) (gn:rple) (gtcfc:10.3) (ec:) (rl5\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3226 ECOLI\_3226 Escherichia coli 562 10124012

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832939	8693	30849	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832950	8694	30850	261	86

#### Description

6500729689 rplx:b3309 50s ribosomal subunit protein 124:50s ribosomal protein 124 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3309 b3309 Escherichia coli 562 -11533547 7000688952 rplx ribosomal protein 124 (cl:escherichia coli ribosomal protein 124) (db:pir1.dat) (mp:73 min) R5EC24 H65123 Escherichia coli 562 -11533547 238283 rplx 50s ribosomal subunit protein 124 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 243) (le:228201) (re:228515) (di:complement) ECOUW67 U18997 g606243 Escherichia coli 562 -11533547 7500953542 (db:genpept-bct1) (de:escherichia coli spc ribosomal protein operon.) (nt:l24 (rplx) (aa 1-104)) (le:622) (re:936) (di:direct) ECSPC X01563 g42980 Escherichia coli 562 -11533547 236542 rplx 50s ribosomal subunit protein 124 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 298 of 400 of the completegenome.) (nt:fl04; cg site no. 243; 100 pct identical amino) (le:4980) (re:5294) (di:complement) AE000408 AE000408 g1789705 Escherichia coli 562 -11533547 5000690768 (de:(ecoli\_3227) (pn:50s ribosomal subunit protein 124) (gn:rplx) (gtcfc:10.3) (ec:) (rl24\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3227 ECOLI\_3227 Escherichia coli 562 10124013

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832954	8695	30851	351	116

#### Description

6500729690 rpln:b3310 50s ribosomal subunit protein 114:50s ribosomal protein 114 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3310 b3310 Escherichia coli 562 -11533548 7500889939 rpln (de:50s ribosomal protein 114) (db:swissprot) RL14\_ECOLI P02411 ESCHERICHIA COLI 562 -11533548 7000686354 rpln ribosomal protein 114 (cl:escherichia coli ribosomal protein 114) (db:pir1.dat) (mp:73 min) R5EC14 A65124 Escherichia coli 562 -11533548 238282 rpln 50s ribosomal subunit protein 114 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 252) (le:228526) (re:228897) (di:complement) ECOUW67 U18997 g606244 Escherichia coli 562 -11533548 5000690769 (db:genpept-bct1) (de:escherichia coli spc ribosomal protein operon.) (nt:l14 (rpln) (aa 1-123)) (le:240) (re:611) (di:direct) ECSPC X01563 g42979 Escherichia coli 562 -11533548 236543 rpln 50s ribosomal subunit protein 114 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 298 of 400 of the completegenome.) (nt:fl123; cg site no. 252; 100 pct identical amino) (le:5305) (re:5676) (di:complement) AE000408 AE000408 g1789706 Escherichia coli 562 -11533548 94792 rpln (de:50s ribosomal protein 114) (db:swissprot) RL14\_ECOLI P02411 ESCHERICHIA COLI 562 -11533548

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832957	8696	30852	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501832975	8697	30853	291	96

Description

6500729691 rpsq:neaa:b3311 30s ribosomal subunit protein s17:30s ribosomal protein s17 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3311 b3311 Escherichia coli 562 -11533549 128806 rpsq ribosomal protein s17 (cl:escherichia coli ribosomal protein s17) (db:pir1.dat) (mp:73 min) R3EC17 A37519 Escherichia coli 562 -11533549 238156 rpsq 30s ribosomal subunit protein s17 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 215; alternate name neaa) (le:229062) (re:229316) (di:complement) ECOUW67 U18997 g606245 Escherichia coli 562 -11533549 7500953514 (db:genpept-bct1) (de:escherichia coli ribosomal protein operon s10.) (nt:ribosomal protein s17 (rpsq) (aa 1-84)) (le:5020) (re:5274) (di:direct) ECRPOS10 X02613 g42835 Escherichia coli 562 -11533549 236544 rpsq 30s ribosomal subunit protein s17 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 298 of 400 of the completegenome.) (nt:f84; cg site no. 215; alternate name neaa; 100 pct) (le:5841) (re:6095) (di:complement) AE000408 AE000408 g1789707 Escherichia coli 562 -11533549 5000690770 (de:(ecoli\_3229) (pn:30s ribosomal subunit protein s17) (gn:rpsq) (gtcfc:10.3) (ec:) (rs17\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3229 ECOLI\_3229 Escherichia coli 562 10067216

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501832986	8698	30854	1599	532

Description

6500729692 rpmc:b3312 50s ribosomal subunit protein 129:50s ribosomal protein 129 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3312 b3312 Escherichia coli 562 -11533550 7500890144 rpmc (de:50s ribosomal protein 129) (db:swissprot) RL29\_ECOLI P02429 ESCHERICHIA COLI 562 -11533550 129139 rpmc ribosomal protein 129 (cl:escherichia coli ribosomal protein 129) (db:pir1.dat) (mp:73 min) R5EC29 B37519 Escherichia coli 562 -11533550 238155 rpmc 50s ribosomal subunit protein 129 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 239) (le:229316) (re:229507) (di:complement) ECOUW67 U18997 g606246 Escherichia coli 562 -11533550 5000690771 (db:genpept-bct1) (de:escherichia coli ribosomal protein operon s10.) (nt:ribosomal protein 129 (rpmc) (aa 1-63)) (le:4829) (re:5020) (di:direct) ECRPOS10 X02613 g42834 Escherichia coli 562 -11533550 236545 rpmc 50s ribosomal subunit protein 129 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 298 of 400 of the completegenome.) (nt:f63; cg site no. 239; 100 pct identical amino) (le:6095) (re:6286) (di:complement) AE000408 AE000408 g1789708 Escherichia coli 562 -11533550 95076 rpmc (de:50s ribosomal protein 129) (db:swissprot) RL29\_ECOLI P02429 ESCHERICHIA COLI 562 -11533550

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833015	8699	30855	1878	626

Description

GTC ORF with score 697 to: (db:genpept) (de:aureobasidium pullulans cosmid ppsr-22 hydroxylase, multidrugresistance-like protein (apmdr1), and peptide synthetase genes,complete cds.) (le:13308:13350:13743:13878) (re:19541:19541:19541:19541) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833024	8700	30856	261	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833025	8701	30857	963	320

Description

6500729693 rplp:b3313 50s ribosomal subunit protein l16:50s ribosomal protein l16 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3313 b3313 Escherichia coli 562 -11533551 7500889977 rplp (de:50s ribosomal protein l16) (db:swissprot) RL16\_ECOLI P02414 ESCHERICHIA COLI 562 -11533551 129056 rplp ribosomal protein l16 (cl:escherichia coli ribosomal protein l16) (db:pir1.dat) (mp:73 min) R5EC16 I23129 Escherichia coli 562 -11533551 238154 rplp 50s ribosomal subunit protein l16 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 250) (le:229507) (re:229917) (di:complement) ECOUW67 U18997 g606247 Escherichia coli 562 -11533551 5000690772 (db:genpept-bct1) (de:escherichia coli ribosomal protein operon s10.) (nt:ribosomal protein l16 (rplp) (aa 1-136)) (le:4419) (re:4829) (di:direct) ECRPOS10 X02613 g42833 Escherichia coli 562 -11533551 236546 rplp 50s ribosomal subunit protein l16 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 298 of 400 of the completegenome.) (nt:f136; cg site no. 250; 100 pct identical amino) (le:6286) (re:6696) (di:complement) AE000408 AE000408 g1789709 Escherichia coli 562 -11533551 94837 rplp (de:50s ribosomal protein l16) (db:swissprot) RL16\_ECOLI P02414 ESCHERICHIA COLI 562 -11533551

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833026	8702	30858	213	70

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833045	8703	30859	516	171

Description

6500729694 rpsc:b3314 30s ribosomal subunit protein s3:30s ribosomal protein s3 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3314 b3314 Escherichia coli 562 -11533552 128645 rpsc ribosomal protein s3 (cl:escherichia coli ribosomal protein s3) (db:pirl.dat) (mp:73 min) R3EC3 H23129 Escherichia coli 562 -11533552 238153 rpsc 30s ribosomal subunit protein s3 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 228) (le:229930) (re:230631) (di:complement) ECOUW67 U18997 g606248 Escherichia coli 562 -11533552 7500953496 (db:genpept-bct1) (de:escherichia coli ribosomal protein operon s10.) (nt:ribosomal protein s3 (rpsc) (aa 1-233)) (le:3705) (re:4406) (di:direct) ECRPOS10 X02613 g42832 Escherichia coli 562 -11533552 236547 rpsc 30s ribosomal subunit protein s3 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 298 of 400 of the completegenome.) (nt:f233; cg site no. 228; 100 pct identical amino) (le:6709) (re:7410) (di:complement) AE000408 AE000408 g1789710 Escherichia coli 562 -11533552 5000690773 (de:(ecoli\_3232) (pn:30s ribosomal subunit protein s3) (gn:rpsc) (gtcfc:10.3) (ec:) (rs3\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3232 ECOLI\_3232 Escherichia coli 562 10067164

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833048	8704	30860	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833063	8705	30861	315	104

Description

GTC ORF with score 180 to: (or:Fusarium lateritium) (sr:fusarium lateritium (library: commonwealth mycological institut) (db:genpept-pln1) (de:fusarium lateritium cyanide hydratase (chyl) mrna, complete cds.) (nt:putative) (le:36) (re:1109) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833065	8706	30862	315	104

Description

6500729695 rplv:eryb:b3315 50s ribosomal subunit protein l22:50s ribosomal protein l22 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3315 b3315 Escherichia coli 562 -11533553 7500890065 rplv:eryb (de:50s ribosomal protein l22) (db:swissprot) RL22\_ECOLI P02423 ESCHERICHIA COLI 562 -11533553 129102 rplv ribosomal protein l22 (cl:escherichia coli ribosomal protein l22) (db:pir1.dat) (mp:73 min) R5EC22 G23129 Escherichia coli 562 -11533553 238152 rplv 50s ribosomal subunit protein l22 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 245) (le:230649) (re:230981) (di:complement) ECOUW67 U18997 g606249 Escherichia coli 562 -11533553 5000690774 (db:genpept-bct1) (de:escherichia coli ribosomal protein operon s10.) (nt:ribosomal protein l22 (rplv) (aa 1-110)) (le:3355) (re:3687) (di:direct) ECRPOS10 X02613 g42831 Escherichia coli 562 -11533553 236548 rplv 50s ribosomal subunit protein l22 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 298 of 400 of the completgenome.) (nt:f110; cg site no. 245; 100 pct identical amino) (le:7428) (re:7760) (di:complement) AE000408 AE000408 g1789711 Escherichia coli 562 -11533553 94976 rplv:eryb (de:50s ribosomal protein l22) (db:swissprot) RL22\_ECOLI P02423 ESCHERICHIA COLI 562 -11533553

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833066	8707	30863	270	89

Description

6500729696 rpss:b3316 30s ribosomal subunit protein s19:30s ribosomal protein s19 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3316 b3316 Escherichia coli 562 -11533554 128822 rpss ribosomal protein s19 (cl:escherichia coli ribosomal protein s19) (db:pir1.dat) (mp:73 min) R3EC19 F23129 Escherichia coli 562 -11533554 238151 rpss 30s ribosomal subunit protein s19 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 213) (le:230996) (re:231274) (di:complement) ECOUW67 U18997 g606250 Escherichia coli 562 -11533554 7500953518 (db:genpept-bct1) (de:escherichia coli ribosomal protein operon s10.) (nt:ribosomal protein s19 (rpss) (aa 1-273)) (le:3062) (re:3340) (di:direct) ECRPOS10 X02613 g42830 Escherichia coli 562 -11533554 236549 rpss 30s ribosomal subunit protein s19 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 298 of 400 of the completgenome.) (nt:f92; cg site no. 213; 100 pct identical amino) (le:7775) (re:8053) (di:complement) AE000408 AE000408 g1789712 Escherichia coli 562 -11533554 5000690775 (de:(ecoli\_3234) (pn:30s ribosomal subunit protein s19) (gn:rpss) (gtcfc:10.3) (ec:) (rs19\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3234 ECOLI\_3234 Escherichia coli 562 10067221

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833073	8708	30864	690	229

Description

6500729697 rplb:b3317 50s ribosomal subunit protein 12:50s ribosomal protein 12 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3317 b3317 Escherichia coli 562 -11533555 128884 rplb ribosomal protein 12 (cl:escherichia coli ribosomal protein 12) (db:pir1.dat) (mp:73 min) R5EC2 E23129 Escherichia coli 562 -11533555 238150 rplb 50s ribosomal subunit protein 12 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 262) (le:231291) (re:232112) (di:complement) ECOUW67 U18997 g606251 Escherichia coli 562 -11533555 7500953523 (db:genpept-bct1) (de:escherichia coli ribosomal protein operon s10.) (nt:ribosomal protein 12 (rplb) (aa 1-273)) (le:2224) (re:3045) (di:direct) ECRPOS10 X02613 g42829 Escherichia coli 562 -11533555 236550 rplb 50s ribosomal subunit protein 12 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 298 of 400 of the completegenome.) (nt:f273; cg site no. 262; 100 pct identical amino) (le:8070) (re:8891) (di:complement) AE000408 AE000408 g1789713 Escherichia coli 562 -11533555 5000690776 (de:(ecoli\_3235) (pn:50s ribosomal subunit protein 12) (gn:rplb) (gtcfc:10.3) (ec:) (rl2\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3235 ECOLI\_3235 Escherichia coli 562 10067246

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833091	8709	30865	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833103	8710	30866	1578	526

Description

6500729698 rplw:b3318 50s ribosomal subunit protein 123:50s ribosomal protein 123 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3318 b3318 Escherichia coli 562 -11533556 7500890087 rplw (de:50s ribosomal protein 123) (db:swissprot) RL23\_ECOLI P02424 ESCHERICHIA COLI 562 -11533556 7000686370 rplw ribosomal protein 123 (cl:escherichia coli ribosomal protein 123) (db:pir1.dat) (mp:73 min) R5EC23 A65125 Escherichia coli 562 -11533556 238149 rplw 50s ribosomal subunit protein 123 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 244) (le:232130) (re:232432) (di:complement) ECOUW67 U18997 g606252 Escherichia coli 562 -11533556 5000690777 (db:genpept-bct1) (de:escherichia coli ribosomal protein operon s10.) (nt:ribosomal protein 123 (rplw) (aa 1-100)) (le:1904) (re:2206) (di:direct) ECRPOS10 X02613 g534975 Escherichia coli 562 -11533556 236551 rplw 50s ribosomal subunit protein 123 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 298 of 400 of the completegenome.) (nt:f100; cg site no. 244; 100 pct identical amino) (le:8909) (re:9211) (di:complement) AE000408 AE000408 g1789714 Escherichia coli 562 -11533556 94996 rplw (de:50s ribosomal protein 123) (db:swissprot) RL23\_ECOLI P02424 ESCHERICHIA COLI 562 -11533556

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833108	8711	30867	720	239

Description

6500729699 rpld:erya:b3319 50s ribosomal subunit protein 14:50s ribosomal protein 14 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3319 b3319 Escherichia coli 562 -11533557 7500890309 rpld:erya (de:50s ribosomal protein 14) (db:swissprot) RL4\_ECOLI P02388 ESCHERICHIA COLI 562 -11533557 128896 rpld ribosomal protein 14 (cl:escherichia coli ribosomal protein 14) (db:pir1.dat) (mp:73 min) R5EC4 C23129 Escherichia coli 562 -11533557 238148 rpld 50s ribosomal subunit protein 14 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 260; alternate name erya) (le:232429) (re:233034) (di:complement) ECOUW67 U18997 g606253 Escherichia coli 562 -11533557 5000690778 (db:genpept-bct1) (de:escherichia coli ribosomal protein operon s10.) (nt:ribosomal protein 14 (rpld) (aa 1-201)) (le:1302) (re:1907) (di:direct) ECRPOS10 X02613 g42828 Escherichia coli 562 -11533557 236552 rpld 50s ribosomal subunit protein 14:regulates (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 298 of 400 of the completegenome.) (nt:f201; cg site no. 260; alternate name erya; 100 pct) (le:9208) (re:9813) (di:complement) AE000408 AE000408 g1789715 Escherichia coli 562 -11533557 95361 rpld:erya (de:50s ribosomal protein 14) (db:swissprot) RL4\_ECOLI P02388 ESCHERICHIA COLI 562 -11533557

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833110	8712	30868	654	217

Description

6500729700 rplc:b3320 50s ribosomal subunit protein 13:50s ribosomal protein 13 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3320 b3320 Escherichia coli 562 -11533558 7500890269 rplc (de:50s ribosomal protein 13) (db:swissprot) RL3\_ECOLI P02386 ESCHERICHIA COLI 562 -11533558 128876 rplc ribosomal protein 13 (cl:escherichia coli ribosomal protein 13) (db:pir1.dat) (mp:73 min) R5EC3 A02757 Escherichia coli 562 -11533558 238147 rplc 50s ribosomal subunit protein 13 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 261) (le:233045) (re:233674) (di:complement) ECOUW67 U18997 g606254 Escherichia coli 562 -11533558 5000690779 (db:genpept-bct1) (de:escherichia coli ribosomal protein operon s10.) (nt:ribosomal protein 13 (rplc) (aa 1-209)) (le:662) (re:1291) (di:direct) ECRPOS10 X02613 g42827 Escherichia coli 562 -11533558 236553 rplc 50s ribosomal subunit protein 13 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 298 of 400 of the completegenome.) (nt:f209; cg site no. 261; 100 pct identical amino) (le:9824) (re:10453) (di:complement) AE000408 AE000408 g1789716 Escherichia coli 562 -11533558 95291 rplc (de:50s ribosomal protein 13) (db:swissprot) RL3\_ECOLI P02386 ESCHERICHIA COLI 562 -11533558

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833144	8713	30869	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833150	8714	30870	684	227

Description

6500729701 rpsj:nuse:b3321 30s ribosomal subunit protein s10:30s ribosomal protein s10 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3321 b3321 Escherichia coli 562 -11533559 7500890841 rpsj:nuse (de:30s ribosomal protein s10) (db:swissprot) RS10\_ECOLI P02364 ESCHERICHIA COLI 562 -11533559 128715 rpsj ribosomal protein s10 (cl:escherichia coli ribosomal protein s10) (db:pir1.dat) (mp:73 min) R3EC10 A02720 Escherichia coli 562 -11533559 238146 rpsj 30s ribosomal subunit protein s10 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 222) (le:233707) (re:234018) (di:complement) ECOUW67 U18997 g606255 Escherichia coli 562 -11533559 238171 (db:genpept-bct1) (de:escherichia coli ribosomal protein operon s10.) (nt:ribosomal protein s10 (rpsj) (aa 1-103)) (le:318) (re:629) (di:direct) ECRPOS10 X02613 g42826 Escherichia coli 562 -11533559 5000690780 rpsj ribosomal protein s10 (db:genpept-bct1) (de:e. coli genes rpsj and rplc for ribosomal proteins s10 and l3.) (le:658) (re:969) (di:direct) ECRPSL V00344 g42857 Escherichia coli 562 -11533559 236554 rpsj 30s ribosomal subunit protein s10 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 298 of 400 of the completegenome.) (nt:f103; cg site no. 222; 100 pct identical amino) (le:10486) (re:10797) (di:complement) AE000408 AE000408 g1789717 Escherichia coli 562 -11533559 96892 rpsj:nuse (de:30s ribosomal protein s10) (db:swissprot) RS10\_ECOLI P02364 ESCHERICHIA COLI 562 -11533559

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833151	8715	30871	279	92

Description

6500729702 rpsg:b3341 30s ribosomal subunit protein s7:30s ribosomal protein s7 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3341 b3341 Escherichia coli 562 -11533560 7000688944 rpsg:strb ribosomal protein s7 (cl:escherichia coli ribosomal protein s7) (db:pir1.dat) (mp:73 min) R3EC7K H65127 Escherichia coli 562 -11533560 7500953502 rpsg 30s ribosomal subunit protein s7 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 224) (le:254290) (re:254829) (di:complement) ECOUW67 U18997 g606275 Escherichia coli 562 -11533560 236574 rpsg 30s ribosomal subunit protein s7:initiates (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 300 of 400 of the completegenome.) (nt:f179; cg site no. 224; 100 pct identical amino) (le:6811) (re:7350) (di:complement) AE000410 AE000410 g1789739 Escherichia coli 562 -11533560 5000690781 (de:(ecoli\_3259) (pn:30s ribosomal subunit protein s7, initiates assembly) (gn:rpsg) (gtcfc:10.3) (ec:) (rs7\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3259 ECOLI\_3259 Escherichia coli 562 10124015

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501833155	8716	30872	405	134

# Description

6500729703 rpsl:strab3342 30s ribosomal subunit protein s12:30s ribosomal protein s12 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3342 b3342 Escherichia coli 562 -11533561 128743 rpsl:stra ribosomal protein s12 (cl:escherichia coli ribosomal protein s12) (db:pir1.dat) (mp:73 min) R3EC12 S13738 Escherichia coli 562 -11533561 148521 rpsl ribosomal protein s12 (cl:escherichia coli ribosomal protein s12) (db:pir2.dat) JH0443 JH0443 Salmonella typhimurium 602 -11533561 236575 rpsl (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli str operon with rpsl and rpsg genes coding for ribosomal proteins s12 and s7.) (nt:ribosomal protein s12) (le:303) (re:677) (di:direct) ECOSTR1 J01688 g147892 Escherichia coli 562 -11533561 238306 rpsl 30s ribosomal subunit protein s12 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 220; alternate name stra) (le:254926) (re:255300) (di:complement) ECOUW67 U18997 g606276 Escherichia coli 562 -11533561 264473 (db:genpept-bct1) (de:part of the e. coli str operon including the gene (str or rpsl) forribosomal protein s12 and the beginning of the gene (rpsg) for s7.) (nt:reading frame (s12 protein)) (le:130) (re:504) (di:direct) ECSTR1 V00355 g43010 Escherichia coli 562 -11533561 407980 rpsl ribosomal protein s12 (sr:salmonella typhimurium (strain lt2) dna) (db:genpept-bct1) (de:salmonella typhimurium ribosomal protein s12 and ribosomal proteins7 (rpsl) gene, complete cds and 5' end.) (le:125) (re:499) (di:direct) STYRPSL M68548 g154357 Salmonella typhimurium 602 -11533561 236045 rpsl 30s ribosomal subunit protein s12 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 300 of 400 of the completegenome.) (nt:f124; cg site no. 220; alternate name stra; 100 pct) (le:7447) (re:7821) (di:complement) AE000410 AE000410 g1789740 Escherichia coli 562 -11533561 5500686714 small ribosomal protein (fn:streptomycin sensitivity) (db:genpept-syn) (de:cloning vector pal-f insertion sequence is1 galactokinase (galk), aminoglycoside 3'-phosphotransferase (kn), beta-galactosidase(lacz), small ribosomal protein and beta-lactamase (ap) genes, complete cds.... CVU87107 U87107 g2501803 Cloning vector pAL-F 56954 -11533561 7500953508 ribosomal protein s12 (sr:clones puc9 (ap-r gene region) and pno1523 (stra+ gene) dna, fro) (db:genpept-syn) (de:synthetic cloning vector plasmid phsg664, complete genome.) (le:232) (re:606) (di:direct) SYNG664CG M12787 g208392 unidentified cloning vector 45196 -11533561 5000690782 (de:(ecoli\_3260) (pn:30s ribosomal subunit protein s12) (gn:rpsl) (gtcfc:10.3) (ec:) (rs12\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3260 ECOLI\_3260 Escherichia coli 562 10067193

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833166	8717	30873	2145	714

Description

6500729704 rpmg:b3636 50s ribosomal subunit protein 133:50s ribosomal protein 133 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3636 b3636 Escherichia coli 562 -11533562 129180 rpmg ribosomal protein 133 (cl:escherichia coli ribosomal protein 133) (db:pir1.dat) (mp:82 min) R5EC33 S42444 Escherichia coli 562 -11533562 236874 rpmg ribosomal protein 133 (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli rpmb and rpmg genes coding for ribosomal proteins 128 and133.) (le:481) (re:648) (di:direct) ECORPMBG J01677 g147709 Escherichia coli 562 -11533562 7000688955 rpmg::cg site no. 236 50s ribosomal subunit protein 133 (sr:escherichia coli k12 strain mg1655; lambda clones ecl4-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:642) (re:809) (di:complement) ECOUW82 L10328 g290486 Escherichia coli 562 -11533562 7500953555 rpmg 133 (db:genpept-bct1) (de:salmonella typhimurium ribosomal protein 128 (rpmb), ribosomalprotein 133 (rpmg) and 8-hydroxyguanine-dna glycosylase (mutmst)genes, compete cds.) (nt:ribosomal protein 133) (le:553) (re:720) (di:direct) STU23405 U23405 g2842792 Salmonella typhimurium 602 -11533562 235875 rpmg 50s ribosomal subunit protein 133 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 331 of 400 of the completegenome.) (nt:f55; 100 pct identical amino acid sequence and) (le:3145) (re:3312) (di:complement) AE000441 AE000441 g1790067 Escherichia coli 562 -11533562 5000690783 (de:(ecoli\_3556) (pn:50s ribosomal subunit protein 133) (gn:rpmg) (gtcfc:10.3) (ec:) (rl33\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3556 ECOLI\_3556 Escherichia coli 562 10067345

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833190	8718	30874	207	68

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833199	8719	30875	357	118

Description

6500729705 rpmb:b3637 50s ribosomal subunit protein 128:50s ribosomal protein 128 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3637 b3637 Escherichia coli 562 -11533563 129137 rpmb ribosomal protein 128 (cl:escherichia coli ribosomal protein 128) (db:pir1.dat) (mp:82 min) R5EC28 S42443 Escherichia coli 562 -11533563 236875 rpmb ribosomal protein 128 (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli rpmb and rpmg genes coding for ribosomal proteins 128 and133.) (le:224) (re:460) (di:direct) ECORPMBG J01677 g147708 Escherichia coli 562 -11533563 7500953546 rpmb::cg site no. 240 50s ribosomal subunit protein 128 (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:830) (re:1066) (di:complement) ECOUW82 L10328 g290487 Escherichia coli 562 -11533563 235874 rpmb 50s ribosomal subunit protein 128 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 331 of 400 of the completegenome.) (nt:f78; 100 pct identical amino acid sequence and) (le:3333) (re:3569) (di:complement) AE000441 AE000441 g1790068 Escherichia coli 562 -11533563 5000690784 (de:(ecoli\_3557) (pn:50s ribosomal subunit protein 128) (gn:rpmb) (gtcfc:10.3) (ec:) (rl28\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3557 ECOLI\_3557 Escherichia coli 562 10067330

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833223	8720	30876	333	110

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833231	8721	30877	453	150

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833238	8722	30878	942	313

Description

6500729706 rpmh:ssaf:rima:b3703 50s ribosomal subunit protein 134:50s ribosomal protein 134 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3703 b3703 Escherichia coli 562 -11533564 7500890221 rpmh:ssaf:rima (de:50s ribosomal protein 134) (db:swissprot) RL34\_ECOLI P02437 ESCHERICHIA COLI 562 -11533564 129188 rpmh ribosomal protein 134 (cl:escherichia coli ribosomal protein 134) (db:pir1.dat) (mp:83 min) R5EC34 C21915 Escherichia coli 562 -11533564 235852 rpmh (sr:escherichia coli (strain k-12) (clone: ptc884 .) dna; escherichi) (db:genpept-bct1) (de:e.coli dnaa operon: dnaa, dnan, and rpmh genes coding for dnaaprotein, dna polymerase iii beta subunit, and ribosomal proteinl34.) (nt:ribosomal protein 134) (l... ECODNAAOP J01602 g145759 Escherichia coli 562 -11533564 236939 rpmh (sr:e.coli k12 dna, clones pfhc507 and pfhc508) (db:genpept-bct1) (de:e.coli rnpa and rpmh genes coding for the protein component ofribonuclease p (rnase p) and ribosomal protein 134.) (nt:ribosomal protein 134) (le:322) (re:462) (di:direct) ECORNPA M11056 g147682 Escherichia coli 562 -11533564 238131 rpmh::cg site no. 235 50s ribosomal subunit protein 134 (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:73734) (re:73874) (di:direct) ECOUW82 L10328 g290551 Escherichia coli 562 -11533564 5000690785 (db:genpept-bct1) (de:e. coli rpmh gene for ribosomal protein 134.) (nt:l34 (rpmh) (aa 1-46)) (le:673) (re:813) (di:direct) ECRPMH X01861 g42804 Escherichia coli 562 -11533564 234178 rpmh 50s ribosomal subunit protein 134 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 337 of 400 of the completegenome.) (nt:o46; 100 pct identical amino acid sequence and) (le:7350) (re:7490) (di:direct) AE000447 AE000447 g1790138 Escherichia coli 562 -11533564 95196 rpmh:ssaf:rima (de:50s ribosomal protein 134) (db:swissprot) RL34\_ECOLI P02437 ESCHERICHIA COLI 562 -11533564

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833254	8723	30879	1335	444

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833267	8724	30880	1371	456

Description

6500729707 rpme:b3936 50s ribosomal protein l31 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3936 b3936 Escherichia coli 562 -11533565 7500890187 rpme (de:50s ribosomal protein l31) (db:swissprot) RL31\_ECOLI P02432 ESCHERICHIA COLI 562 -11533565 129151 rpme ribosomal protein l31 (cl:escherichia coli ribosomal protein l31) (db:pir1.dat) (mp:89 min) R5EC31 S40879 Escherichia coli 562 -11533565 238022 rpme 50s ribosomal protein l31 (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 237) (le:88646) (re:88858) (di:direct) ECOUW87 L19201 g305039 Escherichia coli 562 -11533565 5000690786 rhs-l31 ribosomal protein l31 (db:genpept-bct1) (de:e.coli (0111:nm) rhs-l31 gene for ribosomal protein l31.) (le:274) (re:486) (di:direct) ECRBSL31 X78541 g469093 Escherichia coli 562 -11533565 237153 rpme 50s ribosomal subunit protein l31 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 357 of 400 of the completegenome.) (nt:o70; cg site no. 237) (le:14139) (re:14351) (di:direct) AE000467 AE000467 g1790371 Escherichia coli 562 -11533565 95146 rpme (de:50s ribosomal protein l31) (db:swissprot) RL31\_ECOLI P02432 ESCHERICHIA COLI 562 -11533565

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833270	8725	30881	333	110

Description

GTC ORF with score 90 to: (sr:arabidopsis thaliana (strain columbia) (library: lambda-yes-r) cdn) (db:genpept-pln1) (de:arabidopsis thaliana recombination and dna-damage resistanceprotein (drt111) mrna, complete cds.) (le:61) (re:1212) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833277	8726	30882	513	170

Description

6500729708 rplk:relc:b3983 50s ribosomal subunit protein l11:50s ribosomal protein l11 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3983 b3983 Escherichia coli 562 -11533566 129016 rplk ribosomal protein l11 (cl:escherichia coli ribosomal protein l11) (db:pir1.dat) (mp:90 min) R5EC11 S12572 Escherichia coli 562 -11533566 7500953539 rplk 50s ribosomal subunit protein l11 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 362 of 400 of the completegenome.) (nt:o142; 99 pct identical amino acid sequence and) (le:3410) (re:3838) (di:direct) AE000472 AE000472 g2367334 Escherichia coli 562 -11533566

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833286	8727	30883	1584	527

Description

6500729709 rpla:b3984 50s ribosomal subunit protein l1:50s ribosomal protein l1 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3984 b3984 Escherichia coli 562 -11533567 128860 rpla ribosomal protein l1 (cl:escherichia coli ribosomal protein l1) (db:pir1.dat) (mp:90 min) R5EC1 S12573 Escherichia coli 562 -11533567 238138 rpla::l1 (db:genpept-bct1) (de:e. coli operon rpobc coding for the beta- and beta'-subunits of rnapolymerase (genes rpoc and rpob), and genes rpll, rlpj, rpla, andrplk coding for 50s ribosomal subunit proteins l7/l12, l10, l1, andl11, respectively. (map positio... ECRPOBC V00339 g42815 Escherichia coli 562 -11533567 237194 rpla 50s ribosomal subunit protein l1:regulates (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 362 of 400 of the completgenome.) (nt:o234b; 100 pct identical to rll\_ecoli sw: p02384;) (le:3842) (re:4546) (di:direct) AE000472 AE000472 g1790416 Escherichia coli 562 -11533567 7500953522 rpla 50s ribosomal subunit protein l1 (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 263) (le:44120) (re:44824) (di:direct) ECOUW89 U00006 g396323 Escherichia coli 562 -11533567 5000690788 (de:(ecoli\_3874) (pn:50s ribosomal subunit protein l1, regulates synthesis of l1 and l11) (gn:rpla) (gtcfc:10.3) (ec:) (rll\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3874 ECOLI\_3874 Escherichia coli 562 10067236

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833289	8728	30884	408	135

Description

6500729710 rplj:b3985 50s ribosomal subunit protein l10:50s ribosomal protein l10:l8 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3985 b3985 Escherichia coli 562 -11533568 129013 rplj ribosomal protein l10 (cl:escherichia coli ribosomal protein l10) (db:pir1.dat) (mp:90 min) R5EC10 S12574 Escherichia coli 562 -11533568 238139 rplj::l10 (db:genpept-bct1) (de:e. coli operon rpobc coding for the beta- and beta'-subunits of rnapolymerase (genes rpoc and rpob), and genes rpl1, rlpj, rpla, andrplk coding for 50s ribosomal subunit proteins 17/112, 110, 11, andl11, respectively. (map positio... ECRPOBC V00339 g42816 Escherichia coli 562 -11533568 237195 rplj 50s ribosomal subunit protein l10 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 362 of 400 of the completgenome.) (nt:ol65; 100 pct identical to rl10\_ecoli sw: p02408;) (le:4959) (re:5456) (di:direct) AE000472 AE000472 g1790417 Escherichia coli 562 -11533568 7500953538 rplj 50s ribosomal subunit protein l10 (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 256) (le:45237) (re:45734) (di:direct) ECOUW89 U00006 g396324 Escherichia coli 562 -11533568 5000690789 (de:(ecoli\_3875) (pn:50s ribosomal subunit protein l10) (gn:rplj) (gtcfc:10.3) (ec:) (rl10\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3875 ECOLI\_3875 Escherichia coli 562 10067292

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833304	8729	30885	375	124

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833306	8730	30886	798	265

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833309	8731	30887	186	61

Description

GTC ORF with score 92 to: (sr:plasmodium vivax (isolate:patient) merozoite dna, clone:td430a) (db:genpept-inv) (de:plasmodium vivax clone td430a dna for merozoite surface protein,partial cds.) (nt:polymorphic region and flanking regions) (le:<1) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833323	8732	30888	1890	630

Description

6500729711 rp11:b3986 50s ribosomal subunit protein 17/112:50s ribosomal protein 17/112:18 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b3986 b3986 Escherichia coli 562 -11533569 128935 rp11 ribosomal protein 17/112 (cl:escherichia coli ribosomal protein 112) (db:pir1.dat) (mp:90 min) R5EC7 S12575 Escherichia coli 562 -11533569 238140 rp11::17/112 (db:genpept-bct1) (de:e. coli operon rpobc coding for the beta- and beta'-subunits of rnapolymerase (genes rpoc and rpob), and genes rp11, rlpj, rpla, andrplk coding for 50s ribosomal subunit proteins 17/112, 110, 11, andl11, respectively. (map positio... ECRPOBC V00339 g42817 Escherichia coli 562 -11533569 237196 rp11 50s ribosomal subunit protein 17/112 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 362 of 400 of the completegenome.) (nt:o121; 100 pct identical to rl7\_ecoli sw: p02392; cg) (le:5523) (re:5888) (di:direct) AE000472 AE000472 g1790418 Escherichia coli 562 -11533569 7500953531 rp11 50s ribosomal subunit protein 17/112 (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 254) (le:45801) (re:46166) (di:direct) ECOUW89 U00006 g396325 Escherichia coli 562 -11533569 5000690790 (de:(ecoli\_3876) (pn:50s ribosomal subunit protein 17) (gn:rp11) (gtcfc:10.3) (ec:) (rl7\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_3876 ECOLI\_3876 Escherichia coli 562 10067264

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833335	8733	30889	2343	780

Description

6500729712 rpsf:b4200 30s ribosomal subunit protein s6:30s ribosomal protein s6 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b4200 b4200 Escherichia coli 562 -11533570 7000688943 rpsf ribosomal protein s6 (cl:escherichia coli ribosomal protein s6) (db:pir1.dat) (mp:95 min) R3EC6 C65231 Escherichia coli 562 -11533570 238162 rpsf 30s ribosomal subunit protein s6 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 225) (le:115950) (re:116345) (di:direct) ECOUW93 U14003 g537041 Escherichia coli 562 -11533570 7500953501 (db:genpept-bct1) (de:e. coli genes rpsf, rpsr and rpli for ribosomal proteins s6, s18,19.) (nt:ribosomal protein s6 (aa 1-131)) (le:448) (re:843) (di:direct) ECRPSFRI X04022 g42845 Escherichia coli 562 -11533570 237405 rpsf 30s ribosomal subunit protein s6 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 381 of 400 of the completegenome.) (nt:o131; 100 pct identical to rs6\_ecoli sw: p02358; cg) (le:8784) (re:9179) (di:direct) AE000491 AE000491 g1790644 Escherichia coli 562 -11533570 5000690791 (de:(ecoli\_4083) (pn:30s ribosomal subunit protein s6) (gn:rpsf) (gtcfc:10.3) (ec:) (rs6\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_4083 ECOLI\_4083 Escherichia coli 562 10124154

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833359	8734	30890	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833374	8735	30891	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833375	8736	30892	405	135

Description

6500729713 rpsr:b4202 30s ribosomal subunit protein s18:30s ribosomal protein s18 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b4202 b4202 Escherichia coli 562 -11533571 128811 rpsr ribosomal protein s18 (cl:escherichia coli ribosomal protein s18) (db:pir1.dat) (mp:96 min) R3EC18 S56427 Escherichia coli 562 -11533571 238164 rpsr 30s ribosomal subunit protein s18 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 214) (le:116671) (re:116898) (di:direct) ECOUW93 U14003 g537043 Escherichia coli 562 -11533571 7500953516 (db:genpept-bct1) (de:e. coli genes rpsf, rpsr and rpli for ribosomal proteins s6, s18,19.) (nt:ribosomal protein s18 (aa 1-75)) (le:1169) (re:1396) (di:direct) ECRPSFRI X04022 g42847 Escherichia coli 562 -11533571 237407 rpsr 30s ribosomal subunit protein s18 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 381 of 400 of the completegenome.) (nt:o75; 100 pct identical to rs18\_ecoli sw: p02374; cg) (le:9505) (re:9732) (di:direct) AE000491 AE000491 g1790646 Escherichia coli 562 -11533571 5000690792 (de:(ecoli\_4085) (pn:30s ribosomal subunit protein s18) (gn:rpsr) (gtcfc:10.3) (ec:) (rs18\_ecoli) (keggfc:11.2) (rileyfc:3.1.2) (db:gtc-escherichia coli)) ECOLI\_4085 ECOLI\_4085 Escherichia coli 562 10067218

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833392	8737	30893	630	209

Description

GTC ORF with score 128 to: (sr:information) (db:genpept) (de:homo sapiens bac clone rg054d04 from 7q31, complete sequence.) (nt:similar to calcium-independent phospholipase a2;) (le:79671:86454:95029) (re:79945:86649:95223) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833393	8738	30894	471	157

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833433	8739	30895	501	166

Description

6500729714 rpli:b4203 50s ribosomal subunit protein 19:50s ribosomal protein 19 (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.2) (db:gtc-escherichia coli) b4203 b4203 Escherichia coli 562 -11533572 238165 rpli (de:50s ribosomal protein 19) (db:swissprot) RL9\_ECOLI P02418 ESCHERICHIA COLI 562 -11533572 148917 rpli ribosomal protein 19 (cl:escherichia coli ribosomal protein 19) (db:pir1.dat) (mp:96 min) R5EC9 F65231 Escherichia coli 562 -11533572 237408 rpli 50s ribosomal subunit protein 19 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 257) (le:116940) (re:117389) (di:direct) ECOUW93 U14003 g537044 Escherichia coli 562 -11533572 5000690793 (db:genpept-bct1) (de:e. coli genes rpsf, rpsr and rpli for ribosomal proteins s6, s18,19.) (nt:ribosome protein 19 (aa 1-149)) (le:1439) (re:1888) (di:direct) ECRPSFRI X04022 g42848 Escherichia coli 562 -11533572 7500890362 rpli 50s ribosomal subunit protein 19 (fn:structural component; ribosomal proteins -) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 381 of 400 of the completegenome.) (nt:ol49; cg site no. 257) (le:9774) (re:10223) (di:direct) AE000491 AE000491 g1790647 Escherichia coli 562 -11533572 95495 rpli (de:50s ribosomal protein 19) (db:swissprot) RL9\_ECOLI P02418 ESCHERICHIA COLI 562 -11533572 7000686410 rpli ribosomal protein 19 (cl:escherichia coli ribosomal protein 19) (db:pir) (mp:96 min) R5EC9 S56428 Escherichia coli 562 -11533572

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833438	8740	30896	348	115

Description

GTC ORF with score 100 to: (sr:thale cress) (db:genpept) (de:arabidopsis thaliana chromosome 1 bac t2k10 sequence, complete sequence.) (nt:strong similarity to gb|af039376 evelknivel) (le:29207:32167) (re:32031:32926) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833459	8741	30897	1995	664

Description

6500729715 rimk:b0852 ribosomal protein s6 modification protein (gtcfc:10.5) (keggfc:14.2) (rileyfc:3.1.3) (db:gtc-escherichia coli) b0852 b0852 Escherichia coli 562 -11533573 94361 rimk (de:ribosomal protein s6 modification protein) (db:swissprot) RIMK\_ECOLI P17116 ESCHERICHIA COLI 562 -11533573 7000686332 rimk ribosomal protein s6--glutamic acid ligase::ribosomal protein s6 modification protein (cl:ribosomal protein s6--glutamic acid ligase) (ec:6.3.2.-) (db:pir1.dat) (mp:18.7-19.0 min) D64823 D64823 Escherichia coli 562 -11533573 7500889789 rimk ribosomal protein s6 modification protein (fn:structural component; ribosomes - maturation) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 77 of 400 of the completegenome.) (nt:o300; 100 pct identical to 282 residues) (le:3951) (re:4853) (di:direct) AE000187 AE000187 g1787076 Escherichia coli 562 -11533573 5000690794 (de:(ecoli\_819) (pn:ribosomal protein s6 modification protein) (gn:rimk) (gtcfc:10.4:10.5) (ec:) (rimk\_ecoli) (keggfc:11.2) (rileyfc:3.1.3) (db:gtc-escherichia coli)) ECOLI\_819 ECOLI\_819 Escherichia coli 562 10123039

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833464	8742	30898	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833470	8743	30899	294	97

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833477	8744	30900	783	260

Description

6500729716 rmf:b0953 ribosome modulation factor:protein e (gtcfc:10.5)  
(keggfc:14.2) (rileyfc:3.1.3) (db:gtc-escherichia coli) b0953 b0953  
Escherichia coli 562 -11533574 95666 rmf (de:ribosome modulation factor  
(protein e)) (db:swissprot) RMF\_ECOLI P22986 ESCHERICHIA COLI 562 -11533574  
7000686419 rmf:rfm ribosome modulation factor:protein e (db:pir2.dat)  
(mp:22 min) H64835 H64835 Escherichia coli 562 -11533574 223296 rmf  
ribosome modulation factor protein e (sr:escherichia coli(strain:k12) dna,  
clone:kohara clone #222) (db:genpept-bct1) (de:escherichia coli genomic dna.  
(21.6 - 22.0 min).) (le:9067) (re:9234) (di:direct) D90733 D90733 g1651464  
Escherichia coli 562 -11533574 7500890426 rmf ribosome modulation factor  
(fn:factor; ribosomes - maturation and) (db:genpept-bct2) (de:escherichia  
coli k-12 mg1655 section 87 of 400 of the completegenome.) (nt:o55; 98 pct  
identical to rmf\_ecoli sw: p22986) (le:8023) (re:8190) (di:direct) AE000197  
AE000197 g1787186 Escherichia coli 562 -11533574 5000690795 rmf ribosome  
modulation factor protein e . (sr:escherichia coli(strain:k12) dna,  
clone:kohara clone #222) (db:genpept) (de:escherichia coli genomic dna.  
(21.7 - 22.1 min).) (nt:orf\_id:o222#6; similar to swissprot accession)  
(le:9067) (re:9234) (di:direct) D90733 D90733 g1651464 Escherichia coli 562  
-11533574

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833484	8745	30901	1434	477

Description

6500729717 rimj:b1066 ribosomal-protein-alanine  
acetyltransferase:acetylating enzyme for n-terminal of ribosomal protein s5  
(gtcfc:10.5) (ec:2.3.1.128) (keggfc:14.1) (rileyfc:3.1.3)  
(db:gtc-escherichia coli) b1066 b1066 Escherichia coli 562 -11533575  
7500889788 rimj (ec:2.3.1.128) (de:(acetylating enzyme for n-terminal of  
ribosomal protein s5)) (db:swissprot) RIMJ\_ECOLI P09454 ESCHERICHIA COLI 562  
-11533575 164253 rimj ribosomal-protein-alanine n-acetyltransferase  
(cl:hypothetical protein yoaa) (ec:2.3.1.128) (db:pir2.dat) (mp:23.7 min)  
S01084 S01084 Escherichia coli 562 -11533575 223347 rimj  
ribosomal-protein-alanine acetyltransferase (sr:escherichia coli(strain:k12)  
dna, clone:kohara clone #233) (db:genpept-bct1) (de:escherichia coli genomic  
dna. (24.0 - 24.4 min).) (le:11928) (re:12512) (di:direct) D90743 D90743  
g1651524 Escherichia coli 562 -11533575 238087 rimj acetylase  
(sr:escherichia coli (individual\_isolate mc4100, strain k-12) dna)  
(db:genpept-bct1) (de:e. coli acetylase (rimj) gene, complete cds.) (le:289)  
(re:873) (di:direct) ECORIMJA M99278 g147655 Escherichia coli 562 -11533575  
5000690796 (db:genpept-bct1) (de:e.coli rimj gene for acetylation of  
ribosomal protein s5.) (nt:s5 (aa 1-194)) (le:227) (re:811) (di:direct)  
ECRIMJ X06118 g42744 Escherichia coli 562 -11533575 235833 rimj acetylation  
of n-terminal alanine of 30s (fn:enzyme; ribosomes - maturation and)  
(db:genpept-bct2) (ec:2.3.1.128) (de:escherichia coli k-12 mg1655 section 97  
of 400 of the completegenome.) (nt:o194; 100 pct identical to rimj\_ecoli sw:  
p09454) (le:8898) (re:9482) (di:direct) AE000207 AE000207 g1787305  
Escherichia coli 562 -11533575 7502851940 rimj ribosomal-protein-alanine  
acetyltransferase ec (sr:escherichia coli(strain:k12) dna, clone:kohara  
clone #233) (db:genpept) (de:escherichia coli genomic dna. (24.1 - 24.5  
min).) (nt:orf\_id:o233#14; similar to swissprot accession) (le:11928)  
(re:12512) (di:direct) D90743 D90743 g1651524 Escherichia coli 562 -11533575  
94360 rimj (ec:2.3.1.128) (de:(acetylating enzyme for n-terminal of  
ribosomal protein s5)) (db:swissprot) RIMJ\_ECOLI P09454 ESCHERICHIA COLI 562  
-11533575

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833503	8746	30902	1071	357

Description

GTC ORF with score 478 to: (db:genpept) (de:aureobasidium pullulans  
multidrug resistance protein 1 (mdr1) gene,promoter region and complete  
cds.) (nt:atp-binding cassette (abc) transporter protein) (le:542) (re:4450)  
(di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833511	8747	30903	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833512	8748	30904	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833516	8749	30905	285	94

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833517	8750	30906	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833537	8751	30907	264	88

Description

6500729718 rimi:b4373 ribosomal-protein-alanine acetyltransferase  
 (gtcfc:10.5) (ec:2.3.1.128) (keggfc:14.1) (rileyfc:3.1.3)  
 (db:gtc-escherichia coli) b4373 b4373 Escherichia coli 562 -11533576  
 7500889784 rimi (ec:2.3.1.128) (de:(acetylating enzyme for n-terminal of  
 ribosomal protein s18)) (db:swissprot) RIMI\_ECOLI P09453 ESCHERICHIA COLI  
 562 -11533576 7000691911 rimi ribosomal-protein-alanine n-acetyltransferase  
 (cl:escherichia coli peptide n-acetyltransferase rimi) (ec:2.3.1.128)  
 (db:pir2.dat) D65252 D65252 Escherichia coli 562 -11533576 7500889786 rimi  
 acyltransferase for 30s ribosomal subunit (fn:enzyme; ribosomes - maturation  
 and) (db:genpept-bct2) (ec:2.3.1.128) (de:escherichia coli k-12 mg1655  
 section 397 of 400 of the completegenome.) (nt:ol48; sequence change  
 shortens and) (le:11134) (re:11580) (di:direct) AE000507 AE000507 g2367381  
 Escherichia coli 562 -11533576

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833545	8752	30908	585	194

Description

6500729719 quea:b0405 trna ribosyltransferase-isomerase:s-adenosyl  
methionine trna ribosyltransferase-isomerase:queuosine biosynthesis protein  
quea (gtcfc:10.6:5.4) (ec:5.-.-.-) (keggfc:14.1) (rileyfc:3.1.5)  
(db:gtc-escherichia coli) b0405 b0405 Escherichia coli 562 -11533577 92737  
quea (ec:5.-.-.-) (de:(queuosine biosynthesis protein quea)) (db:swissprot)  
QUEA\_ECOLI P21516 ESCHERICHIA COLI 562 -11533577 164452 quea  
s-adenosylmethionine:trna ribosyltransferase-isomerase::queuosine  
biosynthesis protein quea (cl:s-adenosylmethionine:trna  
ribosyltransferase-isomerase) (ec:5.-.-.-) (db:pir2.dat) B38530 B38530  
Escherichia coli 562 -11533577 240182 quea (sr:e.coli (strain k12) isolate  
p2257 dna) (db:genpept-bct1) (de:e. coli queuosine biosynthesis (quea) gene,  
complete cds.) (le:1923) (re:2993) (di:direct) ECOQBIO M37702 g147485  
Escherichia coli 562 -11533577 7500889219 quea s-adenosylmethionine:trna  
(db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.)  
(le:4461) (re:5531) (di:direct) ECU82664 U82664 g1773089 Escherichia coli  
562 -11533577 235671 quea synthesis of queuine in trna:probably (fn:enzyme;  
aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:5.-.-.-)  
(de:escherichia coli k-12 mgl655 section 37 of 400 of the completegenome.)  
(nt:o356; 100 pct identical to quea\_ecoli sw: p21516) (le:2604) (re:3674)  
(di:direct) AE000147 AE000147 g1786606 Escherichia coli 562 -11533577  
5000690798 (de:(ecoli\_389) (pn:synthesis of queuine in trna; probably s-  
adenosylmethionine:trna ribosyltransferase-isomerase:synthesis of queuine in  
trna; probably s- adenosylmethionine, trna ribosyltransferase-isomerase)  
(gn:quea) (gtcfc:10.6)) ECOLI\_389 ECOLI\_389 Escherichia coli 562 10034765

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833560	8753	30909	1770	589
<u>Description</u>				
6500729720 tgt:b0406 queueine trna-ribosyltransferase:trna-guanine transglycosylase:guanine insertion enzyme (gtcfc:10.6:4.1) (ec:2.4.2.29) (keggfc:14.1) (rileyfc:3.1.5) (db:gtc-escherichia coli) b0406 b0406 Escherichia coli 562 -11533578 164451 tgt queueine trna-ribosyltransferase (cl:queueine trna-ribosyltransferase) (ec:2.4.2.29) (db:pir2.dat) (mp:9 min) C38530 C38530 Escherichia coli 562 -11533578 7500960444 tgt transfer rna-guanine transglycosylase (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:5587) (re:6714) (di:direct) ECU82664 U82664 g1773090 Escherichia coli 562 -11533578 240183 tgt trna-guanine transglycosylase (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:2.4.2.29) (de:escherichia coli k-12 mg1655 section 37 of 400 of the completegenome.) (nt:o375; 99 pct identical to tgt_ecoli sw: p19675) (le:3730) (re:4857) (di:direct) AE000147 AE000147 g1786607 Escherichia coli 562 -11533578 5000690799 (de:(ecoli_390) (pn:trna-guanine transglycosylase) (gn:tgt) (gtcfc:10.6) (ec:2.4.2.29) (tgt_ecoli) (keggfc:11.1) (rileyfc:3.1.5) (db:gtc-escherichia coli)) ECOLI_390 ECOLI_390 Escherichia coli 562 10087322				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833569	8754	30910	558	185

Description

6500729721 aat:b0885 leucyl/phenylalanyl-trna--protein transferase  
(gtcfc:10.6:5.13:5.7) (ec:2.3.2.6) (keggfc:14.1) (rileyfc:3.1.5)  
(db:gtc-escherichia coli) b0885 b0885 Escherichia coli 562 -11533579 82435  
aat (ec:2.3.2.-) (de:leucyl/phenylalanyl-trna--protein transferase,)  
(db:swissprot) LPTP\_ECOLI P23885 ESCHERICHIA COLI 562 -11533579 163996 aat  
leucyl:phenylalanyl-trna--protein transferase::l/f-transferase (ec:2.3.2.-)  
(db:pir2.dat) (mp:20 min) A36888 A36888 Escherichia coli 562 -11533579  
223246 aat 27k protein (sr:escherichia coli(strain:k12) dna, clone:kohara  
clone #214) (db:genpept-bct1) (de:escherichia coli genomic dna.(19.9 - 20.2  
min).) (le:2608) (re:3312) (di:complement) D90726 D90726 g1651407  
Escherichia coli 562 -11533579 234867 aat leu/phe-trna-protein transferase  
(fn:n-terminal protein aminoacylation) (sr:escherichia coli dna)  
(db:genpept-bct1) (de:e. coli leucyl/phenylalanyl trna protein transferase  
(aat) gene,mdrh gene, initiation factor (infa) gene, and serine transfer  
rna(serw) gene, complete cds's.) (nt:pu... ECOAAT L10383 g145166 Escherichia  
coli 562 -11533579 233704 aat leucyl:phenylalanyl-trna-protein transferase  
(fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:2.3.2.-)  
(de:escherichia coli k-12 mg1655 section 80 of 400 of the completegenome.)  
(nt:f234; 100 pct identical to lptp\_ecoli sw: p23885) (le:4429) (re:5133)  
(di:complement) AE000190 AE000190 g1787111 Escherichia coli 562 -11533579  
7500885135 (sr:e.coli, dna) (db:genpept-bct2) (de:escherichia coli infa  
operon and transfer rna-ser(gga), completesequence.) (nt:orf 2) (le:420)  
(re:1124) (di:direct) ECOINFSERW M63145 g146481 Escherichia coli 562  
-11533579 5000690800 aat leucyltransferase ec 2.3.2.6 . (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #214) (db:genpept) (de:escherichia  
coli genomic dna. (19.9 - 20.3 min).) (nt:orf\_id:o214#4; similar to pir  
accession number) (le:2608) (re:3312) (di:complement) D90726 D90726 g1651407  
Escherichia coli 562 -11533579

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833576	8755	30911	216	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833591	8756	30912	369	122

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833615	8757	30913	1053	350

Description

GTC ORF with score 269 to: (db:genpept-bct2) (de:yersinia pestis trna-asn gene, complete sequence; cp4-like integrase (int), ybts (ybts), ybtx (ybtx), ybtq (ybtq), ybtp (ybtp), arac-like regulator ybta (ybta), ybt peptide synthetase hmw2 (irp2), ybt ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833616	8758	30914	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833617	8759	30915	312	103

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833626	8760	30916	231	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833635	8761	30917	411	136

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833639	8762	30918	621	206

Description

6500729722 pth:b1204 peptidyl-trna hydrolase (gtcfc:10.6) (ec:3.1.1.29) (keggfc:14.1) (rileyfc:3.1.5) (db:gtc-escherichia coli) b1204 b1204 Escherichia coli 562 -11533580 304612 pth (ec:3.1.1.29) (de:peptidyl-trna hydrolase, (pth)) (db:swissprot) PTH\_ECOLI P23932 ESCHERICHIA COLI 562 -11533580 162717 pth aminoacyl-trna hydrolase (cl:peptidyl-trna hydrolase) (ec:3.1.1.29) (db:pir2.dat) S16753 S16753 Escherichia coli 562 -11533580 223409 pth aminoacyl-trna hydrolase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #247) (db:genpept-bct1) (de:escherichia coli genomic dna.(27.0 -27.4 min).) (le:2191) (re:2775) (di:complement) D90756 D90756 g1651597 Escherichia coli 562 -11533580 5000690801 pth peptidyl-trna hydrolase (db:genpept-bct1) (ec:3.1.1.29) (de:e.coli pth gene for peptidyl-trna hydrolase.) (nt:pth may be involved in the hydrolysis of) (le:703) (re:1287) (di:direct) ECPTHG X61941 g581202 Escherichia coli 562 -11533580 237944 pth peptidyl-trna hydrolase (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:3.1.1.29) (de:escherichia coli k-12 mg1655 section 109 of 400 of the completegenome.) (nt:f194; 100 pct identical to pth\_ecoli sw: p23932) (le:1623) (re:2207) (di:complement) AE000219 AE000219 g1787455 Escherichia coli 562 -11533580 7502851941 pth aminoacyl-trna hydrolase ec 3.1.1.29 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #247) (db:genpept) (de:escherichia coli genomic dna.(27.1 - 27.5 min).) (nt:orf\_id:o247#2; similar to pir accession number) (le:2191) (re:2775) (di:complement) D90756 D90756 g1651597 Escherichia coli 562 -11533580 92198 pth (ec:3.1.1.29) (de:peptidyl-trna hydrolase, (pth)) (db:swissprot) PTH\_ECOLI P23932 ESCHERICHIA COLI 562 -11533580

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501833640	8763	30919	399	132

Description

6500729723 phem:phtl:b1715 phenylalanyl-trna synthetase operon leader peptide:phenylalanyl-trna synthetase:phest operon leader peptide (gtcfc:10.6:5.13) (keggfc:14.2) (rileyfc:3.1.5) (db:gtc-escherichia coli) b1715 b1715 Escherichia coli 562 -11533581 7500885116 phem:phtl (de:peptide)) (db:swissprot) LPF2\_ECOLI P06985 ESCHERICHIA COLI 562 -11533581 131601 phem phest operon leader peptide (cl:phest leader peptide) (db:pir1.dat) (mp:37 min) LFECFS S11551 Escherichia coli 562 -11533581 235413 (sr:e.coli dna) (db:genpept-bct1) (de:e.coli rplt gene (3' end) coding for ribosomal protein l20 andphest operon: gene for leader peptide and phes gene (5' end) codingfor the small subunit of phenylalanyl-trna synthetase.) (nt:phest operon leader pepti... ECOHIMB M10423 g146350 Escherichia coli 562 -11533581 238351 (sr:plasmid pbls (derived plasmid pbl) dna, from e.coli) (db:genpept-bct1) (de:e.coli phes,t operon attenuator region from plasmid pbls with is4insertion, 5' junction.) (nt:phes,t attenuator protein) (le:70) (re:114) (di:direct) ECOPHEIS1 M13251 g147185 Escherichia coli 562 -11533581 5000690802 (db:genpept-bct1) (de:e.coli thrs, infc, rplt, phes, phet and hima genes encodingthreonyl-trna synthetase, initiation factor if3, ribosomal proteinl20, phenylalanyl-trna synthetase and the alpha-subunit of the hostintegration factor.) (nt:phenylalanyl-... ECTHRINF V00291 g43069 Escherichia coli 562 -11533581 234653 phem phenylalanyl-trna synthetase phest operon (fn:leader; aminoacyl trna synthetases, trna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 156 of 400 of the completegenome.) (nt:f14; 100 pct identical to lpf2\_ecoli sw: p06985;) (le:9709) (re:9753) (di:complement) AE000266 AE000266 g1788008 Escherichia coli 562 -11533581 82379 phem:phtl (de:phenylalanyl-trna synthetase (phest) operon leader peptide) (db:swissprot) LPF2\_ECOLI P06985 ESCHERICHIA COLI 562 -11533581

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833641	8764	30920	489	162

Description

6500729724 trmd:b2607 guanine-7methyltransferase:trna  
 guanine-n1-methyltransferase:mlg-methyltransferase (gtcfc:10.6:4.1)  
 (ec:2.1.1.31) (keggfc:14.1) (rileyfc:3.1.5) (db:gtc-escherichia coli) b2607  
 b2607 Escherichia coli 562 -11533582 7500893405 trmd (ec:2.1.1.31)  
 (de:methyltransferase) (trna (gm37) methyltransferase)) (db:swissprot)  
 TRMD\_ECOLI P07020 ESCHERICHIA COLI 562 -11533582 123223 trmd trna  
 guanine-n1--methyltransferase (cl:trna (guanine-n1) methyltransferase)  
 (ec:2.1.1.31) (db:pir1.dat) (mp:57 min) XYECG1 A30380 Escherichia coli 562  
 -11533582 225182 trmd trna guanine-n1--methyltransferase ec (sr:escherichia  
 coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
 (de:e.coli genomic dna, kohara clone #438(58.9-59.3 min.)) (nt:similar to  
 (pir accession number a30380)) (le:7458) (re:8225) (di:complement) D90888  
 D90888 g1800012 Escherichia coli 562 -11533582 5000690803 (db:genpept-bct1)  
 (de:e. coli trmd operon and nearby regions.) (nt:trna (mlg) methyltransferase  
 (trmd gene) (aa 1-255)) (le:2617) (re:3384) (di:direct) ECTRMD X01818 g43144  
 Escherichia coli 562 -11533582 238405 trmd trna methyltransferase:trna  
 (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2)  
 (ec:2.1.1.31) (de:escherichia coli k-12 mg1655 section 236 of 400 of the  
 completegenome.) (nt:f255; 100 pct identical to trmd\_ecoli sw: p07020;)  
 (le:10364) (re:11131) (di:complement) AE000346 AE000346 g1788959 Escherichia  
 coli 562 -11533582 102276 trmd (ec:2.1.1.31) (de:methyltransferase))  
 (db:swissprot) TRMD\_ECOLI P07020 ESCHERICHIA COLI 562 -11533582

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833667	8765	30921	873	290

Description

6500729725 cca:b3056 trna nucleotidyltransferase:trna  
adenylyltransferase:trna -pyrophosphorylase (gtcfc:10.6:4.1) (ec:2.7.7.25)  
(keggfc:14.1) (rileyfc:3.1.5) (db:gtc-escherichia coli) b3056 b3056  
Escherichia coli 562 -11533583 63387 cca (ec:2.7.7.25) (de:(trna  
cca-pyrophosphorylase) (cca-adding enzyme)) (db:swissprot) CCA\_ECOLI P06961  
ESCHERICHIA COLI 562 -11533583 124057 cca trna adenylyltransferase::trna  
cca-pyrophosphorylase:trna nucleotidyltransferase (cl:escherichia coli trna  
adenylyltransferase) (ec:2.7.7.25) (db:pir1.dat) (mp:67 min) RNECTA A25215  
Escherichia coli 562 -11533583 239261 cca trna nucleotidyltransferase  
(sr:e.coli dna, clones lambda-c(1,4,11)) (db:genpept-bct1) (ec:2.7.7.25)  
(de:e.coli cca gene encoding trna nucleotidyltransferase, complete cds.)  
(le:450) (re:1688) (di:direct) ECOCCA M12788 g145468 Escherichia coli 562  
-11533583 7500878337 cca (fn:trna nucleotidyltransferase) (db:genpept-bct1)  
(ec:2.7.7.25) (de:escherichia coli k-12 genome; approximately 68 minutes.)  
(nt:cg site no. 933) (le:6686) (re:7924) (di:direct) ECU28379 U28379 g882578  
Escherichia coli 562 -11533583 233942 cca trna nucleotidyl transferase  
(fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2)  
(ec:2.7.7.25) (de:escherichia coli k-12 mg1655 section 277 of 400 of the  
completegenome.) (nt:o412; 100 pct identical to cca\_ecoli sw: p06961; cg)  
(le:6811) (re:8049) (di:direct) AE000387 AE000387 g1789436 Escherichia coli  
562 -11533583 5000690804 (de:(ecoli\_2979) (pn:trna nucleotidyl transferase)  
(gn:cca) (gtcfc:10.6) (ec:2.7.7.25) (cca\_ecoli) (keggfc:11.1)  
(rileyfc:3.1.5) (db:gtc-escherichia coli)) ECOLI\_2979 ECOLI\_2979 Escherichia  
coli 562 10006057

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833675	8766	30922	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833682	8767	30923	648	215

Description

GTC ORF with score 225 to: (db:genpept-bct2) (de:bordetella pertussis  
d-3-phosphoglycerate dehydrogenase homolog(sera) and brg1 (brg1) genes,  
complete cds.) (nt:orf4; similar to salicylate hydroxylase) (le:7172)  
(re:8392) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833689	8768	30924	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833692	8769	30925	231	76

Description

6500729726 trma:b3965

uracil-5-methyltransferase:uracil-5--methyltransferase:trna:m-5-u54-methyltransferase:rumt (gtcfc:10.6:4.2) (ec:2.1.1.35) (keggfc:14.1) (rileyfc:3.1.5) (db:gtc-escherichia coli) b3965 b3965 Escherichia coli 562 -11533584 102272 trma (ec:2.1.1.35) (de:methyltransferase) (rumt)) (db:swissprot) TRMA\_ECOLI P23003 ESCHERICHIA COLI 562 -11533584 164772 trna trna uracil-5--methyltransferase (ec:2.1.1.35) (db:pir2.dat) (mp:90 min) A37321 A37321 Escherichia coli 562 -11533584 237183 trna m-5-u54 transfer rna methyltransferase (sr:e.coli dna) (db:genpept-bct1) (ec:2.1.1.35) (de:e.coli trna(m-5-u54)methyltransferase (trma) gene, complete cds andvitamin b-12 binding protein (btub) gene, 5' end.) (le:385) (re:1485) (di:direct) ECOTRMA M57568 g148051 Escherichia coli 562 -11533584 236145 trna trna uracil-5--methyltransferase (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (ec:2.1.1.35) (de:escherichia coli k-12 mg1655 section 360 of 400 of the completegenome.) (nt:f366; 100 pct identical to trma\_ecoli sw: p23003;) (le:9056) (re:10156) (di:complement) AE000470 AE000470 g1790403 Escherichia coli 562 -11533584 7500893403 trna trna uracil-5 -methyltransferase (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (ec:2.1.1.35) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 79) (le:27412) (re:28512) (di:complement) ECOUW89 U00006 g396312 Escherichia coli 562 -11533584 5000690805 (de:(ecoli\_3863) (pn:trna methyltransferase; trna:uracil-5--methyltransferase) (gn:trma) (gtcfc:10.6) (ec:2.1.1.35) (trma\_ecoli) (keggfc:11.1) (rileyfc:3.1.5) (db:gtc-escherichia coli)) ECOLI\_3863 ECOLI\_3863 Escherichia coli 562 10044091

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501833693	8770	30926	207	68

# Description

6500729727 miaa:trpx:b4171 trna delta-2-isopentenylpyrophosphate:trna  
delta:2-isopentenylpyrophosphate transferase:ipp transferase  
(gtcfc:10.6:13.10) (ec:2.5.1.8) (keggfc:14.1) (rileyfc:3.1.5)  
(db:gtc-escherichia coli) b4171 b4171 Escherichia coli 562 -11533585 83700  
miaa:trpx (ec:2.5.1.8) (de:(ipp transferase)) (db:swissprot) MIAA\_ECOLI  
P16384 ESCHERICHIA COLI 562 -11533585 7502851942 miaa:trpx (ec:2.5.1.8)  
(de:(ipp transferase)) (db:swissprot) MIAA\_ECOLI P16384 SHIGELLA FLEXNERI  
623 -11533585 162912 miaa delta 2 -isopentenylpyrophosphate transferase  
(cl:delta(2)-isopentenylpyrophosphate transferase) (ec:2.5.1.-)  
(db:pir2.dat) (mp:95 min) B37318 B37318 Escherichia coli 562 -11533585  
235142 miaa trna delta 2-isopentenylpyrophosphate (sr:shigella flexneri  
(strain:2a, isolate:ysh6000) dna) (db:genpept-bct1) (de:shigella flexneri  
gene for trna delta 2-isopentenylpyrophosphatetransferase, complete cds.)  
(le:56) (re:1006) (di:direct) AB000785 AB000785 g2506034 Shigella flexneri  
623 -11533585 5500684619 miaa delta-2-isopentenyl pyrophosphate transferase  
(sr:e.coli k-12 dna, clone pnul27) (db:genpept-bct1) (de:e.coli  
(delta)2-isopentenyl pyrophosphate transferase (miaa) gene,complete cds, and  
mutator protein (mut1) gene, 3' end.) (le:56) (re:1006) (di:direct) ECOMIAA  
M63655 g146860 Escherichia coli 562 -11533585 7500885626 miaa trna  
delta-2-isopentenylpyrophosphate ipp (db:genpept-bct1) (de:escherichia coli  
k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 18160;  
alternate gene name trpx) (le:90080) (re:91030) (di:direct) ECOUW93 U14003  
g537012 Escherichia coli 562 -11533585 237376 miaa delta 2  
-isopentenylpyrophosphate trna-adenosine (fn:enzyme; aminoacyl trna  
synthetases, trna) (db:genpept-bct2) (ec:2.5.1.-) (de:escherichia coli k-12  
mg1655 section 379 of 400 of the completegenome.) (nt:o316; 100 pct  
identical to miaa\_ecoli sw: p16384;) (le:6966) (re:7916) (di:direct)  
AE000489 AE000489 g1790613 Escherichia coli 562 -11533585 5000690806  
(de:(ecoli\_4054) (pn:delta:2-isopentenylpyrophosphate trna-adenosine  
transferase) (gn:miaa) (gtcfc:10.6) (ec:2.5.1.8) (miaa\_ecoli) (keggfc:11.1)  
(rileyfc:3.1.5) (db:gtc-escherichia coli)) ECOLI\_4054 ECOLI\_4054 Escherichia  
coli 562 10025914

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501833694	8771	30927	495	165

Description

6500729728 map:b0168 methionine aminopeptidase:map:peptidase m (gtcfc:10.7) (ec:3.4.11.18) (keggfc:14.1) (rileyfc:3.1.8) (db:gtc-escherichia coli) b0168 b0168 Escherichia coli 562 -11533586 59383 map (ec:3.4.11.18) (de:methionine aminopeptidase, (map) (peptidase m)) (db:swissprot) AMPM\_ECOLI P07906 ESCHERICHIA COLI 562 -11533586 124730 map methionyl aminopeptidase::metallooligopeptidase:methionine aminopeptidase:peptidase m (cl:escherichia coli methionyl aminopeptidase) (ec:3.4.11.18) (db:pir1.dat) (mp:4 min) DPECM A27761 Escherichia coli 562 -11533586 235059 map methionine aminopeptidase (sr:escherichia coli (sub\_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (ec:3.4.11.18) (de:escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0 min).) (le:77306) (re:78100) (di:complement) ECO82K D26562 g473823 Escherichia coli 562 -11533586 239796 (sr:e.coli (strain cm89) dna, clone psyc1174) (db:genpept-bct1) (de:e.coli map gene, encoding methionine amino peptidase, complete cds.) (nt:methionine amino peptidase) (le:219) (re:1013) (di:direct) ECOMAP M15106 g146727 Escherichia coli 562 -11533586 301634 map methionine aminopeptidase (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:19787) (re:20581) (di:complement) ECU70214 U70214 g1552745 Escherichia coli 562 -11533586 233696 map methionine aminopeptidase (fn:enzyme; proteins - translation and) (db:genpept-bct2) (ec:3.4.11.18) (de:escherichia coli k-12 mg1655 section 16 of 400 of the completegenome.) (nt:f264; 100 pct identical to ampm\_ecoli sw: p07906) (le:5078) (re:5872) (di:complement) AE000126 AE000126 g1786364 Escherichia coli 562 -11533586 5000690807 (de:(ecoli\_168) (pn:methionine aminopeptidase) (gn:map) (gtcfc:10.7) (ec:3.4.11.18) (ampm\_ecoli) (keggfc:11.1) (rileyfc:3.1.8) (db:gtc-escherichia coli)) ECOLI\_168 ECOLI\_168 Escherichia coli 562 10002120



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833706	8772	30928	846	281

Description

6500729729 tsf:b0170 elongation factor ts:ef-ts (gtcfc:10.7) (keggfc:14.2) (rileyfc:3.1.8) (db:gtc-escherichia coli) b0170 b0170 Escherichia coli 562 -11533587 131243 tsf translation elongation factor ef-ts (cl:translation elongation factor ef-ts) (db:pir1.dat) (mp:4 min) EFEC5 A03525 Escherichia coli 562 -11533587 236161 tsf elongation factor ef-ts (sr:escherichia coli (sub\_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0 min.)) (le:79451) (re:80302) (di:direct) ECO82K D26562 g473825 Escherichia coli 562 -11533587 303238 tsf elongation factor ts (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (le:381) (re:1232) (di:direct) ECOTSF D83536 g1208943 Escherichia coli 562 -11533587 239798 tsf elongation factor ts (db:genpept-bct1) (de:e. coli genes tsf and rpsb, encoding elongation factor ts andribosomal protein s2.) (le:1266) (re:2117) (di:direct) ECRPSB V00343 g42843 Escherichia coli 562 -11533587 301636 tsf elongation factor ef-ts (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:21932) (re:22783) (di:direct) ECU70214 U70214 g1552747 Escherichia coli 562 -11533587 233698 tsf protein chain elongation factor ef-ts (fn:factor; proteins - translation and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 16 of 400 of the completegenome.) (nt:o283; 100 pct identical to efts\_ecoli sw: p02997) (le:7223) (re:8074) (di:direct) AE000126 AE000126 g1786366 Escherichia coli 562 -11533587 5000690808 tsf elongation factor ts (db:genpept) (de:e. coli genes tsf and rpsb, encoding elongation factor ts andribosomal protein s2.) (le:1266) (re:2117) (di:direct) ECRPSB V00343 g42843 Escherichia coli 562 -11533587 238161 tsf elongation factor ts (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (le:381) (re:1232) (di:direct) ECOTSF D83536 g1208943 Escherichia coli 562 -11533587

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833710	8773	30929	222	73

Description

6500729730 frr:rrf:b0172 ribosome recycling factor:ribosome releasing factor:rrf (gtcfc:10.7) (keggfc:14.2) (rileyfc:3.1.8) (db:gtc-escherichia coli) b0172 b0172 Escherichia coli 562 -11533588 96608 frr:rrf (de:ribosome recycling factor (ribosome releasing factor) (rrf)) (db:swissprot) RRF\_ECOLI P16174 ESCHERICHIA COLI 562 -11533588 164741 frr:rrf ribosome releasing factor:ribosome recycling factor:translation releasing factor (cl:ribosome releasing factor) (db:pir1.dat) (mp:4 min) A34495 A34495 Escherichia coli 562 -11533588 235923 frr ribosome releasing factor (sr:escherichia coli (sub\_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0 min).) (le:81466) (re:82023) (di:direct) EC082K D26562 g473827 Escherichia coli 562 -11533588 236001 (sr:e.coli (strain cs520) dna, clone plc6-32) (db:genpept-bct1) (de:e.coli ribosome releasing factor gene, complete cds.) (nt:ribosome releasing factor (gtg start codon)) (le:77) (re:634) (di:direct) ECORRFX J05113 g147771 Escherichia coli 562 -11533588 236163 frr ribosome releasing factor frr (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli smba gene.) (le:1482) (re:2039) (di:direct) ECOSMBA D13334 g806329 Escherichia coli 562 -11533588 303240 ribosome releasing factor (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (nt:alternate gene name is rrf) (le:2396) (re:2953) (di:direct) ECOTSF D83536 g1208945 Escherichia coli 562 -11533588 301638 frr ribosome release factor (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:23947) (re:24504) (di:direct) ECU70214 U70214 g1552749 Escherichia coli 562 -11533588 233700 frr ribosome releasing factor (fn:factor; proteins - translation and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 16 of 400 of the completengenome.) (nt:o185; 100 pct identical to rrf\_ecoli sw: p16174;) (le:9238) (re:9795) (di:direct) AE000126 AE000126 g1786368 Escherichia coli 562 -11533588 239800 ribosome releasing factor (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (nt:alternate gene name is rrf) (le:2396) (re:2953) (di:direct) ECOTSF D83536 g1208945 Escherichia coli 562 -11533588 5000690809 (de:(ecoli\_172) (pn:ribosome releasing factor) (gn:frr) (gtcfc:10.7) (ec:) (rrf\_ecoli) (keggfc:11.2) (rileyfc:3.1.8) (db:gtc-escherichia coli)) ECOLI\_172 ECOLI\_172 Escherichia coli 562 10038540

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833711	8774	30930	450	149

Description

6500729731 prfh:b0236 peptide chain release factor homolog:rf-h (gtcfc:10.7) (keggfc:14.2) (rileyfc:3.1.8) (db:gtc-escherichia coli) b0236 b0236 Escherichia coli 562 -11533589 7000691880 prfh peptide chain release factor homolog prfh (db:pir2.dat) E64748 E64748 Escherichia coli 562 -11533589 7500960405 prfh prfh (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:similar to peptide chain release factor) (le:84777) (re:85277) (di:direct) ECU70214 U70214 g1552804 Escherichia coli 562 -11533589 239855 prfh probable peptide chain release factor (fn:putative factor; proteins - translation and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 22 of 400 of the completegenome.) (nt:o166; 100 pct identical to 135 residues of a 141 aa) (le:418) (re:918) (di:direct) AE000132 AE000132 g1786431 Escherichia coli 562 -11533589 5000690810 (de:(ecoli\_229) (pn:probable peptide chain release factor) (gn:prfh) (gtcfc:10.7) (ec:) (rfh\_ecoli) (keggfc:11.2) (rileyfc:3.1.8) (db:gtc-escherichia coli)) ECOLI\_229 ECOLI\_229 Escherichia coli 562 10122715

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833726	8775	30931	501	166

Description

6500729732 hha:b0460 haemolysin expression modulating protein (gtcfc:10.7) (keggfc:14.2) (rileyfc:3.1.8) (db:gtc-escherichia coli) b0460 b0460 Escherichia coli 562 -11533590 7500883247 hha (de:haemolysin expression modulating protein) (db:swissprot) HHA\_ECOLI P23870 ESCHERICHIA COLI 562 -11533590 7000685527 hha hemolysin expression modulating protein (cl:modulating protein ymoa) (db:pir2.dat) C64776 C64776 Escherichia coli 562 -11533590 5000690811 hha hha protein (db:genpept-bct1) (de:e.coli hha gene for haemolysin expression modulating protein hha.) (le:343) (re:561) (di:direct) ECHHAE X57977 g48850 Escherichia coli 562 -11533590 233087 hha haemolysin expression modulating protein (fn:regulator; proteins - translation and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 42 of 400 of the completegenome.) (nt:f72; 100 pct identical to hha\_ecoli sw: p23870) (le:3504) (re:3722) (di:complement) AE000152 AE000152 g1786665 Escherichia coli 562 -11533590 76961 hha (de:haemolysin expression modulating protein) (db:swissprot) HHA\_ECOLI P23870 ESCHERICHIA COLI 562 -11533590

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833727	8776	30932	777	259

Description

6500729733 ppib:b0525 peptidyl-prolyl cis-trans isomerase b:ppiase  
b:rotamase b (gtcfc:10.7) (ec:5.2.1.8) (keggfc:14.1) (rileyfc:3.1.8)  
(db:gtc-escherichia coli) b0525 b0525 Escherichia coli 562 -11533591 67559  
ppib (ec:5.2.1.8) (de:(rotamase b)) (db:swissprot) CYPB\_ECOLI P23869  
ESCHERICHIA COLI 562 -11533591 7000684965 ppib peptidylprolyl  
isomerase:b:cyclophilin b:cyclosporin a-binding protein b (cl:peptidylprolyl  
isomerase) (ec:5.2.1.8) (db:pir1.dat) CSECB D64784 Escherichia coli 562  
-11533591 7500879876 ppib peptidyl-prolyl cis-trans isomerase b rotamase  
(fn:enzyme; proteins - translation and) (db:genpept-bct2) (ec:5.2.1.8)  
(de:escherichia coli k-12 mg1655 section 48 of 400 of the completegenome.)  
(nt:f164; 99 pct identical to cypb\_ecoli sw: p23869) (le:7451) (re:7945)  
(di:complement) AE000158 AE000158 g1786736 Escherichia coli 562 -11533591  
5000690812 (de:(ecoli\_508) (pn:peptidyl-prolyl cis-trans isomerase  
b:rotamase b) (gn:ppib) (gtcfc:10.7) (ec:5.2.1.8) (cypb\_ecoli) (keggfc:11.1)  
(rileyfc:3.1.8) (db:gtc-escherichia coli)) ECOLI\_508 ECOLI\_508 Escherichia  
coli 562 10122878

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833728	8777	30933	699	232

Description

GTC ORF with score 280 to: (sr:caenorhabditis elegans strain=bristol n2)  
(db:genpept-inv) (de:caenorhabditis elegans cosmid f35h12.) (nt:coded for by  
c. elegans cdna yk42d12.5; coded for) (le:14147:14504:14623:14747)  
(re:14191:14572:14699:14875) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501833740	8778	30934	396	132

# Description

6500729734 infa:b0884 initiation factor if-1:translation initiation factor if-1 (gtcfc:10.7) (keggfc:14.2) (rileyfc:3.1.8) (db:gtc-escherichia coli) b0884 b0884 Escherichia coli 562 -11533592 131255 infa translation initiation factor if-1:translation initiation factor eif-1 (cl:translation initiation factor if-1) (db:pir1.dat) (mp:20 min) FIEC1 A27855 Escherichia coli 562 -11533592 223242 infa translation initiation factor eif-1 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #212) (db:genpept-bct1) (de:escherichia coli genomic dna.(19.6 - 19.9 min).) (le:13162) (re:13380) (di:complement) D90725 D90725 g1651402 Escherichia coli 562 -11533592 223245 infa translation initiation factor eif-1 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #214) (db:genpept-bct1) (de:escherichia coli genomic dna.(19.9 - 20.2 min).) (le:2105) (re:2323) (di:complement) D90726 D90726 g1651406 Escherichia coli 562 -11533592 233705 (db:genpept-bct1) (de:e. coli infa gene for initiation factor if1.) (nt:initiation factor if1 (aa 1 -72)) (le:39) (re:257) (di:direct) ECINFA Y00373 g41808 Escherichia coli 562 -11533592 7500953630 infa (fn:initiation factor) (sr:escherichia coli dna) (db:genpept-bct1) (de:e. coli leucyl/phenylalanyl trna protein transferase (aat) gene,mdrh gene, initiation factor (infa) gene, and serine transfer rna(serw) gene, complete cds's.) (nt:putative) (le:2776... ECOAAT L10383 g145167 Escherichia coli 562 -11533592 233222 infa protein chain initiation factor if-1 (fn:factor; proteins - translation and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 80 of 400 of the completegenome.) (nt:f72; 100 pct identical to if1\_ecoli sw: p02998) (le:3926) (re:4144) (di:complement) AE000190 AE000190 g1787110 Escherichia coli 562 -11533592 5000690813 infa translation initiation factor if-1 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #212) (db:genpept) (de:escherichia coli genomic dna.(19.7 - 20.0 min).) (nt:orf\_id:o214#1; similar to pir accession number) (le:13162) (re:13380) (di:complement) D90725 D90725 g1651402 Escherichia coli 562 -11533592 7502851943 infa translation initiation factor if-1 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #214) (db:genpept) (de:escherichia coli genomic dna.(19.9 - 20.3 min).) (nt:orf\_id:o214#1; similar to pir accession number) (le:2105) (re:2323) (di:complement) D90726 D90726 g1651406 Escherichia coli 562 -11533592

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833743	8779	30935	201	66

Description

6500729735 prfa:sueb:uar:b1211 peptide chain release factor 1:rf-1 (gtcfc:10.7) (keggfc:14.2) (rileyfc:3.1.8) (db:gtc-escherichia coli) b1211 b1211 Escherichia coli 562 -11533593 94087 prfa:sueb:uar (de:peptide chain release factor 1 (rf-1)) (db:swissprot) RF1\_ECOLI P07011 ESCHERICHIA COLI 562 -11533593 7000686307 prfa:rf-1:sueb:uar translation releasing factor rf-1:peptide chain release factor 1 (cl:translation releasing factor) (db:pir1.dat) (mp:27 min) FCECR1 H64867 Escherichia coli 562 -11533593 223413 prfa peptide chain release factor 1 rf-1 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #247) (db:genpept-bct1) (de:escherichia coli genomic dna. (27.0 -27.4 min).) (le:9274) (re:10356) (di:direct) D90756 D90756 g1651601 Escherichia coli 562 -11533593 223420 prfa peptide chain release factor 1 rf-1 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #248) (db:genpept-bct1) (de:escherichia coli genomic dna (27.2-27.6 min).) (le:136) (re:1218) (di:direct) D90757 D90757 g1651609 Escherichia coli 562 -11533593 7500889654 prfa peptide chain release factor rf-1 (fn:factor; proteins - translation and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 109 of 400 of the completegenome.) (nt:o360; 99 pct identical to rf1\_ecoli sw: p07011) (le:8706) (re:9788) (di:direct) AE000219 AE000219 g1787462 Escherichia coli 562 -11533593 5000690814 prfa peptide chain release factor 1 rf-1 . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #247) (db:genpept) (de:escherichia coli genomic dna. (27.1 - 27.5 min).) (nt:orf\_id:o248#1; similar to swissprot accession) (le:9274) (re:10356) (di:direct) D90756 D90756 g1651601 Escherichia coli 562 -11533593 7502851944 prfa peptide chain release factor 1 rf-1 . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #248) (db:genpept) (de:escherichia coli genomic dna. (27.3 - 27.7 min).) (nt:orf\_id:o248#1; similar to swissprot accession) (le:136) (re:1218) (di:direct) D90757 D90757 g1651609 Escherichia coli 562 -11533593

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833756	8780	30936	558	185

Description

GTC ORF with score 116 to: (sr:homo sapiens male adult liver cdna to mrna) (db:genpept-pri2) (ec:2.7.1.1) (de:human liver glucokinase (atp:d-hexose 6-phosphotransferase) mrna,complete cds.) (nt:liver isoform, minor; atp:d-hexose) (le:286) (re:1680) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833757	8781	30937	1314	437

Description

6500729736 infc:fit:b1718 initiation factor if-3:translation initiation factor if-3 (gtcfc:10.7) (keggfc:14.2) (rileyfc:3.1.8) (db:gtc-escherichia coli) b1718 b1718 Escherichia coli 562 -11533594 78893 infc:fit (de:translation initiation factor if-3) (db:swissprot) IF3\_ECOLI P02999 ESCHERICHIA COLI 562 -11533594 131258 infc translation initiation factor if-3 (cl:translation initiation factor if-3) (db:pir1.dat) (mp:38 min) FIEC3 S13748 Escherichia coli 562 -11533594 224164 infc:fit initiation factor if-3. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #322(38.4-38.8 min.)) (nt:orf\_id:o322#18; similar to (swissprot accession) (le:16841) (re:17383) (di:complement) D90813 D90813 g1742797 Escherichia coli 562 -11533594 224176 infc:fit initiation factor if-3. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #323(38.6-39.0 min.)) (nt:orf\_id:o322#18; similar to (swissprot accession) (le:9681) (re:10223) (di:complement) D90814 D90814 g1742810 Escherichia coli 562 -11533594 300833 (db:genpept-bct1) (de:e.coli thrs, infc, rplt, phes, phet and hima genes encodingthreonyl-trna synthetase, initiation factor if3, ribosomal proteinl20, phenylalanyl-trna synthetase and the alpha-subunit of the hostintegration factor.) (nt:initiation fa... ECTHRINF V00291 g43067 Escherichia coli 562 -11533594 238349 infc protein chain initiation factor if-3 (fn:factor; proteins - translation and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 157 of 400 of the completegenome.) (nt:f180; 99 pct identical to if3\_ecoli sw: p02999;) (le:79) (re:621) (di:complement) AE000267 AE000267 g1788012 Escherichia coli 562 -11533594 5000690815 (de:(ecoli\_1675) (pn:protein chain initiation factor if-3) (gn:infc) (gtcfc:10.7) (ec:) (if3\_ecoli) (keggfc:11.2) (rileyfc:3.1.8) (db:gtc-escherichia coli)) ECOLI\_1675 ECOLI\_1675 Escherichia coli 562 10021228

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833765	8782	30938	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833770	8783	30939	468	155

Description

6500729737 pcm:b2743 l-isoaspartyl protein carboxyl methyltransferase type ii:protein-l-isoaspartate o-methyltransferase:protein-beta-aspartate methyltransferase:pimt:protein l-isoaspartyl methyltransferase:l-isoaspartyl protein carboxyl methyltransferase (gtcfc:10.7) (ec:2.1.1.77) (keggfc:14.1) (rileyfc:3.1.8) (db:gtc-escherichia coli) b2743 b2743 Escherichia coli 562 -11533595 164423 pcm protein-l-isoaspartate d-aspartate o-methyltransferase:type ii:l-isoaspartyl protein carboxyl methyltransferase (cl:escherichia coli protein-l-isoaspartate (d-aspartate) o-methyltransferase type ii:bioc homology) (ec:2.1.1.77) (db:pir2.dat) (mp:59 min) JH0242 JH0242 Escherichia coli 562 -11533595 239317 pcm l-isoaspartyl protein carboxyl (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (ec:2.1.1.77) (de:escherichia coli l-isoaspartyl protein carboxyl methyltransferasetype ii (pcm) gene,complete cds.) (le:349) (re:975) (di:direct) ECOPCM M63493 g147115 Escherichia coli 562 -11533595 7500960434 pcm l-isoaspartyl protein carboxyl methyltransferase (db:genpept-bct1) (ec:2.1.1.77) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg site no. 33221) (le:41198) (re:41824) (di:complement) ECU29579 U29579 g882636 Escherichia coli 562 -11533595 235363 pcm l-isoaspartate protein carboxylmethyltransferase (fn:enzyme; proteins - translation and) (db:genpept-bct2) (ec:2.1.1.77) (de:escherichia coli k-12 mg1655 section 248 of 400 of the completegenome.) (nt:f208; 100 pct identical to pimt\_ecoli sw: p24206) (le:3867) (re:4493) (di:complement) AE000358 AE000358 g1789100 Escherichia coli 562 -11533595 5000690816 (de:(ecoli\_2672) (pn:l-isoaspartate protein carboxylmethyltransferase type ii) (gn:pcm) (gtcfc:10.7) (ec:2.1.1.77) (pimt\_ecoli) (keggfc:11.1) (rileyfc:3.1.8) (db:gtc-escherichia coli)) ECOLI\_2672 ECOLI\_2672 Escherichia coli 562 10087311



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833787	8784	30940	459	152

Description

6500729738 iap:b2753 iap:alkaline phosphatase isozyme conversion protein precursor (gtcfc:10.7) (ec:3.4.11.-) (keggfc:14.1) (rileyfc:3.1.8) (db:gtc-escherichia coli) b2753 b2753 Escherichia coli 562 -11533596 78582 iap (ec:3.4.11.-) (de:(ec 3.4.11.-)) (db:swissprot) IAP\_ECOLI P10423 ESCHERICHIA COLI 562 -11533596 124729 iap alkaline phosphatase isozyme conversion protein:precursor (cl:alkaline phosphatase isozyme conversion protein) (ec:3.4.11.-) (db:pir1.dat) (mp:59 min) KZEC A28382 Escherichia coli 562 -11533596 239327 (sr:e.coli dna, clone psn143) (db:genpept-bct1) (de:e.coli iap gene encoding potential aminopeptidase, complete cds.) (nt:put. aminopeptidase; putative) (le:332) (re:1369) (di:direct) ECOIAP M18270 g146430 Escherichia coli 562 -11533596 7500883780 iap (fn:alkaline phosphatase isozyme conversion) (db:genpept-bct1) (ec:3.4.11.-) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg site no. 616) (le:48884) (re:49921) (di:direct) ECU29579 U29579 g882646 Escherichia coli 562 -11533596 234830 iap alkaline phosphatase isozyme conversion (fn:enzyme; proteins - translation and) (db:genpept-bct2) (ec:3.4.11.-) (de:escherichia coli k-12 mg1655 section 249 of 400 of the completegenome.) (nt:o345; 100 pct identical to iap\_ecoli sw: p10423; cg) (le:156) (re:1193) (di:direct) AE000359 AE000359 g1789111 Escherichia coli 562 -11533596 5000690817 (de:(ecoli\_2682) (pn:alkaline phosphatase isozyme conversion, aminopeptidase) (gn:iap) (gtcfc:10.7) (ec:3.4.11.-) (iap\_ecoli) (keggfc:11.1) (rileyfc:3.1.8) (db:gtc-escherichia coli)) ECOLI\_2682 ECOLI\_2682 Escherichia coli 562 10020921

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833807	8785	30941	1491	496

Description

6500729739 prfb:supk:b2891 peptide chain release factor 2:rf-2 (gtcfc:10.7) (keggfc:14.2) (rileyfc:3.1.8) (db:gtc-escherichia coli) b2891 b2891 Escherichia coli 562 -11533597 94097 prfb:supk (de:peptide chain release factor 2 (rf-2)) (db:swissprot) RF2\_ECOLI P07012 ESCHERICHIA COLI 562 -11533597 7000686309 prfb translation releasing factor rf-2:peptide chain release factor 2 (cl:translation releasing factor) (db:pir1.dat) (mp:62 min) FCECR2 C65073 Escherichia coli 562 -11533597 7500889660 prfb peptide chain release factor rf-2 (fn:factor; proteins - translation and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 262 of 400 of the completegenome.) (le:10973:11997) (re:11995:12071) (di:complementjoin) AE000372 AE000372 g2367172 Escherichia coli 562 -11533597

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833829	8786	30942	933	310

Description

6500729740 glne:b3053 adenylyl-transferase:glutamate-ammonia-ligase  
adenylyltransferase:glutamine-synthetase adenylyltransferase:atase  
(gtcfc:10.7) (ec:2.7.7.42) (keggfc:14.1) (rileyfc:3.1.8) (db:gtc-escherichia  
coli) b3053 b3053 Escherichia coli 562 -11533598 73985 glne (ec:2.7.7.42)  
(de:synthetase adenylyltransferase) (atase)) (db:swissprot) GLNE\_ECOLI  
P30870 ESCHERICHIA COLI 562 -11533598 7000685409 glne  
glutamate--ammonia-ligase adenylyltransferase,) (ec:2.7.7.42) (db:pir2.dat)  
C65093 C65093 Escherichia coli 562 -11533598 7500882471 glne adenylylating  
enzyme for glutamine synthetase (fn:enzyme; proteins - translation and)  
(db:genpept-bct2) (ec:2.7.7.42) (de:escherichia coli k-12 mg1655 section 277  
of 400 of the completegenome.) (nt:f946; 99 pct identical (1 gap) to  
glne\_ecoli) (le:1721) (re:4561) (di:complement) AE000387 AE000387 g1789433  
Escherichia coli 562 -11533598 5000690819 (de:(ecoli\_2976)  
(pn:adenylylating enzyme for glutamine synthetase,) (gn:glne) (gtcfc:10.7)  
(ec:2.7.7.42) (glne\_ecoli) (keggfc:11.1) (rileyfc:3.1.8) (db:gtc-escherichia  
coli)) ECOLI\_2976 ECOLI\_2976 Escherichia coli 562 10123962

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833830	8787	30943	246	81

# Description

6500729741 infb:ssyg:b3168 protein chain initiation factor 2:translation initiation factor if-2 (gtcfc:10.7) (keggfc:14.2) (rileyfc:3.1.8) (db:gtc-escherichia coli) b3168 b3168 Escherichia coli 562 -11533599 78880 infb:ssyg (de:translation initiation factor if-2) (db:swissprot) IF2\_ECOLI P02995 ESCHERICHIA COLI 562 -11533599 7000685609 infb translation initiation factor if-2 (cl:translation initiation factor if-2:translation elongation factor tu homology) (db:pirl.dat) (mp:69 min) FIEC2 D65107 Escherichia coli 562 -11533599 236407 infb initiation factor if2-alpha (fn:translation initiation factor) (db:genpept-bct1) (de:escherichia coli (strain ecoau9301) infb gene encodingtranslational initiation factor if2.) (le:1) (re:2673) (di:direct) ECAJ2537 AJ002537 g2597861 Escherichia coli 562 -11533599 304595 infb initiation factor if2-alpha (fn:translation initiation factor) (db:genpept-bct1) (de:escherichia coli (strain ecoau9308) infb gene encodingtranslational initiation factor if2.) (le:1) (re:2673) (di:direct) ECAJ2542 AJ002542 g2597881 Escherichia coli 562 -11533599 5500684575 (db:genpept-bct1) (de:e.coli nusa operon including genes for met-trna-f2 (mety), 15 kdprotein, nusa protein (nusa), and initiation factor if2 (infb).) (nt:initiation factor if2-alpha (infb)) (le:2362) (re:5034) (di:direct) ECNUSA2 X00513 g42145 Escherichia coli 562 -11533599 5500684576 infb protein chain initiation factor 2 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 597; alternate name ssyg) (le:94094) (re:96766) (di:complement) ECOUW67 U18997 g606108 Escherichia coli 562 -11533599 233534 infb protein chain initiation factor if-2 (fn:factor; proteins - translation and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 287 of 400 of the completegenome.) (nt:f890; cg site no. 597; alternate name ssyg; 100 pct) (le:9965) (re:12637) (di:complement) AE000397 AE000397 g1789559 Escherichia coli 562 -11533599 5000690820 infb initiation factor if2-alpha (fn:translation initiation factor) (db:genpept) (de:escherichia coli (strain ecoau9301) infb gene encodingtranslational initiation factor if2.) (le:1) (re:2673) (di:direct) ECAJ2537 AJ002537 g2597861 Escherichia coli 562 -11533599 7502851945 infb initiation factor if2-alpha (fn:translation initiation factor) (db:genpept) (de:escherichia coli (strain ecoau9308) infb gene encodingtranslational initiation factor if2.) (le:1) (re:2673) (di:direct) ECAJ2542 AJ002542 g2597881 Escherichia coli 562 -11533599

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833833	8788	30944	549	182

Description

5000690821 grea (gtcfc:10.7) (keggfc:14.2) (rileyfc:3.1.8)  
(db:gtc-escherichia coli) b3181 b3181 Escherichia coli 562 -11533600  
7000690900 grea transcription elongation factor grea:suppressor protein  
grea (cl:transcription elongation factor greb) (db:pir2.dat) G65108 G65108  
Escherichia coli 562 -11533600 7500960466 grea (db:genpept-bct1)  
(de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.)  
(le:108991) (re:109452) (di:complement) ECOUW67 U18997 g606119 Escherichia  
coli 562 -11533600 236418 grea transcription elongation factor:cleaves 3  
(fn:regulator; proteins - translation and) (db:genpept-bct2) (de:escherichia  
coli k-12 mg1655 section 288 of 400 of the completegenome.) (nt:f153; this  
153 aa orf is 100 pct identical to) (le:10100) (re:10561) (di:complement)  
AE000398 AE000398 g1789571 Escherichia coli 562 -11533600 6500729742 grea  
(gtcfc:10.7) (keggfc:14.2) (rileyfc:3.1.8) (db:gtc-escherichia coli) b3181  
b3181 Escherichia coli 562 -11533600

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833834	8789	30945	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833835	8790	30946	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833843	8791	30947	504	167

Description

6500729743 tufa:b3339 elongation factor tu:ef-tu:p-43 (gtcfc:10.7) (keggfc:14.2) (rileyfc:3.1.8) (db:gtc-escherichia coli) b3339 b3339 Escherichia coli 562 -11533601 131219 tufa:strd translation elongation factor ef-tu.a (cl:translation elongation factor tu:translation elongation factor tu homology) (db:pir1.dat) (mp:74 min) EFECTA A91475 Escherichia coli 562 -11533601 236572 tufa elongation factor tu (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli str operon with fusa and tufa genes coding for elongationfactors g and tu.) (nt:gtg start codon) (le:140) (re:1324) (di:direct) ECOSTR3 J01690 g147897 Escherichia coli 562 -11533601 7500953626 tufa (fn:protein chain elongation factor ef-tu) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 61) (le:250893) (re:252077) (di:complement) ECOUW67 U18997 g606273 Escherichia coli 562 -11533601 236050 tufa protein chain elongation factor ef-tu duplicate (fn:factor; proteins - translation and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 300 of 400 of the completegenome.) (nt:f394; cg site no. 61; 99 pct identical amino) (le:3414) (re:4598) (di:complement) AE000410 AE000410 g1789737 Escherichia coli 562 -11533601 5000690822 (de:(ecoli\_3257) (pn:protein chain elongation factor ef-tu:duplicate of tufb) (gn:tufa) (gtcfc:10.7) (ec:) (eftu\_ecoli) (keggfc:11.2) (rileyfc:3.1.8) (db:gtc-escherichia coli)) ECOLI\_3257 ECOLI\_3257 Escherichia coli 562 10068059

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833851	8792	30948	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833855	8793	30949	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833888	8794	30950	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833900	8795	30951	582	193

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833919	8796	30952	378	125

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501833920	8797	30953	510	169

Description

6500729744 fusa:fus:far:b3340 fusa:elongation factor g:ef-g (gtcfc:10.7) (keggfc:14.2) (rileyfc:3.1.8) (db:gtc-escherichia coli) b3340 b3340 Escherichia coli 562 -11533602 7000688978 fusa:strc translation elongation factor ef-g:fusa protein (cl:translation elongation factor g:translation elongation factor tu homology) (db:pirl.dat) (mp:73 min) EFECG G65127 Escherichia coli 562 -11533602 236573 (db:genpept-bct1) (de:e.coli fus gene encoding elongation factor g.) (nt:elongation factor g) (le:31) (re:2145) (di:direct) ECFUSG X00415 g41517 Escherichia coli 562 -11533602 7500953627 fusa (fn:protein chain elongation factor ef-g) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 732; alternate name far) (le:252148) (re:254262) (di:complement) ECOUW67 U18997 g606274 Escherichia coli 562 -11533602 232942 fusa gtp-binding protein chain elongation factor (fn:factor; proteins - translation and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 300 of 400 of the completegenome.) (nt:f704; cg site no. 732; alternate name far; 100 pct) (le:4669) (re:6783) (di:complement) AE000410 AE000410 g1789738 Escherichia coli 562 -11533602 5000690823 (de:(ecoli\_3258) (pn:protein chain elongation factor ef-g) (gn:fusa) (gtcfc:10.7) (ec:) (efg\_ecoli) (keggfc:11.2) (rileyfc:3.1.8) (db:gtc-escherichia coli)) ECOLI\_3258 ECOLI\_3258 Escherichia coli 562 10124014

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833925	8798	30954	387	128

Description

6500729745 slyd:b3349 probable fkbp-type peptidyl-prolyl cis-trans isomerase:fkbp-type peptidyl-prolyl cis-trans isomerase  
slyd:ppiase:rotamase:histidine rich protein:whp (gtcfc:10.7) (ec:5.2.1.8) (keggfc:14.1) (rileyfc:3.1.8) (db:gtc-escherichia coli) b3349 b3349  
Escherichia coli 562 -11533603 235994 slyd (ec:5.2.1.8) (de:(ppiase) (rotamase) (histidine rich protein) (whp)) (db:swissprot) SLYD\_ECOLI P30856  
ESCHERICHIA COLI 562 -11533603 164061 slyd probable fkbp-type peptidyl-prolyl cis-trans isomerase slyd:histidine-rich protein:metal-binding protein whp:slyd protein (db:pir2.dat) A49987 A49987  
Escherichia coli 562 -11533603 5000690824 histidine rich protein (fn:the protein binds ni2+ and zn2+ with high) (db:genpept-bct1) (de:e.coli gene for histidine rich protein.) (nt:the sequence 186..890 has been determined from 4) (le:216) (re:806) (di:direct) ECHISRP Z21496 g394720 Escherichia coli 562 -11533603 235997 slyd (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli slyd gene, complete cds.) (nt:sensitivity to lysis gene) (le:337) (re:927) (di:complement) ECOSLYDX L13261 g475995 Escherichia coli 562 -11533603 236582 histidine rich protein (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf\_f196; hisrp) (le:258655) (re:259245) (di:complement) ECOUW67 U18997 g606283 Escherichia coli 562 -11533603 233108 slyd fkbp-type peptidyl-prolyl cis-trans isomerase (fn:enzyme; proteins - translation and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 301 of 400 of the completegenome.) (nt:f196; 100 pct identical amino acid sequence and) (le:408) (re:998) (di:complement) AE000411 AE000411 g1789748 Escherichia coli 562 -11533603 7500891708 slyd (sr:escherichia coli (strain cs109) dna) (db:genpept-bct2) (de:escherichia coli (slyd) gene, complete cds, (fkpa) gene, completecds.) (le:51) (re:641) (di:direct) ECOSLYD L28082 g862299 Escherichia coli 562 -11533603 98639 slyd (ec:5.2.1.8) (de:(ppiase) (rotamase) (histidine rich protein) (whp)) (db:swissprot) SLYD\_ECOLI P30856  
ESCHERICHIA COLI 562 -11533603

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833951	8799	30955	702	234
<u>Description</u>				
6500729746 ppia:rota:rot:b3363 peptidyl-prolyl cis-trans isomerase a:peptidyl-prolyl cis-trans isomerase a precursor:ppiase a:rotamase a:cyclophilin a (gtcfc:10.7) (ec:5.2.1.8) (keggfc:14.1) (rileyfc:3.1.8) (db:gtc-escherichia coli) b3363 b3363 Escherichia coli 562 -11533604 67583 ppia:rota:rot (ec:5.2.1.8) (de:a) (rotamase a) (cyclophilin a)) (db:swissprot) CYPH_ECOLI P20752 ESCHERICHIA COLI 562 -11533604 125766 ppia peptidylprolyl isomerase:a precursor:cyclophilin a:cyclosporin a-binding protein a (cl:peptidylprolyl isomerase) (ec:5.2.1.8) (db:pir1.dat) (mp:74 min) CSECA A37964 Escherichia coli 562 -11533604 234342 ppia peptidyl-prolyl cis-trans isomerase a (sr:e.coli dna) (db:genpept-bct1) (de:e.coli peptidyl-prolyl cis-trans isomerase a (ppia) and fic genes,complete cds and 3' end.) (le:194) (re:766) (di:direct) ECOAPPPIA M55429 g145287 Escherichia coli 562 -11533604 236596 (sr:e.coli (strain k12) dna) (db:genpept-bct1) (de:e.coli cell division protein (fic), and orf190 genes, complete cds,and para-aminobenzoate (paba) and orf77 genes, 5' end.) (nt:orf190) (le:589) (re:1161) (di:direct) ECOFIC1 M28363 g145954 Escherichia coli 562 -11533604 7500879886 ppia peptidyl-prolyl cis-trans isomerase a (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (le:272472) (re:273044) (di:complement) ECOUW67 U18997 g606297 Escherichia coli 562 -11533604 233810 ppia peptidyl-prolyl cis-trans isomerase a rotamase (fn:enzyme; proteins - translation and) (db:genpept-bct2) (ec:5.2.1.8) (de:escherichia coli k-12 mg1655 section 302 of 400 of the completegenome.) (nt:f190; 100 pct identical amino acid sequence and) (le:2829) (re:3401) (di:complement) AE000412 AE000412 g1789763 Escherichia coli 562 -11533604 5000690825 (de:(ecoli_3281) (pn:peptidyl-prolyl cis-trans isomerase a:rotamase a) (gn:ppia) (gtcfc:10.7) (ec:5.2.1.8) (cyph_ecoli) (keggfc:11.1) (rileyfc:3.1.8) (db:gtc-escherichia coli)) ECOLI_3281 ECOLI_3281 Escherichia coli 562 10010181				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833956	8800	30956	600	199

Description

6500729747 selb (gtcfc:10.7) (keggfc:14.2) (rileyfc:3.1.8)  
(db:gtc-escherichia coli) b3590 b3590 Escherichia coli 562 -11533605 305568  
selb:fdha (de:selenocysteine-specific elongation factor (selb translation  
factor)) (db:swissprot) SELB\_ECOLI P14081 ESCHERICHIA COLI 562 -11533605  
131235 selb translation elongation factor ef-selb (cl:translation  
elongation factor selb:translation elongation factor tu homology)  
(db:pirl.dat) EFECSEB JV0050 Escherichia coli 562 -11533605 7502851946  
(db:genpept-bct1) (de:e.coli selb gene for selb translation factor.) (nt:sel  
b (aa 1-614)) (le:51) (re:1895) (di:direct) ECSELB X16644 g42937 Escherichia  
coli 562 -11533605 238230 selb selenocysteiny1-trna-specific translation  
(fn:factor; proteins - translation and) (db:genpept-bct2) (de:escherichia  
coli k-12 mg1655 section 326 of 400 of the completegenome.) (nt:f614;  
alternate gene name fdha; cg site no.) (le:7090) (re:8934) (di:complement)  
AE000436 AE000436 g2367247 Escherichia coli 562 -11533605 98383 selb:fdha  
(de:selenocysteine-specific elongation factor (selb translation factor))  
(db:swissprot) SELB\_ECOLI P14081 ESCHERICHIA COLI 562 -11533605

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501833958	8801	30957	894	298

#### Description

6500729748 dsba:ppfa:dsf:b3860 dsba:thiol:disulfide interchange protein dsba precursor (gtcfc:10.7) (keggfc:14.2) (rileyfc:3.1.8) (db:gtc-escherichia coli) b3860 b3860 Escherichia coli 562 -11533606 304558 dsba:ppfa:dsf (de:thiol:disulfide interchange protein dsba precursor) (db:swissprot) DSBA\_ECOLI P24991 ESCHERICHIA COLI 562 -11533606 125828 dsba:ppfa protein disulfide-isomerase:dsba precursor:thiol:disulfide interchange protein dsba (cl:protein disulfide-isomerase dsba:thioredoxin homology) (ec:5.3.4.1) (db:pir1.dat) (mp:87.35) A39292 A39292 Escherichia coli 562 -11533606 325694 dsba (db:genpept-bct1) (de:e.coli dsba gene, orfa and orfb.) (le:2094) (re:2720) (di:direct) ECDSBAAB X80762 g762928 Escherichia coli 562 -11533606 237080 (fn:required for disulfide bond formation in vivo) (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli protein required for disulfide bond formation in vivo gene,complete cds.) (nt:putative) (le:16) (re:642) (di:direct) ECODSF M77746 g145813 Escherichia coli 562 -11533606 237868 dsba (fn:disulphide bond formation in vivo) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:5059) (re:5685) (di:direct) ECOUW87 L19201 g304966 Escherichia coli 562 -11533606 5000690827 ppfa ppfa protein (db:genpept-bct1) (de:e.coli ppfa gene.) (le:933) (re:1559) (di:direct) ECPPFA X63186 g42479 Escherichia coli 562 -11533606 232706 dsba protein disulfide isomerase i:essential for (fn:enzyme; proteins - translation and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 351 of 400 of the completegenome.) (nt:o208; 100 pct identical amino acid sequence and) (le:6018) (re:6644) (di:direct) AE000461 AE000461 g1790291 Escherichia coli 562 -11533606 7502851947 pdi peptid pdi (db:genpept-pat) (de:ompa and rbi genes.) (le:1789) (re:2415) (di:direct) A22413 A22413 g641483 unidentified 32644 -11533606 7502851948 orf (db:genpept-pat) (de:gene encoding for disulfidisomerase.) (le:16) (re:639) (di:direct) A22418 A22418 g641487 unidentified 32644 -11533606 69302 dsba:ppfa:dsf (de:thiol:disulfide interchange protein dsba precursor) (db:swissprot) DSBA\_ECOLI P24991 ESCHERICHIA COLI 562 -11533606 234212 dsba (db:genpept-bct1) (de:e.coli dsba gene, orfa and orfb.) (le:2094) (re:2720) (di:direct) ECDSBAAB X80762 g762928 Escherichia coli 562 -11533606

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501833959	8802	30958	405	134

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501833989	8803	30959	513	170

Description

6500729749 tufb:b3980 elongation factor ef-tu:duplicate gene (gtcfc:10.7) (keggfc:14.2) (rileyfc:3.1.8) (db:gtc-escherichia coli) b3980 b3980 Escherichia coli 562 -11533607 131218 tufb translation elongation factor ef-tu.b (cl:translation elongation factor tu:translation elongation factor tu homology) (db:pir1.dat) (mp:90 min) EFECT A91478 Escherichia coli 562 -11533607 237190 tufb (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli tufb gene coding for elongation factor tu & four trnas.) (nt:elongation factor tu) (le:721) (re:1905) (di:direct) ECOTGTUFB J01717 g147969 Escherichia coli 562 -11533607 238438 tufb translation elongation factor ef-tu (db:genpept-bct1) (de:e.coli tufb gene for translation elongation factor ef-tu.) (le:721) (re:1905) (di:direct) ECTUFBT X57091 g297394 Escherichia coli 562 -11533607 236089 tufb protein chain elongation factor ef-tu duplicate (fn:factor; proteins - translation and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 362 of 400 of the completegenome.) (nt:o394; 100 pct identical to eftu\_ecoli sw: p02990;) (le:908) (re:2092) (di:direct) AE000472 AE000472 g1790412 Escherichia coli 562 -11533607 7500953625 tufb elongation factor ef-tu duplicate gene (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 60) (le:41186) (re:42370) (di:direct) ECOUW89 U00006 g396319 Escherichia coli 562 -11533607 5000690828 (de:(ecoli\_3870) (pn:protein chain elongation factor ef-tu:duplicate of tufa) (gn:tufb) (gtcfc:10.7) (ec:) (eftu\_ecoli) (keggfc:11.2) (rileyfc:3.1.8) (db:gtc-escherichia coli)) ECOLI\_3870 ECOLI\_3870 Escherichia coli 562 10068058

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834002	8804	30960	567	188

Description

6500729750 pmba:tlde:b4235 pmba protein:tlde protein (gtcfc:10.7)  
(keggfc:14.2) (rileyfc:3.1.8) (db:gtc-escherichia coli) b4235 b4235  
Escherichia coli 562 -11533608 7500888186 pmba:tlde (de:pmba protein (tlde  
protein)) (db:swissprot) PMBA\_ECOLI P24231 ESCHERICHIA COLI 562 -11533608  
164345 pmba pmba protein (db:pir2.dat) (mp:96 min) S13730 S13730  
Escherichia coli 562 -11533608 237441 tlde tlde protein (fn:modulator of  
interaction between letd protein) (sr:escherichia coli (strain:k12,  
isolate:kp5254) dna, clone:pkp1838) (db:genpept-bct1) (de:escherichia coli  
dna for tlde protein and 2lk protein, completecds.) (le:857) (re:2209)  
(di:direct) ECOTLDE2 D44452 g1732440 Escherichia coli 562 -11533608 237842  
pmba (fn:involved in production of antibiotic mccb17) (db:genpept-bct1)  
(de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.)  
(le:148788) (re:150140) (di:direct) ECOUW93 U14003 g537077 Escherichia coli  
562 -11533608 5000690829 pmba (db:genpept-bct1) (de:e. coli pmba gene  
involved in mccb17 production.) (nt:pmba is involved in the production of  
antibiotic) (le:210) (re:1562) (di:direct) ECPMBA X54152 g42440 Escherichia  
coli 562 -11533608 236106 pmba maturation of antibiotic mccb17:see tld  
genes (fn:phenotype; proteins - translation and) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 384 of 400 of the completegenome.)  
(nt:o450; 100 pct identical amino acid sequence and) (le:9643) (re:10995)  
(di:direct) AE000494 AE000494 g1790682 Escherichia coli 562 -11533608 90061  
pmba:tlde (de:pmba protein (tlde protein)) (db:swissprot) PMBA\_ECOLI P24231  
ESCHERICHIA COLI 562 -11533608

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834020	8805	30961	675	224

Description

6500729751 prfc:tos:miad:b4375 peptide-chain-release factor 3:peptide chain release factor 3:rf-3 (gtcfc:10.7) (keggfc:14.2) (rileyfc:3.1.8) (db:gtc-escherichia coli) b4375 b4375 Escherichia coli 562 -11533609 164255 prfc:tos peptide-chain-release factor 3:translation termination factor rf-3 (cl:translation elongation factor tu homology) (db:pir2.dat) I59305 I59305 Escherichia coli 562 -11533609 237580 prfc/tos rf-3/tos (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:escherichia coli gene for rf-3/tos, complete cds.) (le:703) (re:2292) (di:direct) ECOPRFC D17724 g409377 Escherichia coli 562 -11533609 7500960408 prfc peptide-chain-release factor 3 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:alternate gene name tos) (le:300245) (re:301834) (di:direct) ECOUW93 U14003 g537215 Escherichia coli 562 -11533609 235549 prfc peptide chain release factor rf-3 (fn:factor; proteins - translation and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 398 of 400 of the completegenome.) (nt:o529; 100 pct identical to rf3\_ecoli sw: p33998;) (le:62) (re:1651) (di:direct) AE000508 AE000508 g1790835 Escherichia coli 562 -11533609 5000690830 (de:(ecoli\_4257) (pn:peptide chain release factor rf-3) (gn:prfc) (gtcfc:10.7) (ec:) (rf3\_ecoli) (keggfc:11.2) (rileyfc:3.1.8) (db:gtc-escherichia coli)) ECOLI\_4257 ECOLI\_4257 Escherichia coli 562 10087248

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834029	8806	30962	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834053	8807	30963	282	93

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834068	8808	30964	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834078	8809	30965	1137	378

Description

6500729752 dkas:b0145 dosage-dependent dnaK suppressor protein:dnaK suppressor protein (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b0145 b0145 Escherichia coli 562 -11533610 68723 dkas (de:dnaK suppressor protein) (db:swissprot) DKSA\_ECOLI P18274 ESCHERICHIA COLI 562 -11533610 162966 dkas dosage-dependent dnaK suppressor protein (db:pir2.dat) S45214 S45214 Escherichia coli 562 -11533610 301615 dkas dosage-dependent dnaK suppressor protein (sr:escherichia coli (sub\_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0 min).) (le:48745) (re:49200) (di:complement) ECO82K D26562 g473804 Escherichia coli 562 -11533610 233677 dkas dnaK suppressor protein (fn:phenotype; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 13 of 400 of the completegenome.) (nt:f151; 100 pct identical to dkas\_ecoli sw: p18274;) (le:10521) (re:10976) (di:complement) AE000123 AE000123 g1786338 Escherichia coli 562 -11533610 5000690831 (de:(ecoli\_145) (pn:dnaK suppressor protein) (gn:dkas) (gtcfc:10.8) (ec:)(dkas\_ecoli) (keggfc:11.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_145 ECOLI\_145 Escherichia coli 562 10011308

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834094	8810	30966	384	127

Description

6500729753 pric:b0467 primosomal replication protein n (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b0467 b0467 Escherichia coli 562 -11533611 164365 pric primosomal replication protein n precursor:primosomal replication protein n (db:pir2.dat) JQ1149 JQ1149 Escherichia coli 562 -11533611 240242 pric primosomal replication protein n gtg start (sr:e. coli (strain k12; cell line hms-83) genomic dna, clon) (db:genpept-bct1) (de:e. coli primosomal replication protein n' (pric) gene.) (le:416) (re:943) (di:direct) ECOPRIC D13958 g912452 Escherichia coli 562 -11533611 7500960419 prid primosomal replication protein n (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:69733) (re:70260) (di:complement) ECU82664 U82664 g1773149 Escherichia coli 562 -11533611 235553 pric primosomal replication protein n (fn:factor; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 43 of 400 of the completegenome.) (nt:f175; 100 pct identical to pric\_ecoli sw: p23862) (le:311) (re:838) (di:complement) AE000153 AE000153 g1786673 Escherichia coli 562 -11533611 5000690832 (de:(ecoli\_450) (pn:primosomal replication protein n") (gn:pric) (gtcfc:10.8) (ec:)(pric\_ecoli) (keggfc:11.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_450 ECOLI\_450 Escherichia coli 562 10087292

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834095	8811	30967	948	315

Description

6500729754 seqa:b0687 seqa protein (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b0687 b0687 Escherichia coli 562 -11533612 98407 seqa (de:seqa protein) (db:swissprot) SEQA\_ECOLI P36658 ESCHERICHIA COLI 562 -11533612 164604 seqa seqa protein (db:pir2.dat) A54296 A54296 Escherichia coli 562 -11533612 223148 seqa seqa protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #172) (db:genpept-bct1) (de:escherichia coli genomic dna. (15.0 - 15.4 min).) (le:12814) (re:13359) (di:direct) D90707 D90707 g1651292 Escherichia coli 562 -11533612 223152 seqa seqa protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #173) (db:genpept-bct1) (de:escherichia coli genomic dna. (15.3 - 15.6 min).) (le:2609) (re:3154) (di:direct) D90708 D90708 g1651297 Escherichia coli 562 -11533612 7500891523 seqa seqa (fn:negative regulator of replication initiation) (db:genpept-bct1) (de:escherichia coli k12 negative regulator of replication initiation(seqa) gene, complete cds.) (le:1661) (re:2206) (di:direct) ECU07651 U07651 g464013 Escherichia coli 562 -11533612 238508 seqa negative modulator of initiation of replication (fn:regulator; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 62 of 400 of the completegenome.) (nt:o181; 100 pct identical to seqa\_ecoli sw: p36658) (le:4972) (re:5517) (di:direct) AE000172 AE000172 g1786903 Escherichia coli 562 -11533612 5000690833 seqa seqa protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #172) (db:genpept) (de:escherichia coli genomic dna. (15.1 - 15.5 min).) (nt:orf\_id:o173#5; similar to pir accession number) (le:12814) (re:13359) (di:direct) D90707 D90707 g1651292 Escherichia coli 562 -11533612 7502851949 seqa seqa protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #173) (db:genpept) (de:escherichia coli genomic dna. (15.3 - 15.7 min).) (nt:orf\_id:o173#5; similar to pir accession number) (le:2609) (re:3154) (di:direct) D90708 D90708 g1651297 Escherichia coli 562 -11533612

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834107	8812	30968	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834112	8813	30969	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834129	8814	30970	1266	421

Description

GTC ORF with score 177 to: (sr:thale cress) (db:genpept-pln2)  
 (de:arabidopsis thaliana chromosome v bac t19k24 genomic sequence, complete  
 sequence.) (nt:unknown protein) (le:78837:79069:79265)  
 (re:78971:79182:79367) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834131	8815	30971	495	164

Description

6500729755 phrb:phr:b0708 deoxyribodipyrimidine photolyase:dna  
 photolyase:photoreactivating enzyme (gtcfc:10.8) (ec:4.1.99.3) (keggfc:14.1)  
 (rileyfc:3.1.7) (db:gtc-escherichia coli) b0708 b0708 Escherichia coli 562  
 -11533613 89671 phrb:phr (ec:4.1.99.3) (de:(photoreactivating enzyme))  
 (db:swissprot) PHR\_ECOLI P00914 ESCHERICHIA COLI 562 -11533613 125596  
 phrb:phr deoxyribodipyrimidine photo-lyase::dna photolyase:photoreactivating  
 enzyme (cl:deoxyribodipyrimidine photo-lyase) (ec:4.1.99.3) (db:pir1.dat)  
 (mp:16 min) WZEC D A01137 Escherichia coli 562 -11533613 223165 phr  
 deoxyribodipyrimidine photolyase (sr:escherichia coli(strain:k12) dna,  
 clone:kohara clone #174) (db:genpept-bct1) (de:escherichia coli genomic dna.  
 (15.6 - 15.9 min).) (le:12693) (re:14111) (di:direct) D90709 D90709 g1651311  
 Escherichia coli 562 -11533613 223166 phr deoxyribodipyrimidine photolyase  
 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #175)  
 (db:genpept-bct1) (de:escherichia coli genomic dna. (15.8 - 16.2 min).)  
 (le:2231) (re:3649) (di:direct) D90710 D90710 g1651313 Escherichia coli 562  
 -11533613 7500888066 phr (sr:e.coli k12 genomic dna, plasmid pms2)  
 (db:genpept-bct1) (de:e.coli phr gene coding for deoxyribopyrimidine  
 photolyase.) (nt:deoxyribopyrimidine photolyase) (le:544) (re:1962)  
 (di:direct) ECOPHRORF K01299 g147268 Escherichia coli 562 -11533613 235491  
 phrb deoxyribodipyrimidine photolyase (fn:enzyme; dna - replication,  
 repair,) (db:genpept-bct2) (ec:4.1.99.3) (de:escherichia coli k-12 mg1655  
 section 64 of 400 of the completegenome.) (nt:o472; 100 pct identical to  
 phr\_ecoli sw: p00914;) (le:5376) (re:6794) (di:direct) AE000174 AE000174  
 g1786926 Escherichia coli 562 -11533613 5000690834 phr  
 deoxyribodipyrimidine photolyase ec 4.1.99.3 (sr:escherichia  
 coli(strain:k12) dna, clone:kohara clone #174) (db:genpept) (de:escherichia  
 coli genomic dna. (15.7 - 16.0 min).) (nt:orf\_id:o175#3; similar to  
 swissprot accession) (le:12693) (re:14111) (di:direct) D90709 D90709  
 g1651311 Escherichia coli 562 -11533613 7502851950 phr  
 deoxyribodipyrimidine photolyase ec 4.1.99.3 (sr:escherichia  
 coli(strain:k12) dna, clone:kohara clone #175) (db:genpept) (de:escherichia  
 coli genomic dna. (15.9 - 16.3 min).) (nt:orf\_id:o175#3; similar to  
 swissprot accession) (le:2231) (re:3649) (di:direct) D90710 D90710 g1651313  
 Escherichia coli 562 -11533613



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834164	8816	30972	414	137

Description

6500729756 ding:rarb:b0799 probable atp-dependent helicase  
ding:dna-damage-inducible protein g (gtcfc:10.8) (keggfc:14.2)  
(rileyfc:3.1.7) (db:gtc-escherichia coli) b0799 b0799 Escherichia coli 562  
-11533614 68664 ding:rarb (de:probable atp-dependent helicase ding  
(dna-damage-inducible protein g)) (db:swissprot) DING\_ECOLI P27296  
ESCHERICHIA COLI 562 -11533614 7000685053 ding probable atp-dependent  
helicase ding:dna-damage-inducible protein g (cl:unassigned dead/h box  
helicases:dead/h box helicase homology) (db:pir2.dat) G64816 G64816  
Escherichia coli 562 -11533614 223208 ding probable atp-dependent helicase  
ding (sr:escherichia coli(strain:k12) dna, clone:kohara clone #204)  
(db:genpept-bct1) (de:escherichia coli genomic dna.(17.8 - 18.1 min).)  
(le:4372) (re:6522) (di:direct) D90717 D90717 g1651361 Escherichia coli 562  
-11533614 7500880325 ding or::rarb dna helicase (db:genpept-bct1)  
(de:escherichia coli putative atp-dependent rna helicase (rhle),putative dna  
helicase (ding), ybia, ybib, and ybic genes, completecds.) (nt:swissprot  
number accession p27296; uncertain) (le:2737) (re:4887) (di:direct) ECORHLEA  
L02123 g508648 Escherichia coli 562 -11533614 235789 ding probably  
atp-dependent helicase (fn:putative enzyme; dna - replication, repair,)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 72 of 400 of the  
completegenome.) (nt:o716; 100 pct identical to ding\_ecoli sw: p27296)  
(le:2337) (re:4487) (di:direct) AE000182 AE000182 g1787018 Escherichia coli  
562 -11533614 5000690835 ding probable atp-dependent helicase ding  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #204) (db:genpept)  
(de:escherichia coli genomic dna. (17.9 - 18.2 min).) (nt:orf\_id:o204#5;  
similar to swissprot accession) (le:4372) (re:6522) (di:direct) D90717  
D90717 g1651361 Escherichia coli 562 -11533614

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834165	8817	30973	318	105

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834167	8818	30974	357	118

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834169	8819	30975	342	113

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834179	8820	30976	1380	460

Description

6500729757 himd:hip:b0912 integration host factor beta-subunit:ihf-beta (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b0912 b0912 Escherichia coli 562 -11533615 7500883985 himd:hip (de:integration host factor beta-subunit (ihf-beta)) (db:swissprot) IHFB\_ECOLI P08756 ESCHERICHIA COLI 562 -11533615 7000685617 himd:hip integration host factor beta chain:ihf-beta (cl:bacterial dna-binding protein) (db:pir1.dat) (mp:21 min) IQECAB G64830 Escherichia coli 562 -11533615 223276 himd integration host factor beta-subunit (sr:escherichia coli(strain:k12) dna, clone:kohara clone #217) (db:genpept-bct1) (de:escherichia coli genomic dna. (20.4 - 20.8 min).) (le:11988) (re:12272) (di:direct) D90729 D90729 g1651440 Escherichia coli 562 -11533615 5000690836 ihf aa 1-93 (db:genpept-bct1) (de:e-coli hip gene for integration host factor beta-subunit (ihfbeta).) (le:190) (re:474) (di:direct) ECHIP X04864 g414749 Escherichia coli 562 -11533615 233089 himd integration host factor ihf:beta subunit (fn:factor; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 83 of 400 of the completegenome.) (nt:o94; 100 pct identical to ihfb\_ecoli sw: p08756) (le:7157) (re:7441) (di:direct) AE000193 AE000193 g1787141 Escherichia coli 562 -11533615 7502851951 himd integration host factor beta-subunit (sr:escherichia coli(strain:k12) dna, clone:kohara clone #217) (db:genpept) (de:escherichia coli genomic dna. (20.5 - 20.9 min).) (nt:orf\_id:o217#9; similar to swissprot accession) (le:11988) (re:12272) (di:direct) D90729 D90729 g1651440 Escherichia coli 562 -11533615 79050 himd:hip (de:integration host factor beta-subunit (ihf-beta)) (db:swissprot) IHFB\_ECOLI P08756 ESCHERICHIA COLI 562 -11533615

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834193	8821	30977	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834204	8822	30978	942	313

Description

6500729758 mfd:b1114 transcription-repair coupling factor:trcf (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b1114 b1114 Escherichia coli 562 -11533616 83620 mfd (de:transcription-repair coupling factor (trcf)) (db:swissprot) MFD\_ECOLI P30958 ESCHERICHIA COLI 562 -11533616 7000685838 mfd:trcf transcription/repair-coupling protein:mutation frequency decline protein (cl:transcription-repair coupling protein:dead/h box helicase homology) (db:pir2.dat) G64855 G64855 Escherichia coli 562 -11533616 223367 mfd transcription-repair coupling protein mfd (sr:escherichia coli(strain:k12) dna, clone:kohara clone #237) (db:genpept-bct1) (de:escherichia coli genomic dna.(24.9 - 25.3 min).) (le:12459) (re:15905) (di:complement) D90746 D90746 g1651547 Escherichia coli 562 -11533616 223368 mfd transcription-repair coupling protein mfd (sr:escherichia coli(strain:k12) dna, clone:kohara clone #238) (db:genpept-bct1) (de:escherichia coli genomic dna.(25.1 - 25.5 min).) (le:2205) (re:5651) (di:complement) D90747 D90747 g1651549 Escherichia coli 562 -11533616 7500885576 mfd transcription-repair coupling factor:mutation (fn:factor; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 101 of 400 of the completegenome.) (nt:f1148; 99 pct identical to mfd\_ecoli sw: p30958) (le:8830) (re:12276) (di:complement) AE000211 AE000211 g1787357 Escherichia coli 562 -11533616 5000690837 mfd transcription-repair coupling protein mfd (sr:escherichia coli(strain:k12) dna, clone:kohara clone #237) (db:genpept) (de:escherichia coli genomic dna. (25.0 - 25.4 min).) (nt:orf\_id:o238#3; similar to pir accession number) (le:12459) (re:15905) (di:complement) D90746 D90746 g1651547 Escherichia coli 562 -11533616 7502851952 mfd transcription-repair coupling protein mfd (sr:escherichia coli(strain:k12) dna, clone:kohara clone #238) (db:genpept) (de:escherichia coli genomic dna. (25.2 - 25.6 min).) (nt:orf\_id:o238#3; similar to pir accession number) (le:2205) (re:5651) (di:complement) D90747 D90747 g1651549 Escherichia coli 562 -11533616

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834209	8823	30979	411	136

Description

6500729759 umud:b1183 umud protein (gtcfc:10.8) (ec:3.4.21.-) (keggfc:14.1) (rileyfc:3.1.7) (db:gtc-escherichia coli) b1183 b1183 Escherichia coli 562 -11533617 103695 umud (ec:3.4.21.-) (de:umud protein,) (db:swissprot) UMUD\_ECOLI P04153 ESCHERICHIA COLI 562 -11533617 131422 umud proteinase umud::umud proprotein (cl:lexa repressor) (ec:3.4.21.-) (db:pir1.dat) (mp:26 min) ZWEC A03551 Escherichia coli 562 -11533617 223395 umud umud protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #243) (db:genpept-bct1) (de:escherichia coli genomic dna. (26.2 - 26.6 min).) (le:12658) (re:13077) (di:direct) D90752 D90752 g1651580 Escherichia coli 562 -11533617 223400 umud umud protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #244) (db:genpept-bct1) (de:escherichia coli genomic dna. (26.4 - 26.7 min).) (le:2513) (re:2932) (di:direct) D90753 D90753 g1651586 Escherichia coli 562 -11533617 236261 umud (sr:escherichia coli (strain k-12) dna, clone ptal00) (db:genpept-bct1) (de:e.coli umu operon: umud and umuc genes encoding reca and lexadependent uv repair enzyme.) (nt:umud protein) (le:450) (re:869) (di:direct) ECOUMUCD M10107 g148125 Escherichia coli 562 -11533617 7500893790 umud (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli umudc operon encoding proteins functional in uv mutagenesis,complete cds.) (le:111) (re:530) (di:direct) ECOUMUDC M13387 g148128 Escherichia coli 562 -11533617 236259 umud sos mutagenesis:error-prone repair:processed (fn:putative enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:3.4.21.-) (de:escherichia coli k-12 mg1655 section 106 of 400 of the completegenome.) (nt:ol39; 100 pct identical to umud\_ecoli sw: p04153) (le:9634) (re:10053) (di:direct) AE000216 AE000216 g1787431 Escherichia coli 562 -11533617 5000690838 umud umud protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #243) (db:genpept) (de:escherichia coli genomic dna. (26.3 - 26.7 min).) (nt:orf\_id:o244#3; similar to pir accession number) (le:12658) (re:13077) (di:direct) D90752 D90752 g1651580 Escherichia coli 562 -11533617 7502851953 umud umud protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #244) (db:genpept) (de:escherichia coli genomic dna. (26.5 - 26.8 min).) (nt:orf\_id:o244#3; similar to pir accession number) (le:2513) (re:2932) (di:direct) D90753 D90753 g1651586 Escherichia coli 562 -11533617

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501834213	8824	30980	924	307

# Description

6500729760 umuc:b1184 umuc protein (gtcfc:10.8) (keggfc:14.2)  
(rileyfc:3.1.7) (db:gtc-escherichia coli) b1184 b1184 Escherichia coli 562  
-11533618 103693 umuc (de:umuc protein) (db:swissprot) UMUC\_ECOLI P04152  
ESCHERICHIA COLI 562 -11533618 7000686888 umuc umuc protein (cl:umuc  
protein) (db:pir1.dat) (mp:26 min) ZWECC E64864 Escherichia coli 562  
-11533618 223396 umuc umuc protein (sr:escherichia coli(strain:k12) dna,  
clone:kohara clone #243) (db:genpept-bct1) (de:escherichia coli genomic dna.  
(26.2 - 26.6 min).) (le:13077) (re:14345) (di:direct) D90752 D90752 g1651581  
Escherichia coli 562 -11533618 223401 umuc umuc protein (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #244) (db:genpept-bct1)  
(de:escherichia coli genomic dna. (26.4 - 26.7 min).) (le:2932) (re:4200)  
(di:direct) D90753 D90753 g1651587 Escherichia coli 562 -11533618  
7500893789 umuc (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli  
umudc operon encoding proteins functional in uv mutagenesis,complete cds.)  
(le:530) (re:1798) (di:direct) ECOUMUDC M13387 g148129 Escherichia coli 562  
-11533618 236262 umuc sos mutagenesis and repair (fn:putative enzyme; dna -  
replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655  
section 106 of 400 of the completegenome.) (nt:o422; 99 pct identical to  
umuc\_ecoli sw: p04152) (le:10053) (re:11321) (di:direct) AE000216 AE000216  
g1787432 Escherichia coli 562 -11533618 5000690839 umuc umuc protein.  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #243) (db:genpept)  
(de:escherichia coli genomic dna. (26.3 - 26.7 min).) (nt:orf\_id:o244#4;  
similar to pir accession number) (le:13077) (re:14345) (di:direct) D90752  
D90752 g1651581 Escherichia coli 562 -11533618 7502851954 umuc umuc  
protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #244)  
(db:genpept) (de:escherichia coli genomic dna. (26.5 - 26.8 min).)  
(nt:orf\_id:o244#4; similar to pir accession number) (le:2932) (re:4200)  
(di:direct) D90753 D90753 g1651587 Escherichia coli 562 -11533618

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501834215	8825	30981	459	152

# Description

6500729761 topa:supx:b1274 dna topoisomerase i:omega protein i:dna topoisomerase i:omega-protein:relaxing enzyme:untwisting enzyme:swivelase (gtcfc:10.8) (ec:5.99.1.2) (keggfc:14.1) (rileyfc:3.1.7) (db:gtc-escherichia coli) b1274 b1274 Escherichia coli 562 -11533619 304637 topa:supx (ec:5.99.1.2) (de:(untwisting enzyme) (swivelase)) (db:swissprot) TOP1\_ECOLI P06612 ESCHERICHIA COLI 562 -11533619 7000686810 topa:supx dna topoisomerase::nicking-closing enzyme:omega-protein:relaxing enzyme:swivelase:type i dna topoisomerase:untwisting enzyme (cl:bacterial type i dna topoisomerase) (ec:5.99.1.2) (db:pir1.dat) (mp:28 min) ISECTP E64875 Escherichia coli 562 -11533619 223485 topa:supx dna topoisomerase i ec 5.99.1.2 w-protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #253(28.4-28.7 min.)) (nt:orf\_id:o253#14; similar to (swissprot accession) (le:13668) (re:16265) (di:direct) D90764 D90764 g1742069 Escherichia coli 562 -11533619 300303 topa:supx dna topoisomerase i ec 5.99.1.2 w-protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #254(28.4-28.9 min.)) (nt:orf\_id:o253#14; similar to (swissprot accession) (le:11174) (re:13771) (di:direct) D90765 D90765 g1742085 Escherichia coli 562 -11533619 300288 (db:genpept-bct1) (de:e.coli topa gene for dna topoisomerase i.) (nt:put. dna topoisomerase i (aa 1-864)) (le:1318) (re:3915) (di:direct) ECTOPA X04475 g415338 Escherichia coli 562 -11533619 238377 topa dna topoisomerase type i:omega protein (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:5.99.1.2) (de:escherichia coli k-12 mg1655 section 115 of 400 of the completegenome.) (nt:o865; 100 pct identical to top1\_ecoli sw: p06612;) (le:4332) (re:6929) (di:direct) AE000225 AE000225 g1787529 Escherichia coli 562 -11533619 101784 topa:supx (ec:5.99.1.2) (de:(untwisting enzyme) (swivelase)) (db:swissprot) TOP1\_ECOLI P06612 ESCHERICHIA COLI 562 -11533619 223500 topa:supx dna topoisomerase i ec 5.99.1.2 w-protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #254(28.4-28.9 min.)) (nt:orf\_id:o253#14; similar to (swissprot accession) (le:11174) (re:13771) (di:direct) D90765 D90765 g1742085 Escherichia coli 562 -11533619 5000690840 (de:(ecoli\_1234) (pn:dna topoisomerase type i, omega protein) (gn:topa) (gtcfc:10.8) (ec:5.99.1.2) (top1\_ecoli) (keggfc:11.1) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_1234 ECOLI\_1234 Escherichia coli 562 10043613

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501834217	8826	30982	423	140

# Description

6500729762 ogt:b1335  
o6-methylguanine-dna-alkyltransferase:methylated-dna--protein-cysteine  
methyltransferase:6-o-methylguanine-dna  
methyltransferase:o-6-methylguanine-dna-alkyltransferase (gtcfc:10.8)  
(ec:2.1.1.63) (keggfc:14.1) (rileyfc:3.1.7) (db:gtc-escherichia coli) b1335  
b1335 Escherichia coli 562 -11533620 87534 ogt (ec:2.1.1.63)  
(de:alkyltransferase)) (db:swissprot) OGT\_ECOLI P09168 ESCHERICHIA COLI 562  
-11533620 7000686037 ogt methylated-dna--protein-cysteine  
s-methyltransferase::o 6 -alkylguanine-dna alkyltransferase:o 6  
-methylguanine-dna alkyltransferase:o-methylguanine-dna methyltransferase  
(cl:methylated-dna--protein-cysteine  
s-methyltransferase:methylated-dna--protein-cysteine s-methyltransferase  
homology) (ec:2.1.1.63) (db:pir1.dat) XUECAD B64883 Escherichia coli 562  
-11533620 223601 ogt methylated-dna--protein-cysteine (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #260(29.8-30.2 min.).)  
(nt:orf\_id:o261#7; similar to (pir accession number) (le:18194) (re:18709)  
(di:complement) D90771 D90771 g1742192 Escherichia coli 562 -11533620  
300384 ogt methylated-dna--protein-cysteine (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #261(30.0-30.3 min.).)  
(nt:orf\_id:o261#7; similar to (pir accession number) (le:8259) (re:8774)  
(di:complement) D90772 D90772 g1742203 Escherichia coli 562 -11533620  
300374 ogt o-6-alkylguanine-dna/cysteine-protein (fn:enzyme; dna -  
replication, repair,) (db:genpept-bct2) (ec:2.1.1.63) (de:escherichia coli  
k-12 mg1655 section 121 of 400 of the completegenome.) (nt:f171; 98 pct  
identical to ogt\_ecoli sw: p09168) (le:7823) (re:8338) (di:complement)  
AE000231 AE000231 g1787596 Escherichia coli 562 -11533620 223611 ogt  
methylated-dna--protein-cysteine (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #261(30.0-30.3 min.).) (nt:orf\_id:o261#7; similar to (pir  
accession number) (le:8259) (re:8774) (di:complement) D90772 D90772 g1742203  
Escherichia coli 562 -11533620 5000690841 (de:(ecoli\_1295)  
(pn:o-6-alkylguanine-dna) (gn:ogt) (gtcfc:10.8) (ec:2.1.1.63) (ogt\_ecoli)  
(keggfc:11.1) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_1295  
ECOLI\_1295 Escherichia coli 562 10119539

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834229	8827	30983	1020	339

Description

6500729763 rect:b1349 rect protein:p33 (gtcfc:10.8) (keggfc:14.2)  
(rileyfc:3.1.7) (db:gtc-escherichia coli) b1349 b1349 Escherichia coli 562  
-11533621 93833 rect (de:rect protein (p33)) (db:swissprot) RECT\_ECOLI  
P33228 ESCHERICHIA COLI 562 -11533621 164461 rect rect protein  
(cl:escherichia coli rect protein) (db:pir2.dat) I69516 I69516 Escherichia  
coli 562 -11533621 223622 rect rect protein p33 . (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #262(30.3-30.5 min.)).)  
(nt:orf\_id:o262#8; similar to (swissprot accession) (le:9783) (re:10592)  
(di:complement) D90773 D90773 g1742215 Escherichia coli 562 -11533621  
300395 rect (fn:dna renaturation and synapsis in recombination)  
(sr:escherichia coli (strain k-12) hfr dna) (db:genpept-bct1)  
(de:escherichia coli exonuclease viii (rece) gene, 3' end, and rectgene,  
complete cds.) (nt:putative) (le:617) (re:1426) (di:direct) ECORECEB L23927  
g397681 Escherichia coli 562 -11533621 235721 rect recombinase:dna  
renaturation (fn:enzyme; dna - replication, repair,) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 122 of 400 of the completegenome.)  
(nt:f269; 100 pct identical to rect\_ecoli sw: p33228;) (le:9354) (re:10163)  
(di:complement) AE000232 AE000232 g1787611 Escherichia coli 562 -11533621  
5000690842 (de:(ecoli\_1309) (pn:recombinase, dna renaturation) (gn:rect)  
(gtcfc:10.8) (ec:) (rect\_ecoli) (keggfc:11.2) (rileyfc:3.1.7)  
(db:gtc-escherichia coli)) ECOLI\_1309 ECOLI\_1309 Escherichia coli 562  
10035824

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834243	8828	30984	309	102

Description

Hypothetical protein



ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501834257	8829	30985	825	274

#### Description

6500729764 tus:tau:b1610 dna replication terminus site-binding protein:dna sequence-specific contrahelicase:dna replication terminus site-binding protein:ter protein:ter binding protein (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b1610 b1610 Escherichia coli 562 -11533622 102731 tus:tau (de:binding protein)) (db:swissprot) TUS\_ECOLI P16525 ESCHERICHIA COLI 562 -11533622 128603 tus:tau terminator sequence-binding protein tus:dna replication terminus site-binding protein:dna replication terminus site-binding protein / dna sequence-specific contrahelicase:tau protein:ter-binding protein (cl:terminator sequence-binding protein tus) (db:pir1.dat) (mp:36 min) DNECTS B32161 Escherichia coli 562 -11533622 224026 tus:tau terminator sequence-binding protein tus (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #312(36.0-36.3 min.)) (nt:orf\_id:o312#10; similar to (pir accession number) (le:11965) (re:12894) (di:direct) D90803 D90803 g1742649 Escherichia coli 562 -11533622 224036 tus:tau terminator sequence-binding protein tus (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #313(36.1-36.4 min.)) (nt:orf\_id:o312#10; similar to (pir accession number) (le:8079) (re:9008) (di:direct) D90804 D90804 g1742660 Escherichia coli 562 -11533622 239583 (sr:escherichia coli(k12; isolate w3110) genomic dna) (db:genpept-bct1) (de:e. coli dna replication terminus site-binding (tau) protein.) (nt:tau protein) (le:109) (re:1038) (di:direct) ECOTAU D90037 g216671 Escherichia coli 562 -11533622 300731 tus tus (sr:escherichia coli strain=k-12) (db:genpept-bct1) (de:escherichia coli response regulator homolog (rsta) gene, and sensorkinase homolog (rstb) gene, complete cds, dna replication terminusbinding protein tus (tus) gene, partial cds.) (nt:dna replicati... ECU41101 U41101 g1079809 Escherichia coli 562 -11533622 236067 tus dna-binding protein:inhibition of replication (fn:factor; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 146 of 400 of the completengenome.) (nt:o309; 100 pct identical to tus\_ecoli sw: p16525; cg) (le:6201) (re:7130) (di:direct) AE000256 AE000256 g1787895 Escherichia coli 562 -11533622 5000690843 (de:(ecoli\_1569) (pn:dna-binding protein; inhibition of replication at ter sites) (gn:tus) (gtcfc:10.8) (ec:) (tus\_ecoli) (keggfc:11.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_1569 ECOLI\_1569 Escherichia coli 562 10044549

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834258	8830	30986	195	64

Description

6500729765 hima:hid:b1712 integration host factor alpha-subunit:ihf-alpha (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b1712 b1712 Escherichia coli 562 -11533623 300828 hima:hid (de:integration host factor alpha-subunit (ihf-alpha)) (db:swissprot) IHFA\_ECOLI P06984 ESCHERICHIA COLI 562 -11533623 128605 hima integration host factor alpha chain (cl:bacterial dna-binding protein) (db:pir1.dat) (mp:38 min) IQECAA C23099 Escherichia coli 562 -11533623 224159 hima:hid integration host factor a-subunit ihf-alpha . (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #322(38.4-38.8 min.)) (nt:orf\_id:o322#13; similar to (swissprot accession) (le:11998) (re:12297) (di:complement) D90813 D90813 g1742792 Escherichia coli 562 -11533623 224171 hima:hid integration host factor a-subunit ihf-alpha . (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #323(38.6-39.0 min.)) (nt:orf\_id:o322#13; similar to (swissprot accession) (le:4838) (re:5137) (di:complement) D90814 D90814 g1742805 Escherichia coli 562 -11533623 238354 hima integration host factor alpha subunit (sr:e.coli dna, clone lambda-hima) (db:genpept-bct1) (de:e.coli infc, rplt, phes, phet and hima genes encoding initiationfactor if3, ribosomal protein l20, beta- and alpha-subunits ofphenylalanyl-trna synthetase and the alpha-subunit of integrationhost... ECOHIMA K02844 g146347 Escherichia coli 562 -11533623 5000690844 (db:genpept-bct1) (de:e.coli thrs, infc, rplt, phes, phet and hima genes encodingthreonyl-trna synthetase, initiation factor if3, ribosomal proteinl20, phenylalanyl-trna synthetase and the alpha-subunit of the hostintegration factor.) (nt:integration h... ECTHRINF V00291 g43072 Escherichia coli 562 -11533623 234651 hima integration host factor ihf:alpha subunit (fn:factor; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 156 of 400 of the completegenome.) (nt:f99; 100 pct identical to ihfa\_ecoli sw: p06984; cg) (le:5736) (re:6035) (di:complement) AE000266 AE000266 g1788005 Escherichia coli 562 -11533623 79044 hima:hid (de:integration host factor alpha-subunit (ihf-alpha)) (db:swissprot) IHFA\_ECOLI P06984 ESCHERICHIA COLI 562 -11533623

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501834259	8831	30987	513	170

Description

6500729766 topb:b1763 dna topoisomerase iii (gtcfc:10.8) (ec:5.99.1.2) (keggfc:14.1) (rileyfc:3.1.7) (db:gtc-escherichia coli) b1763 b1763 Escherichia coli 562 -11533624 101814 topb (ec:5.99.1.2) (de:dna topoisomerase iii,) (db:swissprot) TOP3\_ECOLI P14294 ESCHERICHIA COLI 562 -11533624 162948 topb dna topoisomerase:iii (ec:5.99.1.2) (db:pir2.dat) (mp:39 min) JV0049 JV0049 Escherichia coli 562 -11533624 224231 topb dna topoisomerase iii ec 5.99.1.- (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #328(39.4-39.8 min.)) (nt:orf\_id:o328#16; similar to (pir accession number) (le:16513) (re:18474) (di:complement) D90819 D90819 g1742870 Escherichia coli 562 -11533624 300876 topb dna topoisomerase iii ec 5.99.1.- (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #329(39.7-40.0 min.)) (nt:orf\_id:o328#16; similar to (pir accession number) (le:1856) (re:3817) (di:complement) D90820 D90820 g1742874 Escherichia coli 562 -11533624 300873 topb topoisomerase iii (sr:escherichia coli (strain hms-83) (clone: prd15.) dna) (db:genpept-bct1) (de:e.coli topoisomerase iii (topb) gene, complete cds.) (le:345) (re:2306) (di:direct) ECOTOPB J05076 g148026 Escherichia coli 562 -11533624 236127 topb dna topoisomerase iii (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:5.99.1.2) (de:escherichia coli k-12 mg1655 section 161 of 400 of the completgenome.) (nt:f653; 100 pct identical to top3\_ecoli sw: p14294;) (le:2776) (re:4737) (di:complement) AE000271 AE000271 g1788061 Escherichia coli 562 -11533624 224234 topb dna topoisomerase iii ec 5.99.1.- (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #329(39.7-40.0 min.)) (nt:orf\_id:o328#16; similar to (pir accession number) (le:1856) (re:3817) (di:complement) D90820 D90820 g1742874 Escherichia coli 562 -11533624 5000690845 (de:(ecoli\_1720) (pn:dna topoisomerase iii) (gn:topb) (gtcfc:10.8) (ec:5.99.1.2) (top3\_ecoli) (keggfc:11.1) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_1720 ECOLI\_1720 Escherichia coli 562 10043643

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834268	8832	30988	294	97

Description

6500729767 ruvb:b1860 holliday junction dna helicase ruvb (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b1860 b1860 Escherichia coli 562 -11533625 300994 ruvb (de:holliday junction dna helicase ruvb) (db:swissprot) RUVB\_ECOLI P08577 ESCHERICHIA COLI 562 -11533625 131300 ruvb dna-binding protein ruvb:holliday junction dna helicase ruvb (cl:ruvb protein) (db:pir1.dat) (mp:41 min) BVECVB B28533 Escherichia coli 562 -11533625 224354 ruvb holliday junction dna helicase ruvb. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #337(41.9-42.3 min.)) (nt:orf\_id:o337#1; similar to (swissprot accession) (le:1148) (re:2158) (di:complement) D90829 D90829 g1736507 Escherichia coli 562 -11533625 238196 (sr:e.coli (strain k12) dna, clone abl157) (db:genpept-bct1) (de:e.coli ruv operon (ruva and ruvb) genes encoding proteins for filament formation and sensitivity to uv radiation, complete cds.) (nt:ruvb protein) (le:980) (re:1990) (di:direct) ECORUVABA M21298 g147783 Escherichia coli 562 -11533625 5000690846 (db:genpept-bct1) (de:e.coli ruv region.) (nt:ruvb gene product (aa 1 - 336)) (le:937) (re:1947) (di:direct) ECRUVAB X07091 g42903 Escherichia coli 562 -11533625 235944 ruvb holliday junction helicase subunit a:branch (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 170 of 400 of the complete genome.) (nt:f336; 100 pct identical to ruvb\_ecoli sw: p08577;) (le:2765) (re:3775) (di:complement) AE000280 AE000280 g1788167 Escherichia coli 562 -11533625 97682 ruvb (de:holliday junction dna helicase ruvb) (db:swissprot) RUVB\_ECOLI P08577 ESCHERICHIA COLI 562 -11533625

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834281	8833	30989	660	219
<u>Description</u>				
6500729768 ruva:b1861 holliday junction dna helicase ruva (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b1861 b1861 Escherichia coli 562 -11533626 97679 ruva (de:holliday junction dna helicase ruva) (db:swissprot) RUVA_ECOLI P08576 ESCHERICHIA COLI 562 -11533626 7000686531 ruva holliday junction dna helicase ruva (cl:holliday junction dna helicase ruva) (db:pir1.dat) (mp:41 min) BVECRV E64948 Escherichia coli 562 -11533626 224355 ruva ruva protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #337(41.9-42.3 min.)) (nt:orf_id:o337#2; similar to (pir accession number) (le:2167) (re:2778) (di:complement) D90829 D90829 g1736508 Escherichia coli 562 -11533626 300995 (sr:e.coli (strain k12) dna, clone ab1157) (db:genpept-bct1) (de:e.coli ruv operon (ruva and ruvb) genes encoding proteins forfilament formation and sensitivity to uv radiation, complete cds.) (nt:ruva protein (gtg start)) (le:360) (re:971) (di:direct) ECORUVABA M21298 g147782 Escherichia coli 562 -11533626 235943 ruva holliday junction helicase subunit b:branch (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 170 of 400 of the completegenome.) (nt:f203; 99 pct identical to ruva_ecoli sw: p08576; cg) (le:3784) (re:4395) (di:complement) AE000280 AE000280 g1788168 Escherichia coli 562 -11533626 5000690847 (de:(ecoli_1818) (pn:branch migration of holliday structures; repair) (gn:ruva) (gtcfc:10.8) (ec:) (ruva_ecoli) (keggfc:11.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI_1818 ECOLI_1818 Escherichia coli 562 10119881				
<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834296	8834	30990	825	274
<u>Description</u>				
GTC ORF with score 184 to: (fn:splicing factor) (sr:house mouse) (db:genpept-rod) (de:mus musculus suppressor of white apricot homolog 2 (swap2) mrna,complete cds.) (nt:contains rs (arginine/serine-rich) domain) (le:103) (re:1941) (di:direct)				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834297	8835	30991	711	237

Description

6500729769 ruvc:b1863 crossover junction endodeoxyribonuclease ruvc:holliday junction nuclease ruvc:holliday junction resolvase ruvc (gtcfc:10.8) (ec:3.1.22.4) (keggfc:14.1) (rileyfc:3.1.7) (db:gtc-escherichia coli) b1863 b1863 Escherichia coli 562 -11533627 162947 ruvc crossover junction endodeoxyribonuclease:ruvc:dna repair protein ruvc (cl:dna repair protein ruvc) (ec:3.1.22.4) (db:pir2.dat) D38113 D38113 Escherichia coli 562 -11533627 224357 ruvc dna repair protein ruvc (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #337(41.9-42.3 min.)) (nt:orf\_id:o337#4; similar to (pir accession number) (le:3657) (re:4178) (di:complement) D90829 D90829 g1736510 Escherichia coli 562 -11533627 235948 ruvc (db:genpept-bct1) (de:e.coli orf150, orf246, orf11 and ruvc gene for resolvase ofholliday junction intermediates.) (le:1274) (re:1795) (di:direct) ECORFRUFC X59551 g42175 Escherichia coli 562 -11533627 300997 ruvc ruvc (fn:endonuclease) (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e. coli dna for orf17, orf26, ruvc and orf23 genes.) (le:1767) (re:2288) (di:direct) ECORUVC D10165 g216653 Escherichia coli 562 -11533627 235777 ruvc holliday junction nuclease:resolution of (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:3.1.22.4) (de:escherichia coli k-12 mg1655 section 170 of 400 of the completegenome.) (nt:f173; 100 pct identical to ruvc\_ecoli sw: p24239) (le:5274) (re:5795) (di:complement) AE000280 AE000280 g1788170 Escherichia coli 562 -11533627 5000690848 (de:(ecoli\_1820) (pn:holliday junction nuclease; resolution of structures; repair) (gn:ruvc) (gtcfc:10.8) (ec:3.1.22.4) (ruvc\_ecoli) (keggfc:11.1) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_1820 ECOLI\_1820 Escherichia coli 562 10086697

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834303	8836	30992	486	161
<u>Description</u>				
6500729770 dcm:mec:b1961 dna-cytosine methyltransferase (gtcfc:10.8) (ec:2.1.1.73) (keggfc:14.1) (rileyfc:3.1.7) (db:gtc-escherichia coli) b1961 b1961 Escherichia coli 562 -11533628 234131 dcm:mec (ec:2.1.1.73) (de:dna-cytosine methyltransferase,) (db:swissprot) DCM_ECOLI P11876 ESCHERICHIA COLI 562 -11533628 137806 dcm site-specific dna-methyltransferase cytosine-specific::dcm protein (cl:site-specific methyltransferase (cytosine-specific) ecorii) (ec:2.1.1.73) (db:pir2.dat) JS0263 A37754 Escherichia coli 562 -11533628 224471 dcm:mec dna-cytosine methyltransferase ec 2.1.1.73 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #344(43.5-43.9 min.)) (nt:orf_id:o344#8; similar to (swissprot accession) (le:9304) (re:10722) (di:complement) D90835 D90835 g1736630 Escherichia coli 562 -11533628 5000690849 (db:genpept-bct1) (de:e. coli dcm gene for dna-cytosine methyltransferase and 3 orfs.) (nt:dna-cytosine methyltransferase (aa 1 - 472)) (le:298) (re:1716) (di:direct) ECDCM X13330 g41239 Escherichia coli 562 -11533628 301111 (sr:e.coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli dna cytosine methylase (dcm) and patch repair protein genes,complete cds.) (nt:dna cytosine methylase; (dcm)) (le:250) (re:1668) (di:direct) ECODCMA M32307 g145719 Escherichia coli 562 -11533628 232647 dcm dna cytosine methylase (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:2.1.1.73) (de:escherichia coli k-12 mg1655 section 177 of 400 of the completegenome.) (nt:f472; 100 pct identical to dcm_ecoli sw: p11876) (le:9397) (re:10815) (di:complement) AE000287 AE000287 g1788271 Escherichia coli 562 -11533628 68040 dcm:mec (ec:2.1.1.73) (de:dna-cytosine methyltransferase,) (db:swissprot) DCM_ECOLI P11876 ESCHERICHIA COLI 562 -11533628				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501834311	8837	30993	525	174

# Description

6500729771 alka:aida:b2068 dna-3-methyladenine glycosidase  
ii:3-methyladenine-dna glycosylase i:inducible:tag ii (gtcfc:10.8)  
(ec:3.2.2.21) (keggfc:14.1) (rileyfc:3.1.7) (db:gtc-escherichia coli) b2068  
b2068 Escherichia coli 562 -11533629 57519 alka:aida (ec:3.2.2.21)  
(de:glycosylase i, inducible) (tag ii)) (db:swissprot) 3MG2\_ECOLI P04395  
ESCHERICHIA COLI 562 -11533629 124698 alka dna-3-methyladenine glycosidase  
ii (cl:3-methyladenine dna glycosylase ii) (ec:3.2.2.21) (db:pir1.dat)  
(mp:43 min) DGECA A00904 Escherichia coli 562 -11533629 224609 alka:aida  
dna-3-methyladenine glycosidase ii ec 3.2.2.21 (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #356(46.1-46.5 min..))  
(nt:orf\_id:o356#1; similar to (swissprot accession) (le:5413) (re:6261)  
(di:complement) D90845 D90845 g1736778 Escherichia coli 562 -11533629  
301249 alka 3-methyladenine dna glycosylase ii (sr:e. coli k12 (strain  
w363) dna, clone pyn1000) (db:genpept-bct1) (de:e. coli alka gene encoding  
3-methyladenine dna glycosylase ii,complete cds.) (le:572) (re:1420)  
(di:direct) ECOALKA K02498 g145226 Escherichia coli 562 -11533629 233762  
alka 3-methyl-adenine dna glycosylase ii:inducible (fn:enzyme; dna -  
replication, repair,) (db:genpept-bct2) (ec:3.2.2.21) (de:escherichia coli  
k-12 mg1655 section 187 of 400 of the completegenome.) (nt:f282; 100 pct  
identical to 3mg2\_ecoli sw: p04395;) (le:85) (re:933) (di:complement)  
AE000297 AE000297 g1788383 Escherichia coli 562 -11533629 5000690850  
(de:(ecoli\_2016) (pn:3-methyl-adenine dna glycosylase ii, inducible)  
(gn:alka) (gtcfc:10.8) (ec:3.2.2.21) (3mg2\_ecoli) (keggfc:11.1)  
(rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_2016 ECOLI\_2016 Escherichia  
coli 562 10000302



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834312	8838	30994	1035	345

Description

6500729772 alkb:aidd:b2212 alkb protein (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b2212 b2212 Escherichia coli 562 -11533630 59184 alkb:aidd (de:alkb protein) (db:swissprot) ALKB\_ECOLI P05050 ESCHERICHIA COLI 562 -11533630 131294 alkb alkb protein (cl:alkb protein) (db:pir1.dat) (mp:48 min) BVECKB A24605 Escherichia coli 562 -11533630 224679 alkb:aidd alkb protein. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #373(49.5-49.9 min.)) (nt:orf\_id:o373#1; similar to (swissprot accession) (le:8209) (re:8859) (di:complement) D90850 D90850 g1736853 Escherichia coli 562 -11533630 234815 (sr:e.coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli alkb gene encoding the alkb protein, complete cds, and adagene encoding 0-6-methylguanine-dna methyltransferase, partial cds.) (nt:alkb protein (alkb)) (le:207) (re:857) (di:direct) ECOADAB J02607 g145195 Escherichia coli 562 -11533630 301319 alkb (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:centisome 49 region of e.coli k12 bhb2600.) (le:35742) (re:36392) (di:complement) ECOHU49 U00008 g405945 Escherichia coli 562 -11533630 233724 alkb dna repair system specific for alkylated dna (fn:putative enzyme; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 200 of 400 of the completegenome.) (nt:f216; 100 pct identical to alkb\_ecoli sw: p05050) (le:5011) (re:5661) (di:complement) AE000310 AE000310 g1788541 Escherichia coli 562 -11533630 5000690851 (de:(ecoli\_2161) (pn:dna repair system specific for alkylated dna) (gn:alkb) (gtcfc:10.8) (ec:) (alkb\_ecoli) (keggfc:11.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_2161 ECOLI\_2161 Escherichia coli 562 10001923

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834321	8839	30995	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834322	8840	30996	1176	391

Description

6500729773 ada:b2213 ada regulatory protein:regulatory protein:regulatory protein of adaptative response:contains:methylated-dna--protein-cysteine methyltransferase:o-6-methylguanine-dna alkyltransferase (gtcfc:10.8) (ec:2.1.1.63) (keggfc:14.1) (rileyfc:3.1.7) (db:gtc-escherichia coli) b2213 b2213 Escherichia coli 562 -11533631 58596 ada (ec:2.1.1.63) (de:(ec 2.1.1.63) (o-6-methylguanine-dna alkyltransferase))) (db:swissprot) ADA\_ECOLI P06134 ESCHERICHIA COLI 562 -11533631 7000684522 ada adaptive response regulatory protein (cl:adaptive response regulatory protein:methylated-dna--protein-cysteine s-methyltransferase homology:methylphosphotriester-dna methyltransferase homology) (db:pir1.dat) (mp:48 min) XEYCO2 C64991 Escherichia coli 562 -11533631 224680 ada ada regulatory protein regulatory protein of (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #373(49.5-49.9 min.)) (nt:orf\_id:o373#2; similar to (swissprot accession) (le:8859) (re:9923) (di:complement) D90850 D90850 g1736854 Escherichia coli 562 -11533631 301320 ada (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:centisome 49 region of e.coli k12 bhb2600.) (nt:dna repair protein.) (le:36392) (re:37456) (di:complement) ECOHU49 U00008 g405944 Escherichia coli 562 -11533631 234816 ada o6-methylguanine-dna methyltransferase (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:2.1.1.63) (de:escherichia coli k-12 mg1655 section 200 of 400 of the completegenome.) (nt:f354; 100 pct identical to ada\_ecoli sw: p06134) (le:5661) (re:6725) (di:complement) AE000310 AE000310 g1788542 Escherichia coli 562 -11533631 5000690852 (de:(ecoli\_2162) (pn:regulatory protein:regulatory protein of ptative response:contains, methylated-dna--protein-cysteine methyltransferase:o-6-methylguanine-dna alkyltransferase) (gn:ada) (gtcfc:10.8) (ec:2.1.1.63) (ada\_ecoli) () ECOLI\_2162 ECOLI\_2162 Escherichia coli 562 10001344

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834325	8841	30997	1176	391

Description

6500729774 gyra:pard:nala:hisw:b2231 dna gyrase subunit a (gtcfc:10.8) (ec:5.99.1.3) (keggfc:14.1) (rileyfc:3.1.7) (db:gtc-escherichia coli) b2231 b2231 Escherichia coli 562 -11533632 7500882873 gyra:pard:nala:hisw (ec:5.99.1.3) (de:dna gyrase subunit a,) (db:swissprot) GYRA\_ECOLI P09097 ESCHERICHIA COLI 562 -11533632 125862 gyra dna topoisomerase atp-hydrolyzing:chain a:dna gyrase chain a:type ii dna topoisomerase chain a (cl:dna topoisomerase (atp-hydrolyzing) chain a:phage t4 dna topoisomerase (atp-hydrolyzing) medium chain homology) (ec:5.99.1.3) (db:pir1.dat) (mp:48 min) ITECAP S02340 Escherichia coli 562 -11533632 224735 gyra dna gyrase subunit a ec 5.99.1.3 . (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #376(50.2-50.6 min.)) (nt:similar to (swissprot accession number p09097)) (le:10034) (re:12661) (di:complement) D90854 D90854 g1799575 Escherichia coli 562 -11533632 233049 (db:genpept-bct1) (de:e. coli gyra gene for dna gyrase subunit a (ec 5.99.1.3).) (nt:gyra gene product (aa 1-875)) (le:184) (re:2811) (di:direct) ECGYRA X06744 g41634 Escherichia coli 562 -11533632 5000690853 (db:genpept-bct1) (de:e. coli gyra gene for dna gyrase a subunit.) (nt:dna gyrase a subunit (aa 1-875)) (le:388) (re:3015) (di:direct) ECGYRA1 X06373 g41636 Escherichia coli 562 -11533632 233048 gyra dna gyrase:subunit a:type ii topoisomerase (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:5.99.1.3) (de:escherichia coli k-12 mg1655 section 202 of 400 of the completegenome.) (nt:f875; 100 pct identical to gyra\_ecoli sw: p09097) (le:9493) (re:12120) (di:complement) AE000312 AE000312 g1788562 Escherichia coli 562 -11533632 75194 gyra:pard:nala:hisw (ec:5.99.1.3) (de:dna gyrase subunit a,) (db:swissprot) GYRA\_ECOLI P09097 ESCHERICHIA COLI 562 -11533632

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834331	8842	30998	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834343	8843	30999	723	240

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834349	8844	31000	330	109

Description

6500729775 lig:liga:dna:lpdec:lop:b2411 dna ase:dna  
ligase:polydeoxyribonucleotide synthase:nad+ (gtcfc:10.8) (ec:6.5.1.2)  
(keggfc:14.1) (rileyfc:3.1.7) (db:gtc-escherichia coli) b2411 b2411  
Escherichia coli 562 -11533633 69001 liga:liga:dna:lpdec:lop (ec:6.5.1.2)  
(de:dna ligase, (polydeoxyribonucleotide synthase (nad+))) (db:swissprot)  
DNLJ\_ECOLI P15042 ESCHERICHIA COLI 562 -11533633 7000685082 lig dna ligase  
nad+:polydeoxyribonucleotide synthase nad+ (cl:polydeoxyribonucleotide  
synthase (nad+)) (ec:6.5.1.2) (db:pir1.dat) (mp:52 min) LQEC6 B65015  
Escherichia coli 562 -11533633 7500880522 lig (sr:e.coli (strain k12) dna)  
(db:genpept-bct1) (de:e.coli dna ligase (lig) gene, complete cds.) (nt:dna  
ligase (ec 6.5.1.2)) (le:246) (re:2261) (di:direct) ECOLIG M24278 g146613  
Escherichia coli 562 -11533633 234978 lig dna ligase (fn:enzyme; dna -  
replication, repair,) (db:genpept-bct2) (ec:6.5.1.2) (de:escherichia coli  
k-12 mg1655 section 218 of 400 of the completegenome.) (nt:f671; 100 pct  
identical to dnlj\_ecoli sw: p15042) (le:9850) (re:11865) (di:complement)  
AE000328 AE000328 g1788750 Escherichia coli 562 -11533633 5000690854  
(de:(ecoli\_2352) (pn:dna ase) (gn:lig) (gtcfc:10.8) (ec:6.5.1.2)  
(dnlj\_ecoli) (keggfc:11.1) (rileyfc:3.1.7) (db:gtc-escherichia coli))  
ECOLI\_2352 ECOLI\_2352 Escherichia coli 562 10123673

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834367	8845	31001	639	212

Description

6500729776 reco:b2565 dna repair protein reco:recombination protein o (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b2565 b2565 Escherichia coli 562 -11533634 93821 reco (de:dna repair protein reco (recombination protein o)) (db:swissprot) RECO\_ECOLI P15027 ESCHERICHIA COLI 562 -11533634 131411 reco dna repair protein reco (cl:reco protein) (db:pir1.dat) (mp:55 min) BVECRO JS0116 Escherichia coli 562 -11533634 235732 reco protein (sr:escherichia coli (strain k12) (library: kohara) dna, clone 7g4) (db:genpept-bct1) (de:escherichia coli ribonuclease iii and other genes, complete cds.) (le:9209) (re:9937) (di:complement) ECOK12RIII D64044 g987640 Escherichia coli 562 -11533634 235733 reco recombination protein (sr:e.coli (k-12, isolate cs520) dna) (db:genpept-bct1) (de:e.coli recombination protein (reco) gene, complete cds.) (nt:the start codon is putative. other potential start) (le:772) (re:1500) (di:direct) ECORECO M27251 g147552 Escherichia coli 562 -11533634 7500889581 reco (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli reco gene, complete cds.) (le:49) (re:777) (di:direct) ECORECOB M26416 g499369 Escherichia coli 562 -11533634 234890 reco protein interacts with recr and possibly recf (fn:regulator; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 233 of 400 of the completegenome.) (nt:f242; 99 pct identical to reco\_ecoli sw: p15027; cg) (le:1501) (re:2229) (di:complement) AE000343 AE000343 g2367140 Escherichia coli 562 -11533634

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834379	8846	31002	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834381	8847	31003	471	156

Description

GTC ORF with score 99 to: (db:genpept-bct1) (de:rhodobacter sphaeroides magnesium chelatase subunits bchi (bchi)and bchd (bchd) genes, complete cds; and bcho (bcho) gene, partialcds.) (nt:similar to rhodobacter capsulatus bcho) (le:2699) (re:3154) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834382	8848	31004	624	207

Description

GTC ORF with score 101 to: (fn:cinnamoyl ester hydrolase) (sr:butyrivibrio fibrisolvens strain=e14) (db:genpept-bct2) (de:butyrivibrio fibrisolvens cinnamoyl ester hydrolase (cini) gene,complete cds, and aldoketoreductase (akri) gene, partial cds.) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834385	8849	31005	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834386	8850	31006	675	224

Description

GTC ORF with score 172 to: (fn:reduction of 7-oxo position of aklaviketone to) (db:genpept-bct1) (de:streptomyces sp. c5 acyl carrier protein (daua(g)),glycosyltransferase (dauh), and aklaviketone reductase (daue)genes, complete cds.) (le:4746) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834398	8851	31007	306	101

Description

6500729777 ung:b2580 uracil-dna glycosylase (gtcfc:10.8) (ec:3.2.2.-)  
(keggfc:14.1) (rileyfc:3.1.7) (db:gtc-escherichia coli) b2580 b2580  
Escherichia coli 562 -11533635 124700 ung uracil-dna glycosylase  
(cl:uracil-dna glycosylase) (ec:3.2.2.-) (db:pir1.dat) (mp:56 min) DGECU  
A28175 Escherichia coli 562 -11533635 225156 ung uracil-dna glycosylase ec  
3.2.2.- (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda  
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#436(58.4-58.8 min.)) (nt:similar to (pir accession number a28175))  
(le:2057) (re:2746) (di:direct) D90886 D90886 g1799984 Escherichia coli 562  
-11533635 235692 uracil dna glycosylase (sr:escherichia coli (strain k12)  
(library: kohara) dna, clone 7g4) (db:genpept-bct1) (de:escherichia coli  
ribonuclease iii and other genes, complete cds.) (le:24219) (re:24908)  
(di:direct) ECOK12RIII D64044 g987651 Escherichia coli 562 -11533635 236276  
ung uracil dna glycosylase (sr:escherichia coli (strain:k-12) dna)  
(db:genpept-bct1) (de:e.coli genes for l-aspartate oxidase, putative atp  
dependent rnahelicase, and uracil dna glycosylase.) (le:7979) (re:8668)  
(di:direct) ECORBAB D13169 g285778 Escherichia coli 562 -11533635  
7500953303 (sr:e.coli dna) (db:genpept-bct1) (de:e.coli ung gene encoding  
uracil dna glycosylase, complete cds.) (nt:uracil dna glycosylase) (le:533)  
(re:1222) (di:direct) ECOUNG J03725 g148149 Escherichia coli 562 -11533635  
234901 ung uracil-dna-glycosylase (fn:enzyme; dna - replication, repair,)  
(db:genpept-bct2) (ec:3.2.2.-) (de:escherichia coli k-12 mg1655 section 234  
of 400 of the completegenome.) (nt:o229; 100 pct identical to ung\_ecoli sw:  
p12295) (le:6568) (re:7257) (di:direct) AE000344 AE000344 g1788934  
Escherichia coli 562 -11533635 5000690856 (de:(ecoli\_2520)  
(pn:uracil-dna-glycosylase) (gn:ung) (gtcfc:10.8) (ec:3.2.2.-) (ung\_ecoli)  
(keggfc:11.1) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_2520  
ECOLI\_2520 Escherichia coli 562 10066185

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834434	8852	31008	1863	620

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834436	8853	31009	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834447	8854	31010	483	160

Description

6500729778 recn:radb:b2616 recn:dna repair protein recn:recombination protein n (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b2616 b2616 Escherichia coli 562 -11533636 7000688982 recn recn protein (cl:recn protein) (db:pir1.dat) (mp:59 min) RQECN C65040 Escherichia coli 562 -11533636 7500953652 recn protein used in recombination and dna repair (fn:putative enzyme; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 237 of 400 of the completegenome.) (nt:o553; 100 pct identical to gb: ecu36840\_2) (le:5517) (re:7178) (di:direct) AE000347 AE000347 g1788969 Escherichia coli 562 -11533636 5000690857 (de:(ecoli\_2552) (pn:protein in recombination and dna repair) (gn:recn) (gtcfc:10.8) (ec:) (recn\_ecoli) (keggfc:11.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_2552 ECOLI\_2552 Escherichia coli 562 10123749

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834448	8855	31011	276	91

Description

6500729779 reca:lexb:umub:rech:rnmb:tif:zab:b2699 reca protein (gtcfc:10.8) (ec:3.4.99.37) (keggfc:14.1) (rileyfc:3.1.7) (db:gtc-escherichia coli) b2699 b2699 Escherichia coli 562 -11533637 7000688981 reca reca protein (cl:reca protein) (db:pir1.dat) (mp:58 min) RQECA G65049 Escherichia coli 562 -11533637 7500953651 reca reca gene product (db:genpept-bct1) (de:e. coli reca gene.) (le:239) (re:1300) (di:direct) ECRECA V00328 g42673 Escherichia coli 562 -11533637 238026 reca dna strand exchange and renaturation (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 244 of 400 of the completegenome.) (nt:f353; 100 pct identical to reca\_ecoli sw: p03017;) (le:664) (re:1725) (di:complement) AE000354 AE000354 g1789051 Escherichia coli 562 -11533637 5000690858 (de:(ecoli\_2627) (pn:dna strand exchange and renaturation, dna-dependent atpase, dna- and atp-dependent coprotease) (gn:reca) (gtcfc:10.8) (ec:3.4.99.37) (reca\_ecoli) (keggfc:11.1) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_2627 ECOLI\_2627 Escherichia coli 562 10123781



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834449	8856	31012	675	224

Description

6500729780 muts:fdv:b2733 dna mismatch repair protein:dna mismatch repair protein muts (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b2733 b2733 Escherichia coli 562 -11533638 84746 muts:fdv (de:dna mismatch repair protein muts) (db:swissprot) MUTS\_ECOLI P23909 ESCHERICHIA COLI 562 -11533638 162942 muts dna mismatch repair protein (cl:dna mismatch repair protein muts) (db:pir2.dat) I54964 I54964 Escherichia coli 562 -11533638 239307 fdv dna mismatch repair protein (sr:e.coli (strain mc4100) dna) (db:genpept-bct1) (de:escherichia coli dna mismatch repair protein (fdv) gene, completecds.) (le:679) (re:3240) (di:direct) ECOMUTS M64730 g146906 Escherichia coli 562 -11533638 7500886163 muts dna mismatch repair protein (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:alternate gene name fdv?; cg site no. 469;) (le:29397) (re:31958) (di:direct) ECU29579 U29579 g882626 Escherichia coli 562 -11533638 235207 muts methyl-directed mismatch repair (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 247 of 400 of the completegenome.) (nt:o853; 100 pct identical to muts\_ecoli sw: p23909) (le:2822) (re:5383) (di:direct) AE000357 AE000357 g1789089 Escherichia coli 562 -11533638 5000690859 (de:(ecoli\_2662) (pn:methyl-directed mismatch repair) (gn:muts) (gtcfc:10.8) (ec:) (muts\_ecoli) (keggfc:11.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_2662 ECOLI\_2662 Escherichia coli 562 10026937

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834458	8857	31013	273	90

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834479	8858	31014	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834483	8859	31015	321	106

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834484	8860	31016	405	134

Description

GTC ORF with score 387 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome i cosmid c2f3.) (nt:spac2f3.15, putative cell division protein kinase,) (le:32056:33050:33207:33937) (re:33003:33140:33885:34000) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834488	8861	31017	357	118

Description

6500729781 muth:mutr:prv:b2831 muth:dna mismatch repair protein muth (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b2831 b2831 Escherichia coli 562 -11533639 7000688984 muth mutator muth (cl:mutator muth) (db:pir1.dat) (mp:61 min) MVECMH H65065 Escherichia coli 562 -11533639 239402 muth (db:genpept-bct1) (de:escherichia coli muth gene, complete cds.) (le:1) (re:690) (di:direct) ECU16361 U16361 g577425 Escherichia coli 562 -11533639 7500953654 muth (fn:methyl-directed mismatch repair) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:cg site no. 471; alternate gene names mutr, prv) (le:51217) (re:51906) (di:direct) ECU29581 U29581 g882724 Escherichia coli 562 -11533639 238723 muth methyl-directed mismatch repair (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 257 of 400 of the completengenome.) (nt:o229; 100 pct identical to muth\_ecoli sw: p06722;) (le:373) (re:1062) (di:direct) AE000367 AE000367 g1789196 Escherichia coli 562 -11533639 5000690860 (de:(ecoli\_2759) (pn:methyl-directed mismatch repair) (gn:muth) (gtcfc:10.8) (ec:) (muth\_ecoli) (keggfc:11.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_2759 ECOLI\_2759 Escherichia coli 562 10123851

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834489	8862	31018	930	309

Description

6500729782 xerd:xprb:b2894 site-specific integrase/recombinase:with  
xerc:integrase/recombinase xerd (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7)  
(db:gtc-escherichia coli) b2894 b2894 Escherichia coli 562 -11533640 108096  
xerd:xprb (de:integrase/recombinase xerd) (db:swissprot) XERD\_ECOLI P21891  
ESCHERICHIA COLI 562 -11533640 164460 xerd:xprb site-specific  
integrase/recombinase:with xerc:recombinase xerd:xprb protein (cl:probable  
site-specific integrase/recombinase xerc) (db:pir2.dat) A39202 A39202  
Escherichia coli 562 -11533640 239107 xprb (sr:e.coli (strain k-12) dna,  
clone pjc761) (db:genpept-bct1) (de:e.coli recj, xpra, and xprb genes,  
complete cds.) (le:107) (re:1003) (di:direct) ECORECJXPR M54884 g147548  
Escherichia coli 562 -11533640 7500894436 xerd site-specific  
integrase/recombinase:with xerc (db:genpept-bct1) (de:escherichia coli k-12  
genome; approximately 64 to 65 minutes.) (nt:cg site no. 30201; alternate  
gene name xprb; gtg) (le:48661) (re:49557) (di:complement) ECU28375 U28375  
g887844 Escherichia coli 562 -11533640 235729 xerd site-specific  
recombinase (fn:enzyme; dna - replication, repair,) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 263 of 400 of the completegenome.)  
(nt:f298; 100 pct identical to xerd\_ecoli sw: p21891;) (le:2550) (re:3446)  
(di:complement) AE000373 AE000373 g1789261 Escherichia coli 562 -11533640  
5000690861 (de:(ecoli\_2818) (pn:site-specific recombinase) (gn:xerd)  
(gtcfc:10.8) (ec:) (xerd\_ecoli) (keggfc:11.2) (rileyfc:3.1.7)  
(db:gtc-escherichia coli)) ECOLI\_2818 ECOLI\_2818 Escherichia coli 562  
10049828

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834499	8863	31019	693	230

#### Description

6500729783 icia:b2916 chromosome intitiation inhibitor:chromosome initiation inhibitor:oric replication inhibitor (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b2916 b2916 Escherichia coli 562 -11533641 239129 icia (de:chromosome initiation inhibitor (oric replication inhibitor)) (db:swissprot) ICIA\_ECOLI P24194 ESCHERICHIA COLI 562 -11533641 164471 icia chromosome intitiation inhibitor icia:chromosome initiation inhibitor a:chromosome initiation inhibitor a (sr:strain k12-38, , strain k12-38) (sr:strain k12-38, ) (db:pir2.dat) (mp:62.8 min) S22098 S22098 Escherichia coli 562 -11533641 238239 icia chromosome initiation inhibitor (fn:inhibitor of oric replication in vitro) (sr:e.coli (strain w3110) dna, (kohara library) clone ia) (db:genpept-bct1) (de:e.coli chromosome initiation inhibitor (icia) gene, complete cds.) (le:650) (re:1543) (di:direct) ECOICIA M62865 g146436 Escherichia coli 562 -11533641 5000690862 icia inhibitor of chromosome initiaton (db:genpept-bct1) (de:e.coli sera, icia, sbm genes and two open reading frames.) (nt:icia orf) (le:1641) (re:2534) (di:direct) ECSERAICI X66836 g42944 Escherichia coli 562 -11533641 7500883799 icia chromosome intitiation inhibitor (fn:inhibitor of oric replication in vitro) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:cg site no. 28646) (le:14144) (re:15037) (di:direct) ECU28377 U28377 g882445 Escherichia coli 562 -11533641 234836 icia replication initiation inhibitor:binds to (fn:regulator; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 265 of 400 of the completegenome.) (nt:o297; 100 pct identical to icia\_ecoli sw: p24194;) (le:101) (re:994) (di:direct) AE000375 AE000375 g1789283 Escherichia coli 562 -11533641 78714 icia (de:chromosome initiation inhibitor (oric replication inhibitor)) (db:swissprot) ICIA\_ECOLI P24194 ESCHERICHIA COLI 562 -11533641

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834505	8864	31020	186	61

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834508	8865	31021	237	78

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834518	8866	31022	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834523	8867	31023	315	104

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834540	8868	31024	438	145

Description

6500729784 muty:mica:b2961 a/g-specific adenine glycosylase (gtcfc:10.8) (ec:3.2.2.-) (keggfc:14.1) (rileyfc:3.1.7) (db:gtc-escherichia coli) b2961 b2961 Escherichia coli 562 -11533642 235145 muty:mica (ec:3.2.2.-) (de:a/g-specific adenine glycosylase,) (db:swissprot) MUTY\_ECOLI P17802 ESCHERICHIA COLI 562 -11533642 162667 muty a/g-specific adenine glycosylase::mica protein (ec:3.2.2.-) (db:pir2.dat) B38535 B38535 Escherichia coli 562 -11533642 5000690863 (db:genpept-bct1) (de:escherichia coli muty gene for adenine glycosylase.) (nt:adenine glycosylase (aa 1-350)) (le:148) (re:1200) (di:direct) ECMUTY X52391 g42073 Escherichia coli 562 -11533642 239174 mica a/g-specific adenine glycosylase (sr:e.coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli a/g-specific adenine glycosylase (mica) gene, complete cds.) (le:1100) (re:2152) (di:direct) ECOMICA M59471 g146864 Escherichia coli 562 -11533642 7500886172 muty (fn:a/g-specific adenine glycosylase) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:cg site no. 18130; alternate name mica) (le:57406) (re:58458) (di:direct) ECU28377 U28377 g882490 Escherichia coli 562 -11533642 233443 muty adenine glycosylase:g.c --t.a transversions (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:3.2.2.-) (de:escherichia coli k-12 mg1655 section 268 of 400 of the completegenome.) (nt:o350; 100 pct identical to muty\_ecoli sw: p17802;) (le:9034) (re:10086) (di:direct) AE000378 AE000378 g1789331 Escherichia coli 562 -11533642 84757 muty:mica (ec:3.2.2.-) (de:a/g-specific adenine glycosylase,) (db:swissprot) MUTY\_ECOLI P17802 ESCHERICHIA COLI 562 -11533642

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834548	8869	31025	1320	440

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834555	8870	31026	264	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834559	8871	31027	357	118

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834562	8872	31028	291	96

Description

6500729785 parc:b3019 topoisomerase iv subunit:topoisomerase iv subunit a (gtcfc:10.8) (ec:5.99.1.-) (keggfc:14.1) (rileyfc:3.1.7) (db:gtc-escherichia coli) b3019 b3019 Escherichia coli 562 -11533643 88640 parc (ec:5.99.1.-) (de:topoisomerase iv subunit a,) (db:swissprot) PARC\_ECOLI P20082 ESCHERICHIA COLI 562 -11533643 7000686087 parc dna topoisomerase iv:parc chain (cl:dna topoisomerase (atp-hydrolyzing) chain a:phage t4 dna topoisomerase (atp-hydrolyzing) medium chain homology) (ec:5.99.1.-) (db:pir2.dat) (mp:65 min) A65089 A65089 Escherichia coli 562 -11533643 7500887663 parc topoisomerase iv subunit (fn:chromosome partitioning) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (le:118102) (re:120360) (di:complement) ECU28377 U28377 g882549 Escherichia coli 562 -11533643 239233 parc dna topoisomerase iv subunit a (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:5.99.1.-) (de:escherichia coli k-12 mg1655 section 274 of 400 of the completegenome.) (nt:f752; 100 pct identical to parc\_ecoli sw: p20082) (le:2544) (re:4802) (di:complement) AE000384 AE000384 g1789396 Escherichia coli 562 -11533643 5000690864 (de:(ecoli\_2942) (pn:dna topoisomerase iv subunit a) (gn:parc) (gtcfc:10.8) (ec:5.99.1.-) (parc\_ecoli) (keggfc:11.1) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_2942 ECOLI\_2942 Escherichia coli 562 10030767

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834570	8873	31029	249	82
<u>Description</u>				
6500729786 pare:nfxd:b3030 topoisomerase iv subunit:topoisomerase iv subunit b (gtcfc:10.8) (ec:5.99.1.-) (keggfc:14.1) (rileyfc:3.1.7) (db:gtc-escherichia coli) b3030 b3030 Escherichia coli 562 -11533644 88649 pare:nfxd (ec:5.99.1.-) (de:topoisomerase iv subunit b,) (db:swissprot) PARE_ECOLI P20083 ESCHERICHIA COLI 562 -11533644 7000686088 pare topoisomerase iv subunit::pare protein (cl:dna topoisomerase (atp-hydrolyzing) chain b) (ec:5.99.1.-) (db:pir2.dat) D65090 D65090 Escherichia coli 562 -11533644 7500887667 pare topoisomerase iv subunit (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (le:127892) (re:129784) (di:complement) ECU28377 U28377 g882560 Escherichia coli 562 -11533644 239244 pare dna topoisomerase iv subunit b (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:5.99.1.-) (de:escherichia coli k-12 mg1655 section 275 of 400 of the completegenome.) (nt:f630; 100 pct identical to pare_ecoli sw: p20083) (le:1164) (re:3056) (di:complement) AE000385 AE000385 g1789408 Escherichia coli 562 -11533644 5000690865 (de:(ecoli_2953) (pn:dna topoisomerase iv subunit b) (gn:pare) (gtcfc:10.8) (ec:5.99.1.-) (pare_ecoli) (keggfc:11.1) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI_2953 ECOLI_2953 Escherichia coli 562 10030776				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501834584	8874	31030	435	144

# Description

6500729787 fis:b3261 factor-for-inversion stimulation protein:hin recombinational enhancer binding protein:fis protein (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b3261 b3261 Escherichia coli 562 -11533645 71715 fis (de:binding protein) (fis protein)) (db:swissprot) FIS\_ECOLI P11028 ESCHERICHIA COLI 562 -11533645 7502851955 fis (de:binding protein) (fis protein)) (db:swissprot) FIS\_ECOLI P11028 SALMONELLA TYPHIMURIUM 602 -11533645 7500881474 fis dna-binding protein fis:hin recombinational enhancer-binding protein:mu enhancer-binding protein:nbp protein:ndh-binding protein:recombinational enhancer-binding protein fis (cl:dna-binding protein fis) (db:pir1.dat) (mp:72 min) DNECF5 A32142 Escherichia coli 562 -11533645 148296 fis protein:factor for inversion stimulation fis (cl:dna-binding protein fis) (db:pir2.dat) B56267 B56267 Salmonella typhimurium 602 -11533645 234354 fis hin recombinational enhancer binding protein (sr:escherichia coli (strain k-12) (clone: prj741.) dna) (db:genpept-bct1) (de:e.coli fis gene encoding the hin recombinational enhancer bindingprotein, complete cds.) (le:59) (re:355) (di:direct) ECOFIS J03245 g145971 Escherichia coli 562 -11533645 234357 fis (sr:e.coli (strain k12) dna) (db:genpept-bct1) (de:e.coli factor-for-inversion stimulation protein (fis) gene,complete cds.) (nt:factor-for-inversion protein) (le:169) (re:465) (di:direct) ECOFISA J03816 g145973 Escherichia coli 562 -11533645 236501 (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli fis protein gene, orf3, 3'end; orf1, complete cds;orf2, 5'end.) (nt:'fis orf start') (le:1785) (re:2081) (di:direct) ECOFISORFS M95784 g145977 Escherichia coli 562 -11533645 263873 fis (fn:site-specific inversion) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 18328) (le:192017) (re:192313) (di:direct) ECOUW67 U18997 g606202 Escherichia coli 562 -11533645 7000685250 fis fis (fn:factor for inversion stimulation) (db:genpept-bct1) (de:salmonella typhimurium fis factor for inversion stimulation (fis)gene and upstream orf1, complete cds.) (le:1277) (re:1573) (di:direct) STU03101 U03101 g424092 Salmonella typhimurium 602 -11533645 234352 fis site-specific dna inversion stimulation factor (fn:factor; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 295 of 400 of the completegenome.) (nt:o98; cg site no. 18328) (le:1067) (re:1363) (di:direct) AE000405 AE000405 g1789661 Escherichia coli 562 -11533645 7500881475 fis small dna binding protein fis (db:genpept-bct2) (de:serratia marcescens ribosomal protein l11 methyltransferase (prma)gene, partial cds; and yhdg homolog and small dna binding proteinfis (fis) genes, complete cds.) (le:1393) (re:1689) (di:direct) AF040378 AF040378 g2773311 Serratia marcescens 615 -11533645 71716 fis (de:binding protein) (fis protein)) (db:swissprot) FIS\_ECOLI P37404 ESCHERICHIA COLI 562 -11533645 7502851956 fis (de:binding protein) (fis protein)) (db:swissprot) FIS\_ECOLI P37404 SALMONELLA TYPHIMURIUM 602 -11533645 128615 fis protein:factor for inversion stimulation fis (cl:dna-binding protein fis) (db:pir) B56267 B56267 Salmonella typhimurium 602 -11533645 5000690866 (de:(ecoli\_3186) (pn:site-specific dna inversion stimulation factor; dna-binding protein; a trans activator for



stimulation factor; dna-binding protein; a trans activator for  
transcription) (gn:fn) (gtcfc:10.8) (ec:) (fis\_ecoli) (keggfc:11.2)

ORF Name	NT ID	AA ID	NT	AA
			LENGTH	LENGTH
7501834599	8875	31031	1923	640

Description

6500729788 pino:b3322 pino protein (gtcfc:10.8:13.1) (keggfc:14.2)  
(rileyfc:3.1.7:5.1.0) (db:gta-escherichia coli) b3322 b3322 Escherichia coli  
562 -11533646 89799 pino:pino (de:pino protein (pino protein))  
(db:swissprot) P100\_ECOLI P03825 ESCHERICHIA COLI 562 -11533646 7000686144  
pino pino protein (cl:pino protein) (db:pir1.dat) (mp:72 min) QQECRP E65125  
Escherichia coli 562 -11533646 7500888097 (db:genpept-bct1) (de:escherichia  
coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf\_f139)  
(le:234256) (re:234675) (di:complement) ECOUW67 U18997 g606256 Escherichia  
coli 562 -11533646 236555 pino calcium-binding protein required for  
initiation (fn:factor; dna - replication, repair,) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 299 of 400 of the completegenome.)  
(nt:f139; 100 pct identical amino acid sequence and) (le:149) (re:568)  
(di:complement) AE000409 AE000409 g1789719 Escherichia coli 562 -11533646  
5000690867 (de:(ecoli\_3240) (pn:calcium-binding protein required for  
initiation of chromosome replication) (gn:pino) (gtcfc:10.8:13.1) (ec:)  
(pino\_ecoli) (keggfc:11.2:11.2) (rileyfc:3.1.7:5.1.0) (db:gta-escherichia  
coli)) ECOLI\_3240 ECOLI\_3240 Escherichia coli 562 10031919

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834624	8876	31032	357	118

Description

6500729789 dam:b3387 dna adenine methylase:deoxyadenosyl-methyltransferase (gtcfc:10.8) (ec:2.1.1.72) (keggfc:14.1) (rileyfc:3.1.7) (db:gtc-escherichia coli) b3387 b3387 Escherichia coli 562 -11533647 234124 dam (ec:2.1.1.72) (de:dna adenine methylase, (deoxyadenosyl-methyltransferase)) (db:swissprot) DMA\_ECOLI P00475 ESCHERICHIA COLI 562 -11533647 123256 dam site-specific dna-methyltransferase adenine-specific:dam (cl:site-specific methyltransferase (adenine-specific) ecorv) (ec:2.1.1.72) (db:pir1.dat) (mp:74.3 min) XYECDA A00555 Escherichia coli 562 -11533647 232641 (db:genpept-bct1) (de:e.coli dam operon.) (nt:orf, dam. brooks j.e., blumenthal r.m., gingeras) (le:5019) (re:5855) (di:direct) ECDAMOPRA Z19601 g41227 Escherichia coli 562 -11533647 236620 (db:genpept-bct1) (de:e. coli gene coding for the adenine methylase (dam) whichmethylates the sequence gatc.) (nt:coding sequence) (le:195) (re:1031) (di:direct) ECDAMX V00272 g41230 Escherichia coli 562 -11533647 5000690868 dam (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli dam gene coding for dna adenine methylase.) (nt:dna adenine methylase) (le:195) (re:1031) (di:direct) ECODAM J01600 g145706 Escherichia coli 562 -11533647 7500880374 dam dna adenine methylase (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 881) (le:295825) (re:296661) (di:complement) ECOUW67 U18997 g606321 Escherichia coli 562 -11533647 232637 dam dna adenine methylase (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:2.1.1.72) (de:escherichia coli k-12 mg1655 section 304 of 400 of the completegenome.) (nt:f278; cg site no. 881; 100 pct identical amino) (le:4089) (re:4925) (di:complement) AE000414 AE000414 g1789789 Escherichia coli 562 -11533647 68775 dam (ec:2.1.1.72) (de:dna adenine methylase, (deoxyadenosyl-methyltransferase)) (db:swissprot) DMA\_ECOLI P00475 ESCHERICHIA COLI 562 -11533647

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834629	8877	31033	369	122
<u>Description</u>				
6500729790 damx:b3388 damx protein (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b3388 b3388 Escherichia coli 562 -11533648 7000688993 damx damx protein arob-dam intergenic region (cl:damx protein) (db:pir1.dat) (mp:74.3 min) Q4ECAD G65133 Escherichia coli 562 -11533648 7500953697 damx (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (le:296768) (re:298054) (di:complement) ECOUW67 U18997 g606322 Escherichia coli 562 -11533648 236621 damx putative membrane protein:interferes with cell (fn:putative membrane; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 304 of 400 of the completegenome.) (nt:f428; this 428 aa orf is 97 pct identical (1 gap)) (le:5032) (re:6318) (di:complement) AE000414 AE000414 g1789790 Escherichia coli 562 -11533648 5000690869 (de:(ecoli_3306) (pn:damx protein) (gn:damx) (gtcfc:10.8) (ec:) (damx_ecoli) (keggfc:11.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI_3306 ECOLI_3306 Escherichia coli 562 10124021				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834633	8878	31034	417	138

Description

6500729791 tag:b3549 3-methyladenine dna glycosylase  
i:constitutive:dna-3-methyladenine glycosidase i:3-methyladenine-dna  
glycosylase i:constitutive:tag i (gtcfc:10.8) (ec:3.2.2.20) (keggfc:14.1)  
(rileyfc:3.1.7) (db:gtc-escherichia coli) b3549 b3549 Escherichia coli 562  
-11533649 7500876104 tag (ec:3.2.2.20) (de:glycosylase i, constitutive)  
(tag i)) (db:swissprot) 3MG1\_ECOLI P05100 ESCHERICHIA COLI 562 -11533649  
124697 tag:tagi 3-methyladenine-dna glycosylase:i (cl:3-methyladenine dna  
glycosylase i) (ec:3.2.2.-) (db:pir1.dat) (mp:72 min) DGECM1 A24604  
Escherichia coli 562 -11533649 236786 (sr:e.coli (strain k-12) dna, clone  
pcy5) (db:genpept-bct1) (de:e.coli tag gene coding for 3-methyladenine-dna  
glycosylase i,complete cds.) (nt:3-methyladenine-dna glycosylase i (tag))  
(le:134) (re:697) (di:direct) ECOTAG J02606 g147920 Escherichia coli 562  
-11533649 238322 tag 3-methyladenine dna glycosylase i:constitutive  
(sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda)  
(db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.)  
(nt:aug is 4th start; cg site no. 124) (le:127344) (re:127907) (di:direct)  
ECOUW76 U00039 g466687 Escherichia coli 562 -11533649 5000690870  
(db:genpept-bct1) (de:e. coli tag gene for 3-methyladenine dna glycosylase i  
(tagi).) (nt:tagi (aa 1-187)) (le:134) (re:697) (di:direct) ECTAG X03845  
g43030 Escherichia coli 562 -11533649 236060 tag 3-methyl-adenine dna  
glycosylase i (fn:enzyme; dna - replication, repair,) (db:genpept-bct2)  
(ec:3.2.2.20) (de:escherichia coli k-12 mg1655 section 322 of 400 of the  
completegenome.) (nt:o187; 100 pct identical to 3mg1\_ecoli sw: p05100;)  
(le:5331) (re:5894) (di:direct) AE000432 AE000432 g1789971 Escherichia coli  
562 -11533649 57518 tag (ec:3.2.2.20) (de:glycosylase i, constitutive) (tag  
i)) (db:swissprot) 3MG1\_ECOLI P05100 ESCHERICHIA COLI 562 -11533649

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834634	8879	31035	765	254

#### Description

6500729792 dfp:b3639 dfp protein (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b3639 b3639 Escherichia coli 562 -11533650 68310 dfp (de:dna/pantothenate metabolism flavoprotein) (db:swissprot) DFP\_ECOLI P24285 ESCHERICHIA COLI 562 -11533650 7000685021 dfp protein dfp (cl:pantothenate metabolism flavoprotein dfp) (db:pir2.dat) A65165 A65165 Escherichia coli 562 -11533650 7500880201 dfp flavoprotein affecting synthesis of dna and (fn:phenotype; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 331 of 400 of the completegenome.) (nt:o430; 100 pct identical amino acid sequence and) (le:4554) (re:5846) (di:direct) AE000441 AE000441 g1790070 Escherichia coli 562 -11533650 5000690871 (de:(ecoli\_3559) (pn:flavoprotein affecting synthesis of dna and pantothenate metabolism) (gn:dfp) (gtcfc:10.8) (ec:) (dfp\_ecoli) (keggfc:11.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_3559 ECOLI\_3559 Escherichia coli 562 10124048

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834635	8880	31036	333	110

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834642	8881	31037	327	108

#### Description

6500729793 gyrb:para:nalc:acrb:pcba:himb:hisu:b3699 dna gyrase:subunit b:dna gyrase subunit b (gtcfc:10.8) (ec:5.99.1.3) (keggfc:14.1) (rileyfc:3.1.7) (db:gtc-escherichia coli) b3699 b3699 Escherichia coli 562 -11533651 7000688905 gyrb dna topoisomerase atp-hydrolyzing:chain b:dna gyrase b chain:type ii dna topoisomerase b chain (cl:dna topoisomerase (atp-hydrolyzing) chain b) (ec:5.99.1.3) (db:pir1.dat) (mp:83 min) ISECTB D65172 Escherichia coli 562 -11533651 7500953356 gyrb dna gyrase subunit b:type ii topoisomerase (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:5.99.1.3) (de:escherichia coli k-12 mg1655 section 337 of 400 of the completegenome.) (nt:f804; 99 pct identical amino acid sequence and) (le:718) (re:3132) (di:complement) AE000447 AE000447 g1790134 Escherichia coli 562 -11533651 5000690872 (de:(ecoli\_3617) (pn:dna gyrase subunit b, type ii topoisomerase, dna cleavage with transient covalent bonding, atpase activity) (gn:gyrb) (gtcfc:10.8) (ec:5.99.1.3) (gyrb\_ecoli) (keggfc:11.1) (rileyfc:3.1.7) (db:gtc-escherichia) ECOLI\_3617 ECOLI\_3617 Escherichia coli 562 10124074

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834667	8882	31038	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834673	8883	31039	243	80

Description

6500729794 recf:uvrf:b3700 protein:recf protein (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b3700 b3700 Escherichia coli 562 -11533652 131407 recf recf protein (cl:recf protein) (db:pir1.dat) (mp:83 min) RQECF A03547 Escherichia coli 562 -11533652 235725 (db:genpept-bct1) (de:e. coli genes dnan (3'region), recf and gyrb.) (nt:recf protein) (le:78) (re:1151) (di:direct) ECGYRBF X04341 g41645 Escherichia coli 562 -11533652 7500953653 recf (sr:e.coli dna, clone pjc605) (db:genpept-bct1) (de:escherichia coli recf gene with 3' end of dnan gene and 5' end ofgyrb gene.) (nt:recf protein) (le:213) (re:1286) (di:direct) ECORECF K02179 g147539 Escherichia coli 562 -11533652 233056 recf ssdna and dsdna binding:atp binding (fn:regulator; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 337 of 400 of the completgenome.) (nt:f357; 99 pct identical amino acid sequence and) (le:3161) (re:4234) (di:complement) AE000447 AE000447 g1790135 Escherichia coli 562 -11533652 5000690873 (de:(ecoli\_3618) (pn:ssdna and dsdna binding, atp binding) (gn:recf) (gtcfc:10.8) (ec:) (recf\_ecoli) (keggfc:11.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_3618 ECOLI\_3618 Escherichia coli 562 10068112

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834676	8884	31040	372	123

#### Description

6500729795 dnaa:b3702 chromosomal replication initiator protein dnaa (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b3702 b3702 Escherichia coli 562 -11533653 68827 dnaa (de:chromosomal replication initiator protein dnaa) (db:swissprot) DNAA\_ECOLI P03004 ESCHERICHIA COLI 562 -11533653 7000685067 dnaa replication initiation protein dnaa (cl:replication initiation protein dnaa) (db:pir1.dat) (mp:83 min) IQECDA G65172 Escherichia coli 562 -11533653 7500880393 dnaa (sr:escherichia coli (strain k-12) (clone: ptc884 .) dna; escherichi) (db:genpept-bct1) (de:e.coli dnaa operon: dnaa, dnan, and rpmh genes coding for dnaaprotein, dna polymerase iii beta subunit, and ribosomal proteinl34.) (nt:dnaa protein (gtg start c... ECODNAAOP J01602 g145760 Escherichia coli 562 -11533653 234179 dnaa dna biosynthesis:initiation of chromosome (fn:putative regulator; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 337 of 400 of the completegenome.) (nt:f467; 100 pct identical to dnaa\_ecoli sw: p03004;) (le:5339) (re:6742) (di:complement) AE000447 AE000447 g2367267 Escherichia coli 562 -11533653

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834682	8885	31041	1383	460

#### Description

6500729796 gidb:b3740 glucose inhibited division protein:glucose inhibited division protein b (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b3740 b3740 Escherichia coli 562 -11533654 7500882348 gidb (de:glucose inhibited division protein b) (db:swissprot) GIDB\_ECOLI P17113 ESCHERICHIA COLI 562 -11533654 131318 gidb:giab gidb protein (cl:gidb protein) (db:pir1.dat) (mp:84 min) BVECQB C30389 Escherichia coli 562 -11533654 240345 gidb::cg site no. 1... (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:glucose inhibited division protein) (le:112449) (re:113072) (di:complement) ECOUW82 L10328 g290589 Escherichia coli 562 -11533654 5000690875 (db:genpept-bct1) (de:e. coli origin of replication oric and genes gid, unc, ecourf-1 andglms.) (nt:gidb protein) (le:2357) (re:2980) (di:direct) ECUNC X01631 g581247 Escherichia coli 562 -11533654 236977 gidb glucose-inhibited division:chromosome (fn:phenotype; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 341 of 400 of the completegenome.) (nt:f207; 100 pct identical to gidb\_ecoli sw: p17113) (le:154) (re:777) (di:complement) AE000451 AE000451 g1790179 Escherichia coli 562 -11533654 73612 gidb (de:glucose inhibited division protein b) (db:swissprot) GIDB\_ECOLI P17113 ESCHERICHIA COLI 562 -11533654

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834685	8886	31042	207	68

Description

6500729797 gida:b3741 glucose inhibited division protein:glucose inhibited division protein a (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b3741 b3741 Escherichia coli 562 -11533655 7500882335 gida (de:glucose inhibited division protein a) (db:swissprot) GIDA\_ECOLI P17112 ESCHERICHIA COLI 562 -11533655 7000690892 gida glucose inhibited division protein (cl:gida protein) (db:pir1.dat) (mp:84 min) BVECQA F65177 Escherichia coli 562 -11533655 7500882337 gida glucose-inhibited division:chromosome (fn:phenotype; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 341 of 400 of the completegenome.) (nt:f629; 99 pct identical to gida\_ecoli sw: p17112; cg) (le:841) (re:2730) (di:complement) AE000451 AE000451 g2367273 Escherichia coli 562 -11533655

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834705	8887	31043	312	103

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834727	8888	31044	183	60

Description

Hypothetical protein



ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501834732	8889	31045	1485	495

Description

6500729798 mioc:b3742 involved in modulation of initiation at oric:mioc protein (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b3742 b3742 Escherichia coli 562 -11533656 7000688997 mioc mioc protein:hypothetical protein b2790 (cl:mioc protein:flavodoxin homology) (db:pir1.dat) (mp:83 min) QQEC16 G65177 Escherichia coli 562 -11533656 236979 (sr:escherichia coli, clone (minichromosome) pcm959, dna) (db:genpept-bct1) (de:e.coli replication origin (oric) and asna gene coding forasparagine synthetase a.) (nt:16k protein) (le:968) (re:1411) (di:complement) ECOORIASN K00826 g455178 Escherichia coli 562 -11533656 7500953701 mioc::cg site no. 1... (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:involved in modulation of initiation at oric) (le:115401) (re:115844) (di:complement) ECOUW82 L10328 g290591 Escherichia coli 562 -11533656 235309 mioc initiation of chromosome replication (fn:factor; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 341 of 400 of the completegenome.) (nt:f147; 100 pct identical to mioc\_ecoli sw: p03817;) (le:3109) (re:3552) (di:complement) AE000451 AE000451 g1790181 Escherichia coli 562 -11533656 5000690877 (de:(ecoli\_3660) (pn:initiation of chromosome replication) (gn:mioc) (gtcfc:10.8) (ec:) (mioc\_ecoli) (keggfc:11.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_3660 ECOLI\_3660 Escherichia coli 562 10124086

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834755	8890	31046	285	94

Description

6500729799 xerc:b3811 integrase/recombinase xerc (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b3811 b3811 Escherichia coli 562 -11533657 164401 xerc probable site-specific recombinase xerc:integrase/recombinase xerc (cl:probable site-specific integrase/recombinase xerc) (db:pir2.dat) C37841 C37841 Escherichia coli 562 -11533657 7500960432 xerc lambda-integrase (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli lambda-integrase (xerc) gene, complete cds,diaminopimelate (dapf), 3' end, and helicase ii (uvrd) gene, 5'end.) (le:752) (re:1648) (di:direct) ECOXERC M38257 g148270 Escherichia coli 562 -11533657 237641 xerc site-specific recombinase:acts on cer sequence (fn:enzyme; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 347 of 400 of the completegenome.) (nt:o298; 99 pct identical amino acid sequence and) (le:1919) (re:2815) (di:direct) AE000457 AE000457 g1790244 Escherichia coli 562 -11533657 5000690878 (de:(ecoli\_3717) (pn:site-specific recombinase, acts on cer sequence of cole1, effects chromosome segregation at cell division) (gn:xerc) (gtcfc:10.8) (ec:) (xerc\_ecoli) (keggfc:11.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_3717 ECOLI\_3717 Escherichia coli 562 10087305

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834759	8891	31047	642	213

Description

6500729800 pria:b3935 primosomal protein replication factor:primosomal protein n:replication factor y (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b3935 b3935 Escherichia coli 562 -11533658 164366 pria primosomal replication factor y:protein n (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) (mp:88.5 min) A35505 S40878 Escherichia coli 562 -11533658 7500960420 pria primosomal protein replication factor (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:product is either primosomal protein replication) (le:86245) (re:88443) (di:complement) ECOUW87 L19201 g305038 Escherichia coli 562 -11533658 237152 pria primosomal protein n = factor y putative (fn:factor; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 357 of 400 of the completegenome.) (nt:f732; 99 pct identical amino acid sequence and) (le:11738) (re:13936) (di:complement) AE000467 AE000467 g1790370 Escherichia coli 562 -11533658 5000690879 (de:(ecoli\_3833) (pn:factor y:putative helicase:primosomal protein n") (gn:pria) (gtcfc:10.8) (ec:) (pria\_ecoli) (keggfc:11.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_3833 ECOLI\_3833 Escherichia coli 562 10087293

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834762	8892	31048	714	237

Description

GTC ORF with score 195 to: (or:Bacillus subtilis) (fn:unknown)  
(db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21):  
from 3197001to 3414420.) (nt:alternate gene name: yvxa; similar to retinol)  
(le:184692) (re:185534) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834763	8893	31049	354	117

Description

6500729801 uvra:dine:b4058 excision nuclease:excinnuclease abc subunit a  
(gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b4058  
b4058 Escherichia coli 562 -11533659 104032 uvra:dine (de:excinnuclease abc  
subunit a) (db:swissprot) UVRA\_ECOLI P07671 ESCHERICHIA COLI 562 -11533659  
130770 uvra excinnuclease abc chain a:excision endonuclease abc::chain  
a:uvra protein (cl:excinnuclease abc chain a:atp-binding cassette homology)  
(ec:3.1.-.-) (db:pir1.dat) (mp:92 min) BVECUA A23869 Escherichia coli 562  
-11533659 7500893885 uvra (sr:e.coli k12 dna, clone punc1986)  
(db:genpept-bct1) (de:e.coli uvra gene encoding uvra protein, complete cds.)  
(nt:uvra protein) (le:256) (re:3078) (di:direct) ECOUVRAA M13495 g148165  
Escherichia coli 562 -11533659 236306 uvra excision nuclease subunit a  
(fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (de:escherichia  
coli k-12 mg1655 section 369 of 400 of the completegenome.) (nt:o940; 99 pct  
identical amino acid sequence and) (le:2028) (re:4850) (di:complement)  
AE000479 AE000479 g2367343 Escherichia coli 562 -11533659

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501834764	8894	31050	330	109

Description

6500729802 ssb:b4059 single-strand dna-binding protein (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b4059 b4059 Escherichia coli 562 -11533660 7000688938 ssb single-stranded dna-binding protein:helix-destabilizing protein (cl:bacterial single-stranded dna-binding protein:single-stranded dna-binding protein homology) (db:pir1.dat) (mp:92 min) DDEC B65214 Escherichia coli 562 -11533660 237265 ssb ssdna-binding protein (fn:factor; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 369 of 400 of the completegenome.) (nt:ol78; cg site no. 150) (le:5104) (re:5640) (di:direct) AE000479 AE000479 g1790494 Escherichia coli 562 -11533660 7500953489 ssb single-strand dna-binding protein (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 150) (le:139365) (re:139901) (di:direct) ECOUW89 U00006 g396394 Escherichia coli 562 -11533660 5000690881 (de:(ecoli\_3945) (pn:ssdna-binding protein) (gn:ssb) (gtcfc:10.8) (ec:) (ssb\_ecoli) (keggfc:11.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_3945 ECOLI\_3945 Escherichia coli 562 10124143

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501834765	8895	31051	426	141

Description

6500729803 mutl:b4170 dna mismatch repair protein mutl (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b4170 b4170 Escherichia coli 562 -11533661 237375 mutl (de:dna mismatch repair protein mutl) (db:swissprot) MUTL\_ECOLI P23367 ESCHERICHIA COLI 562 -11533661 164064 mutl methyl-directed mismatch repair protein mutl (db:pir2.dat) (mp:95 min) PH0853 PH0853 Escherichia coli 562 -11533661 5000690882 mutl mutl protein (fn:required for methyl-directed dna mismatch) (db:genpept-bct1) (de:e.coli mutl and miaa genes for mutl protein anddelta2-isopentenylpyrophosphate trna transferase (partial).) (le:267) (re:2114) (di:direct) ECMUTLG Z11831 g42067 Escherichia coli 562 -11533661 7500886159 mutl (fn:methyl directed mismatch repair) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 470; alternate gene name mut-25) (le:88240) (re:90087) (di:direct) ECOUW93 U14003 g537011 Escherichia coli 562 -11533661 233437 mutl enzyme in methyl-directed mismatch repair (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 379 of 400 of the completegenome.) (nt:ol15; 100 pct identical to mutl\_ecoli sw: p23367;) (le:5126) (re:6973) (di:direct) AE000489 AE000489 g1790612 Escherichia coli 562 -11533661 84740 mutl (de:dna mismatch repair protein mutl) (db:swissprot) MUTL\_ECOLI P23367 ESCHERICHIA COLI 562 -11533661

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834766	8896	31052	342	114

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834772	8897	31053	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834775	8898	31054	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834778	8899	31055	192	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834780	8900	31056	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834797	8901	31057	795	264

Description

6500729804 aidb:b4187 aidb protein (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b4187 b4187 Escherichia coli 562 -11533662 59003 aidb (de:aidb protein) (db:swissprot) AIDB\_ECOLI P33224 ESCHERICHIA COLI 562 -11533662 233754 (db:genpept-bct1) (de:escherichia coli (aidb) gene, complete cds.) (nt:putative; homology to acyl coa dehydrogenases and) (le:612) (re:2252) (di:direct) ECOAIDB L20915 g457172 Escherichia coli 562 -11533662 237392 aidb (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 18553; induced by alkylating agents; an) (le:105088) (re:106728) (di:direct) ECOUW93 U14003 g537028 Escherichia coli 562 -11533662 7500876703 aidb putative acyl coenzyme a dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 380 of 400 of the completegenome.) (nt:o546; 100 pct identical to aidb\_ecoli sw: p33224;) (le:9944) (re:11584) (di:direct) AE000490 AE000490 g1790630 Escherichia coli 562 -11533662 162665 (de:acyl coa dehydrogenase homolog - escherichia coli) S56412 S56412 Escherichia coli 562 -11533662 5000690883 (de:(ecoli\_4070) (pn:aidb protein) (gn:aidb) (gtcfc:10.8) (ec:) (aidb\_ecoli) (keggfc:11.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_4070 ECOLI\_4070 Escherichia coli 562 10001747

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834819	8902	31058	594	197

Description

6500729805 prib:b4201 primosomal replication protein n (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b4201 b4201 Escherichia coli 562 -11533663 131415 prib primosomal replication protein n:prib protein (cl:primosomal protein n) (db:pir1.dat) (mp:95.5 min) Q4ECFR A30281 Escherichia coli 562 -11533663 238163 prib (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:116352) (re:116666) (di:direct) ECOUW93 U14003 g537042 Escherichia coli 562 -11533663 7500953656 (db:genpept-bct1) (de:e. coli genes rpsf, rpsr and rpli for ribosomal proteins s6, s18,19.) (nt:unidentified reading frame (aa 1-104)) (le:850) (re:1164) (di:direct) ECRPSFRI X04022 g42846 Escherichia coli 562 -11533663 237406 prib primosomal replication protein n (fn:factor; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 381 of 400 of the completegenome.) (nt:o104; 100 pct identical amino acid sequence and) (le:9186) (re:9500) (di:direct) AE000491 AE000491 g1790645 Escherichia coli 562 -11533663 5000690884 (de:(ecoli\_4084) (pn:primosomal replication protein n) (gn:prib) (gtcfc:10.8) (ec:) (prib\_ecoli) (keggfc:11.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_4084 ECOLI\_4084 Escherichia coli 562 10068114

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834825	8903	31059	1032	343

Description

GTC ORF with score 405 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid d1022.) (nt:similar to ubiquitin conjugating enzyme) (le:27076:27352:27489:27642) (re:27297:27436:27594:27979) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834848	8904	31060	279	92

Description

6500729806 hsdS:hss:b4348 type i restriction enzyme ecoki specificity protein:s protein (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b4348 b4348 Escherichia coli 562 -11533664 237554 hsdS:hss (de:type i restriction enzyme ecoki specificity protein (s protein)) (db:swissprot) T1SK\_ECOLI P05719 ESCHERICHIA COLI 562 -11533664 124380 hsdS type i site-specific deoxyribonuclease:ecok chain s:type i restriction enzyme:ecok:s chain:type i restriction-modification system:ecok:s chain (cl:type i site-specific deoxyribonuclease ecok chain s) (ec:3.1.21.3) (db:pir1.dat) (mp:99 min) NDECKS A30369 Escherichia coli 562 -11533664 5000690885 hsdS (db:genpept-bct1) (de:e. coli specificity gene of ecok restriction enzyme (hsdS).) (le:227) (re:1621) (di:direct) ECHSDK V00288 g41746 Escherichia coli 562 -11533664 7500892670 hsdS (fn:specificity determinant for hsdM and hsdR) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 619; alternate gene name hss) (le:270901) (re:272295) (di:complement) ECOUW93 U14003 g537190 Escherichia coli 562 -11533664 233152 hsdS specificity determinant for hsdM and hsdR (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 395 of 400 of the completegenome.) (nt:f464; 100 pct identical to t1sk\_ecoli sw: p05719;) (le:6079) (re:7473) (di:complement) AE000505 AE000505 g1790807 Escherichia coli 562 -11533664 100268 hsdS:hss (de:type i restriction enzyme ecoki specificity protein (s protein)) (db:swissprot) T1SK\_ECOLI P05719 ESCHERICHIA COLI 562 -11533664

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834861	8905	31061	771	256

Description

6500729807 hsdm:hsm:b4349 type i restriction enzyme ecoki m protein:type i restriction enzyme ecok i m protein (gtcfc:10.8) (ec:2.1.1.72) (keggfc:14.1) (rileyfc:3.1.7) (db:gtc-escherichia coli) b4349 b4349 Escherichia coli 562 -11533665 237555 hsdm:hsm (ec:2.1.1.72) (de:type i restriction enzyme ecok i m protein,) (db:swissprot) T1M\_ECOLI P08957 ESCHERICHIA COLI 562 -11533665 123261 hsdm site-specific dna-methyltransferase adenine-specific:ecok:dna methylase m:type i restriction enzyme:ecok:m chain:type i restriction-modification system:ecok:m chain:type i site-specific deoxyribonuclease:ecok:m chain (cl:site-specific methyltransferase (adenine-specific) ecok) (ec:2.1.1.72) (db:pir1.dat) (mp:99 min) XYECHM B30375 Escherichia coli 562 -11533665 5000690886 (db:genpept-bct1) (de:e. coli genes hsdR and hsdM.) (nt:hsdm gene product (aa 1 - 529)) (le:4002) (re:5591) (di:direct) ECHSDRM X06545 g41753 Escherichia coli 562 -11533665 7500892668 hsdm (fn:dna methylase m; host modification) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 621; alternate gene names hs, hsm, hsp,) (le:272292) (re:273881) (di:complement) ECOUW93 U14003 g537191 Escherichia coli 562 -11533665 233157 hsdm host modification:dna methylase m (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:2.1.1.72) (de:escherichia coli k-12 mg1655 section 395 of 400 of the completegenome.) (nt:f529; 100 pct identical to t1m\_ecoli sw: p08957; cg) (le:7470) (re:9059) (di:complement) AE000505 AE000505 g1790808 Escherichia coli 562 -11533665 100258 hsdm:hsm (ec:2.1.1.72) (de:type i restriction enzyme ecok i m protein,) (db:swissprot) T1M\_ECOLI P08957 ESCHERICHIA COLI 562 -11533665

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834862	8906	31062	234	77

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834881	8907	31063	951	316

Description

6500729808 mrr:b4351 restriction system protein (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b4351 b4351 Escherichia coli 562 -11533666 237557 mrr (de:mrr restriction system protein) (db:swissprot) MRR\_ECOLI P24202 ESCHERICHIA COLI 562 -11533666 164104 mrr mrr protein (db:pir2.dat) A40368 A40368 Escherichia coli 562 -11533666 5000690887 mrr mrr protein (db:genpept-bct1) (de:e. coli mrr gene for mrr protein (including hsdR gene (partial) anda downstream orf of unknown function).) (le:215) (re:1129) (di:direct) ECMRR X54198 g42020 Escherichia coli 562 -11533666 7500885888 mrr (fn:restriction of methylated adenine) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 18139) (le:277782) (re:278696) (di:direct) ECOUW93 U14003 g537193 Escherichia coli 562 -11533666 233408 mrr restriction of methylated adenine (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 396 of 400 of the completegenome.) (nt:o304; cg site no. 18139) (le:97) (re:1011) (di:direct) AE000506 AE000506 g1790811 Escherichia coli 562 -11533666 84238 mrr (de:mrr restriction system protein) (db:swissprot) MRR\_ECOLI P24202 ESCHERICHIA COLI 562 -11533666

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834888	8908	31064	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834898	8909	31065	600	199

Description

6500729809 dnac:dnad:b4361 dna replication protein dnac (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b4361 b4361 Escherichia coli 562 -11533667 237569 (sr:e.coli (strain k12 c600) dna (1); clone pjkl37 (2)) (db:genpept-bct1) (de:e.coli dna operon encoding normal and stable dna replication proteins p-14, dnac and p-18, complete cds.) (nt:dnac protein) (le:1065) (re:1802) (di:direct) ECODNATC J04030 g145791 Escherichia coli 562 -11533667 7500974874 dnac (fn:dna biosynthesis; initiation and chain) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 849; alternate gene name dnad) (le:291070) (re:291807) (di:complement) ECOUW93 U14003 g537204 Escherichia coli 562 -11533667 234194 dnac chromosome replication:initiation and chain (fn:putative enzyme; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 397 of 400 of the completegenome.) (nt:f245; 99 pct identical amino acid sequence and) (le:3187) (re:3924) (di:complement) AE000507 AE000507 g1790823 Escherichia coli 562 -11533667 5000690888 (de:(ecoli\_4246) (pn:chromosome replication; initiation and chain elongation) (gn:dnac) (gtcfc:10.8) (ec:) (dnac\_ecoli) (keggfc:11.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_4246 ECOLI\_4246 Escherichia coli 562 10124163

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834905	8910	31066	597	198

Description

6500729810 dnat:b4362 primosomal protein i (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b4362 b4362 Escherichia coli 562 -11533668 154679 dnat replication termination factor dnat:primosomal protein i (cl:primosomal protein i) (db:pir1.dat) (mp:99 min) RMECI S56589 Escherichia coli 562 -11533668 237570 (sr:e.coli (strain k12 c600) dna (1); clone pjki37 (2)) (db:genpept-bct1) (de:e.coli dna operon encoding normal and stable dna replication proteins p-14, dnat, dnac and p-18, complete cds.) (nt:prepriming protein i) (le:523) (re:1062) (di:direct) ECODNATC J04030 g145790 Escherichia coli 562 -11533668 7500953655 dnat (fn:dna biosynthesis; primosomal protein i) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 839) (le:291810) (re:292349) (di:complement) ECOUW93 U14003 g537205 Escherichia coli 562 -11533668 234193 dnat dna biosynthesis:primosomal protein i (fn:factor; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 397 of 400 of the complete genome.) (nt:f179; 99 pct identical amino acid sequence and) (le:3927) (re:4466) (di:complement) AE000507 AE000507 g1790824 Escherichia coli 562 -11533668 5000690889 (de:(ecoli\_4247) (pn:dna biosynthesis; primosomal protein i) (gn:dnat) (gtcfc:10.8) (ec:) (dnat\_ecoli) (keggfc:11.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_4247 ECOLI\_4247 Escherichia coli 562 10081679

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834906	8911	31067	639	212

Description

6500729811 rob:b4396 right origin-binding protein (gtcfc:10.8) (keggfc:14.2) (rileyfc:3.1.7) (db:gtc-escherichia coli) b4396 b4396 Escherichia coli 562 -11533669 95878 rob (de:right origin-binding protein) (db:swissprot) ROB\_ECOLI P27292 ESCHERICHIA COLI 562 -11533669 164561 rob right oric-binding protein:rob protein (db:pir2.dat) (mp:99.8 min) JU0158 JU0158 Escherichia coli 562 -11533669 237601 rob right origin-binding protein (sr:escherichia coli (sub\_strain w3110, strain k-12) (library: embl) (db:genpept-bct1) (de:e.coli right origin-binding protein (rob) gene, complete cds, and positive regulatory protein for pho operon (phom) gene, 5' end.) (le:295) (re:1164) (di:direct) ECOROBPHOM M97495 g147692 Escherichia coli 562 -11533669 7500890484 rob (fn:right origin-binding protein) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:325274) (re:326143) (di:complement) ECOUW93 U14003 g537236 Escherichia coli 562 -11533669 235862 rob right origin-binding protein (fn:factor; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 399 of 400 of the complete genome.) (nt:f289; 100 pct identical to rob\_ecoli sw: p27292) (le:9629) (re:10498) (di:complement) AE000509 AE000509 g1790857 Escherichia coli 562 -11533669 5000690890 (de:(ecoli\_4278) (pn:right origin-binding protein) (gn:rob) (gtcfc:10.8) (ec:) (rob\_ecoli) (keggfc:11.2) (rileyfc:3.1.7) (db:gtc-escherichia coli)) ECOLI\_4278 ECOLI\_4278 Escherichia coli 562 10037825

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834907	8912	31068	411	136

Description

GTC ORF with score 102 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f32e10.) (nt:similar to ldl-receptor ligand-binding repeat.) (le:9240:9361:9553:9954) (re:9316:9505:9665:10011) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834910	8913	31069	201	66
<u>Description</u>				
6500729812 rnhb:b0183 ribonuclease hii:rnase hii (gtcfc:10.9) (ec:3.1.26.4) (keggfc:14.1) (rileyfc:3.2.1) (db:gtc-escherichia coli) b0183 b0183 Escherichia coli 562 -11533670 95718 rnhb (ec:3.1.26.4) (de:ribonuclease hii, (rnase hii)) (db:swissprot) RNH2_ECOLI P10442 ESCHERICHIA COLI 562 -11533670 7000686423 rnhb ribonuclease h:ii:ribonuclease hii:rnase hii (cl:ribonuclease hii) (ec:3.1.26.4) (db:pir1.dat) (mp:4 min) QQECBE G64742 Escherichia coli 562 -11533670 7500890447 rnhb ribonuclease hii (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:35568) (re:36164) (di:direct) ECU70214 U70214 g1552760 Escherichia coli 562 -11533670 239811 rnhb rnase hii:degrades rna of dna-rna hybrids (fn:enzyme; degradation of rna) (db:genpept-bct2) (ec:3.1.26.4) (de:escherichia coli k-12 mg1655 section 17 of 400 of the completegenome.) (nt:o198; 100 pct identical to 195 aa from) (le:9713) (re:10309) (di:direct) AE000127 AE000127 g1786380 Escherichia coli 562 -11533670 5000690894 (de:(ecoli_183) (pn:rnase hii, degrades rna of dna-rna hybrids) (gn:rnhb) (gtcfc:10.9) (ec:3.1.26.4) (rnh2_ecoli) (keggfc:11.1) (rileyfc:3.2.1) (db:gtc-escherichia coli)) ECOLI_183 ECOLI_183 Escherichia coli 562 10122698				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834932	8914	31070	225	74

Description

6500729813 rnha:rnh:dasf:hera:sdra:b0214 ribonuclease hi:rnase  
hi:ribonuclease h:rnase h (gtcfc:10.9) (ec:3.1.26.4) (keggfc:14.1)  
(rileyfc:3.2.1) (db:gtc-escherichia coli) b0214 b0214 Escherichia coli 562  
-11533671 239835 rnha:rnh:dasf:hera:sdra (ec:3.1.26.4) (de:ribonuclease hi,  
(rnase hi) (ribonuclease h) (rnase h)) (db:swissprot) RNH\_ECOLI P00647  
ESCHERICHIA COLI 562 -11533671 124406 rnha:rnh ribonuclease h  
(cl:ribonuclease h) (ec:3.1.26.4) (db:pir1.dat) (mp:5 min) NRECH A92401  
Escherichia coli 562 -11533671 235848 (db:genpept-bct1) (de:e. coli  
mutd(dnaq)-rnh region for dna polymerase iii epsilon subunit and rnaase h.)  
(nt:rnh polypeptide (aa 1-155)) (le:49) (re:516) (di:complement) ECMUTD  
X04027 g42062 Escherichia coli 562 -11533671 235850 (sr:escherichia coli  
k12 dna) (db:genpept-bct1) (de:e.coli rnase h gene coding for ribonuclease h.)  
(nt:ribonuclease h (rnase h)) (le:243) (re:710) (di:direct) ECORNH K00552  
g147677 Escherichia coli 562 -11533671 236192 rnase h ribonuclease h  
(sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli dnaq  
(mutd) gene encoding dna polymerase iii epsilon subunit and ribonuclease h  
(rnase h) gene, complete cds.) (le:1076) (re:1543) (di:direct) ECORNHQ K00985  
g147680 Escherichia coli 562 -11533671 238103 rnase h ribonuclease h  
(sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (ec:3.1.26.4)  
(de:escherichia coli genome, 4.0 - 6.0 min region.) (le:45076) (re:45543)  
(di:complement) ECOTSF D83536 g1208974 Escherichia coli 562 -11533671  
5000690895 rnase h ribonuclease h (db:genpept-bct1) (ec:3.1.26.4) (de:e. coli  
gene rnase h coding for ribonuclease h (rnase, ec 3.1.26.4).) (le:243) (re:710)  
(di:direct) ECRNHX V00337 g42777 Escherichia coli 562 -11533671 303269 rnase h  
ribonuclease h (db:genpept-bct1) (de:escherichia coli chromosome minutes  
4-6.) (le:66610) (re:67077) (di:complement) ECU70214 U70214 g1552784  
Escherichia coli 562 -11533671 233433 rnase h ribonuclease h:degrades rna of dna-rna  
hybrids (fn:enzyme; degradation of rna) (db:genpept-bct2) (ec:3.1.26.4)  
(de:escherichia coli k-12 mg1655 section 20 of 400 of the complete genome.)  
(nt:f155; 100 pct identical to rnase\_h\_coli sw: p00647) (le:4564) (re:5031)  
(di:complement) AE000130 AE000130 g1786408 Escherichia coli 562 -11533671  
95726 rnha:rnh:dasf:hera:sdra (ec:3.1.26.4) (de:ribonuclease hi, (rnase hi)  
(ribonuclease h) (rnase h)) (db:swissprot) RNH\_ECOLI P00647 ESCHERICHIA COLI  
562 -11533671

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501834940	8915	31071	513	170

Description

GTC ORF with score 239 to: (sr:caenorhabditis elegans strain=bristol n2)  
(db:genpept-inv) (de:caenorhabditis elegans cosmid c01g5.) (nt:coded for by  
c. elegans cdna yk134d6.5; coded for) (le:23:333:947:1299)  
(re:283:637:1253:1378) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834945	8916	31072	591	196
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834953	8917	31073	387	128
<u>Description</u>				

6500729814 rna:rnsa:b0611 ribonuclease i precursor:enterobacter  
 ribonuclease:rnase i (gtcfc:10.9) (ec:3.1.27.6) (keggfc:14.1)  
 (rileyfc:3.2.1) (db:gtc-escherichia coli) b0611 b0611 Escherichia coli 562  
 -11533672 95732 rna:rnsa (ec:3.1.27.6) (de:(rnase i)) (db:swissprot)  
 RNI\_ECOLI P21338 ESCHERICHIA COLI 562 -11533672 139887 rna:rnsa  
 enterobacter ribonuclease:i precursor:ribonuclease i (cl:enterobacter  
 ribonuclease) (ec:3.1.27.6) (db:pir2.dat) (mp:14 min) JQ0777 JQ0777  
 Escherichia coli 562 -11533672 223111 rna ribonuclease i precursor  
 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #166)  
 (db:genpept-bct1) (de:escherichia coli genomic dna. (13.5 - 13.9 min).)  
 (le:13953) (re:14759) (di:complement) D90701 D90701 g1651249 Escherichia  
 coli 562 -11533672 223115 rna ribonuclease i precursor rnase i  
 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #167)  
 (db:genpept-bct1) (de:escherichia coli genomic dna. (13.7 - 14.0 min).)  
 (le:6138) (re:6944) (di:complement) D90702 D90702 g1651254 Escherichia coli  
 562 -11533672 7500890452 rna ribonuclease i (sr:escherichia coli k12  
 (strain w3110) dna) (db:genpept-bct1) (ec:3.1.27.6) (de:e.coli ribonuclease  
 i gene, complete cds.) (nt:on the 100 min. genetic map) (le:250) (re:1056)  
 (di:direct) ECORIBI34 M55687 g147653 Escherichia coli 562 -11533672 235832  
 rna rnase i:cleaves phosphodiester bond between any (fn:enzyme; degradation  
 of rna) (db:genpept-bct2) (ec:3.1.27.6) (de:escherichia coli k-12 mg1655  
 section 56 of 400 of the completegenome.) (nt:f268; 100 pct identical to  
 rni\_ecoli sw: p21338;) (le:7585) (re:8391) (di:complement) AE000166 AE000166  
 g1786828 Escherichia coli 562 -11533672 5000690896 rna ribonuclease i  
 precursor ec 3.1.27.6 (sr:escherichia coli(strain:k12) dna, clone:kohara  
 clone #166) (db:genpept) (de:escherichia coli genomic dna. (13.6 - 14.0  
 min).) (nt:orf\_id:o167#6; similar to swissprot accession) (le:13954)  
 (re:14760) (di:complement) D90701 D90701 g1651249 Escherichia coli 562  
 -11533672 7502851957 rna ribonuclease i precursor ec 3.1.27.6  
 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #167) (db:genpept)  
 (de:escherichia coli genomic dna. (13.7 - 14.1 min).) (nt:orf\_id:o167#6;  
 similar to swissprot accession) (le:6138) (re:6944) (di:complement) D90702  
 D90702 g1651254 Escherichia coli 562 -11533672

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834959	8918	31074	342	113

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834965	8919	31075	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834979	8920	31076	552	183

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834992	8921	31077	975	324

Description

6500729815 rnb:b1286 exoribonuclease ii:ribonuclease ii:rnase ii (gtcfc:10.9) (ec:3.1.13.1) (keggfc:14.1) (rileyfc:3.2.1) (db:gtc-escherichia coli) b1286 b1286 Escherichia coli 562 -11533673 95691 rnb (ec:3.1.13.1) (de:exoribonuclease ii, (ribonuclease ii) (rnase ii)) (db:swissprot) RNB\_ECOLI P30850 ESCHERICHIA COLI 562 -11533673 7000686420 rnb exoribonuclease ii::ribonuclease ii (cl:exoribonuclease ii) (ec:3.1.13.1) (db:pir2.dat) A64877 A64877 Escherichia coli 562 -11533673 223514 rnb exoribonuclease ii ec 3.1.13.1 ribonuclease (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #255(28.8-29.2 min.)).) (nt:orf\_id:o255#13; similar to (swissprot accession) (le:9247) (re:11181) (di:complement) D90766 D90766 g1742100 Escherichia coli 562 -11533673 223522 rnb exoribonuclease ii ec 3.1.13.1 ribonuclease (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #256(29.0-29.4 min.)).) (nt:orf\_id:o255#13; similar to (swissprot accession) (le:2642) (re:4576) (di:complement) D90767 D90767 g1742109 Escherichia coli 562 -11533673 300317 rnb rnase ii:mrna degradation (fn:enzyme; degradation of rna) (db:genpept-bct2) (ec:3.1.13.1) (de:escherichia coli k-12 mg1655 section 116 of 400 of the completegenome.) (nt:f644; 99 pct identical to rnb\_ecoli sw: p30850; cg) (le:8470) (re:10404) (di:complement) AE000226 AE000226 g1787542 Escherichia coli 562 -11533673 5000690897 (de:(ecoli\_1246) (pn:rnase ii, mrna degradation) (gn:rnb) (gtcfc:10.9) (ec:3.1.13.1) (rnb\_ecoli) (keggfc:11.1) (rileyfc:3.2.1) (db:gtc-escherichia coli)) ECOLI\_1246 ECOLI\_1246 Escherichia coli 562 10119503



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501834993	8922	31078	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835004	8923	31079	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835005	8924	31080	495	164

Description

6500729816 rnt:b1652 ribonuclease t:exoribonuclease t:rnase t (gtcfc:10.9) (ec:3.1.13.-) (keggfc:14.1) (rileyfc:3.2.1) (db:gtc-escherichia coli) b1652 b1652 Escherichia coli 562 -11533674 95843 rnt (ec:3.1.13.-) (de:ribonuclease t, (exoribonuclease t) (rnase t)) (db:swissprot) RNT\_ECOLI P30014 ESCHERICHIA COLI 562 -11533674 164566 rnt ribonuclease t:rnt:rnase t (ec:3.1.13.-) (db:pir2.dat) A45065 A45065 Escherichia coli 562 -11533674 235858 rnt rnase t:degrades trna (fn:enzyme; degradation of rna) (db:genpept-bct2) (ec:3.1.13.-) (de:escherichia coli k-12 mg1655 section 150 of 400 of the completegenome.) (nt:o215; 100 pct identical to rnt\_ecoli sw: p30014; cg) (le:3682) (re:4329) (di:direct) AE000260 AE000260 g1787941 Escherichia coli 562 -11533674 7500890480 rnt rnaset (sr:escherichia coli (strain k-12) dna) (db:genpept-bct2) (de:e. coli rnaset (rnt) gene, long helicase-related (lhr) gene,complete cds, and glutaredoxin-like (yhdd) gene, 3' end.) (le:193) (re:840) (di:direct) ECORNTLHR L01622 g147688 Escherichia coli 562 -11533674 5000690898 (de:(ecoli\_1611) (pn:rnase t, degrades trna) (gn:rnt) (gtcfc:10.9) (ec:3.1.13.-) (rnt\_ecoli) (keggfc:11.1) (rileyfc:3.2.1) (db:gtc-escherichia coli)) ECOLI\_1611 ECOLI\_1611 Escherichia coli 562 10037790

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835006	8925	31081	372	123

Description

6500729817 rnd:b1804 ribonuclease d:rnase d (gtcfc:10.9) (ec:3.1.26.3) (keggfc:14.1) (rileyfc:3.2.1) (db:gtc-escherichia coli) b1804 b1804 Escherichia coli 562 -11533675 300922 rnd (ec:3.1.26.3) (de:ribonuclease d, (rnase d)) (db:swissprot) RND\_ECOLI P09155 ESCHERICHIA COLI 562 -11533675 124375 rnd ribonuclease iii::ribonuclease d (cl:ribonuclease d) (ec:3.1.26.3) (db:pir1.dat) (mp:40 min) NRECD S01223 Escherichia coli 562 -11533675 224280 rnd ribonuclease d ec 3.1.13.- (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #332(40.4-40.7 min.)) (nt:orf\_id:o332#13; similar to (pir accession number) (le:13060) (re:14187) (di:complement) D90823 D90823 g1736427 Escherichia coli 562 -11533675 300931 rnd ribonuclease d ec 3.1.13.- (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #333(40.5-40.8 min.)) (nt:orf\_id:o332#13; similar to (pir accession number) (le:8530) (re:9657) (di:complement) D90824 D90824 g1736437 Escherichia coli 562 -11533675 5000690899 (db:genpept-bct1) (de:e. coli rnd gene for ribonuclease d.) (nt:ribonuclease d (aa 1-375) (start codon uug)) (le:169) (re:1296) (di:direct) ECRND X07055 g581215 Escherichia coli 562 -11533675 238100 rnd rnase d:processes trna precursor (fn:enzyme; degradation of rna) (db:genpept-bct2) (ec:3.1.26.3) (de:escherichia coli k-12 mg1655 section 164 of 400 of the completegenome.) (nt:f375; 100 pct identical to rnd\_ecoli sw: p09155; cg) (le:12603) (re:13730) (di:complement) AE000274 AE000274 g1788105 Escherichia coli 562 -11533675 95702 rnd (ec:3.1.26.3) (de:ribonuclease d, (rnase d)) (db:swissprot) RND\_ECOLI P09155 ESCHERICHIA COLI 562 -11533675 224289 rnd ribonuclease d ec 3.1.13.- (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #333(40.5-40.8 min.)) (nt:orf\_id:o332#13; similar to (pir accession number) (le:8530) (re:9657) (di:complement) D90824 D90824 g1736437 Escherichia coli 562 -11533675

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835009	8926	31082	258	85

Description

6500729818 rnc:b2567 ribonuclease iii:rnase iii (gtcfc:10.9) (ec:3.1.26.3) (keggfc:14.1) (rileyfc:3.2.1) (db:gtc-escherichia coli) b2567 b2567 Escherichia coli 562 -11533676 239521 rnc (ec:3.1.26.3) (de:ribonuclease iii, (rnase iii)) (db:swissprot) RNC\_ECOLI P05797 ESCHERICHIA COLI 562 -11533676 7000686421 rnc ribonuclease iii (cl:ribonuclease iii:double-stranded rna-binding repeat homology) (ec:3.1.26.3) (db:pir1.dat) NREC3 F65034 Escherichia coli 562 -11533676 238099 ribonuclease iii (sr:escherichia coli (strain k12) (library: kohara) dna, clone 7g4) (db:genpept-bct1) (de:escherichia coli ribonuclease iii and other genes, complete cds.) (le:10851) (re:11531) (di:complement) ECOK12RIII D64044 g987642 Escherichia coli 562 -11533676 5000690900 (db:genpept-bct1) (de:e. coli rnc gene for ribonuclease iii.) (nt:ribonuclease iii (rnc) (aa 1-226)) (le:219) (re:899) (di:direct) ECRNCIII X02946 g42769 Escherichia coli 562 -11533676 7500890438 rnc rnase iii (db:genpept-bct1) (ec:3.1.26.3) (de:escherichia coli k-12 genome, approximately 55 minutes.) (nt:cg site no. 271) (le:14627) (re:15307) (di:complement) ECU36841 U36841 g1033156 Escherichia coli 562 -11533676 234892 rnc rnase iii:ds rna (fn:enzyme; degradation of rna) (db:genpept-bct2) (ec:3.1.26.3) (de:escherichia coli k-12 mg1655 section 233 of 400 of the completegenome.) (nt:f226; 100 pct identical to rnc\_ecoli sw: p05797; cg) (le:3143) (re:3823) (di:complement) AE000343 AE000343 g1788920 Escherichia coli 562 -11533676 95698 rnc (ec:3.1.26.3) (de:ribonuclease iii, (rnase iii)) (db:swissprot) RNC\_ECOLI P05797 ESCHERICHIA COLI 562 -11533676

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835010	8927	31083	297	98

Description

6500729819 rph:b3643 rnase ph (gtcfc:10.9) (ec:2.7.7.56) (keggfc:14.1) (rileyfc:3.2.1) (db:gtc-escherichia coli) b3643 b3643 Escherichia coli 562 -11533677 7500974866 rph rnase ph (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:5255) (re:5941) (di:complement) ECOUW82 L10328 g290493 Escherichia coli 562 -11533677 236881 rph rnase ph (fn:enzyme; degradation of rna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 331 of 400 of the completegenome.) (nt:f228; this 228 aa orf is 100 pct identical (0 gaps)) (le:7758) (re:8444) (di:complement) AE000441 AE000441 g1790074 Escherichia coli 562 -11533677 5000690901 (de:(ecoli\_3563) (pn:rnase ph) (gn:rph) (gtcfc:10.9) (ec:2.7.7.56) (rnph\_ecoli) (keggfc:11.1) (rileyfc:3.2.1) (db:gtc-escherichia coli)) ECOLI\_3563 ECOLI\_3563 Escherichia coli 562 10124050

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835027	8928	31084	1230	409

#### Description

6500729820 rnpa:b3704 rnase p:protein component:ribonuclease p protein component:protein c5:rnase p (gtcfc:10.9) (ec:3.1.26.5) (keggfc:14.1) (rileyfc:3.2.1) (db:gtc-escherichia coli) b3704 b3704 Escherichia coli 562 -11533678 95760 rnase p (ec:3.1.26.5) (de:ribonuclease p protein component, (protein c5) (rnase p)) (db:swissprot) RNPA\_ECOLI P06277 ESCHERICHIA COLI 562 -11533678 124408 rnase p:protein component:protein c5 (cl:ribonuclease p, protein component) (ec:3.1.26.5) (db:pir1.dat) (mp:83 min) NRECP A00794 Escherichia coli 562 -11533678 236940 rnase p (sr:e.coli k12 dna, clones pfhc507 and pfhc508) (db:genpept-bct1) (de:e.coli rnase p and rpmh genes coding for the protein component of ribonuclease p (rnase p) and ribosomal protein l34.) (nt:ribonuclease p protein component (gtg start codon)) (le:479) (r... ECORNPA M11056 g147683 Escherichia coli 562 -11533678 7500890463 rnase p:cg site no. 267 rnase p:protein component (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e.coli; the region from 81.5 to 84.5 minutes.) (le:73891) (re:74250) (di:direct) ECUW82 L10328 g290552 Escherichia coli 562 -11533678 235853 rnase p:protein component:protein c5 (fn:enzyme; degradation of rna) (db:genpept-bct2) (ec:3.1.26.5) (de:escherichia coli k-12 mg1655 section 337 of 400 of the complete genome.) (nt:ol19; 100 pct identical amino acid sequence and) (le:7507) (re:7866) (di:direct) AE000447 AE000447 g1790139 Escherichia coli 562 -11533678 5000690902 (de:(ecoli\_3622) (pn:rnase p, protein component; processes trna, 4) (gn:rnase p) (gtcfc:10.9) (ec:3.1.26.5) (rnase\_p) (keggfc:11.1) (rileyfc:3.2.1) (db:gtc-escherichia coli)) ECOLI\_3622 ECOLI\_3622 Escherichia coli 562 10037709

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835030	8929	31085	420	139

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835037	8930	31086	285	94

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835052	8931	31087	222	73

Description

6500729821 fhua:tona:b0150 ferrichrome-iron receptor precursor:ferric hydroxamate uptake (gtcfc:11.1:12.6) (keggfc:11.1) (rileyfc:3.3.1) (db:gtc-escherichia coli) b0150 b0150 Escherichia coli 562 -11533679 71553 fhua:tona (de:ferrichrome-iron receptor precursor (ferric hydroxamate uptake)) (db:swissprot) FHUA\_ECOLI P06971 ESCHERICHIA COLI 562 -11533679 7000685233 fhua:tona ferrichrome-iron receptor precursor (cl:ferrichrome-iron receptor:tonb-dependent receptor amino-terminal homology:tonb-dependent receptor carboxyl-terminal homology) (db:pir1.dat) (mp:4 min) QRECFE F64738 Escherichia coli 562 -11533679 7500881438 fhua ferrichrome-iron receptor (sr:e.coli k12 dna, clone ppm27 (1), clone ppm18 (2)) (db:genpept-bct1) (de:e.coli fhua, fhuc and fhud genes encoding the ferrichrome-ironreceptor and two ferric aerobactin and ferric coprogen transportproteins, complete cds.) (nt:precursor) (le:540) (... ECOFHUACD M12486 g2226438 Escherichia coli 562 -11533679 4000714805 fhua outer membrane protein receptor for ferrichrome (fn:membrane; outer membrane constituents) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 14 of 400 of the completegenome.) (nt:o747; 99 pct identical to fhua\_ecoli sw: p06971;) (le:6821) (re:9064) (di:direct) AE000124 AE000124 g1786344 Escherichia coli 562 -11533679 5000690903 (de:(ecoli\_150) (pn:outer membrane protein receptor for ferrichrome, colicin m, and phages t1, t5, and phi80) (gn:fhua) (gtcfc:11.1) (ec:) (fhua\_ecoli) (keggfc:11.2) (rileyfc:3.3.1) (db:gtc-escherichia coli)) ECOLI\_150 ECOLI\_150 Escherichia coli 562 10122683

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835063	8932	31088	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835068	8933	31089	963	320
<u>Description</u>				
6500729822 hlp:skp:omph:b0178 histone-like protein hlp-1 precursor:dna-binding 17 kd protein (gtcfc:11.1) (keggfc:14.2) (rileyfc:3.3.1) (db:gtc-escherichia coli) b0178 b0178 Escherichia coli 562 -11533680 77119 hlp:skp:omph (de:histone-like protein hlp-1 precursor (dna-binding 17 kd protein)) (db:swissprot) HLP_AECOLI P11457 ESCHERICHIA COLI 562 -11533680 128604 hlp:skp outer membrane protein hlp precursor:dna-binding 17k protein:histone-like protein hlp (cl:dna-binding 17k protein) (db:pir1.dat) DNEC17 JT0304 Escherichia coli 562 -11533680 236167 (sr:e.coli (strain b) dna, clone pgah317) (db:genpept-bct1) (de:e.coli skp gene encoding the 17k protein, complete cds.) (nt:17k protein (gtg start codon)) (le:25) (re:510) (di:direct) ECOSKP M21118 g147822 Escherichia coli 562 -11533680 239806 hlp protein precursor (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (le:10040) (re:10525) (di:direct) ECOTSF D83536 g1208949 Escherichia coli 562 -11533680 303244 hlp histone-like protein (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:31557) (re:32042) (di:direct) ECU70214 U70214 g1552755 Escherichia coli 562 -11533680 235983 hlp histone-like protein:located in outer membrane (fn:factor; basic proteins - synthesis,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 17 of 400 of the completegenome.) (nt:o161; 100 pct identical to hlp_ecoli sw:) (le:5702) (re:6187) (di:direct) AE000127 AE000127 g1786375 Escherichia coli 562 -11533680 5000690904 (de:(ecoli_178) (pn:histone-like protein, located in outer membrane or nucleoid) (gn:hlp) (gtcfc:11.1) (ec:) (hlp_ecoli) (keggfc:11.2) (rileyfc:3.3.1) (db:gtc-escherichia coli)) ECOLI_178 ECOLI_178 Escherichia coli 562 10019481				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835070	8934	31090	477	158

Description

6500729823 phoe:ompe:b0241 outer membrane pore protein e precursor  
 (gtcfc:11.1) (keggfc:14.2) (rileyfc:3.3.1) (db:gtc-escherichia coli) b0241  
 b0241 Escherichia coli 562 -11533681 303282 phoe:ompe (de:outer membrane  
 pore protein e precursor) (db:swissprot) PHOE\_ECOLI P02932 ESCHERICHIA COLI  
 562 -11533681 130835 phoe outer membrane porin phoe precursor (cl:outer  
 membrane protein phoe) (db:pir1.dat) (mp:6 min) MMECPE A03432 Escherichia  
 coli 562 -11533681 237804 phoe outer membrane pore protein e precursor  
 (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia  
 coli genome, 4.0 - 6.0 min region.) (le:67812) (re:68867) (di:complement)  
 ECOTSF D83536 g1208987 Escherichia coli 562 -11533681 5000690905 phoe phoe  
 protein (db:genpept-bct1) (de:e. coli gene phoe encoding the phosphate  
 limitation inducible outermembrane pore protein.) (le:475) (re:1530)  
 (di:direct) ECPHOE V00316 g42391 Escherichia coli 562 -11533681 236205 phoe  
 outer membrane pore protein e e:ic:nmpab (fn:membrane; outer membrane  
 constituents) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 22  
 of 400 of the completengenome.) (nt:f351; 100 pct identical to phoe\_ecoli sw:  
 p02932) (le:4985) (re:6040) (di:complement) AE000132 AE000132 g1786436  
 Escherichia coli 562 -11533681 89631 phoe:ompe (de:outer membrane pore  
 protein e precursor) (db:swissprot) PHOE\_ECOLI P02932 ESCHERICHIA COLI 562  
 -11533681

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835080	8935	31091	579	192
<u>Description</u>				
<p>6500729824 acra:mtca:lir:b0463 acriflavin resistance protein a precursor (gtcfc:11.1:13.3) (keggfc:14.2) (rileyfc:3.3.1) (db:gtc-escherichia coli) b0463 b0463 Escherichia coli 562 -11533682 58291 acra:mtca:lir (de:acriflavin resistance protein a precursor) (db:swissprot) ACRA_ECOLI P31223 ESCHERICHIA COLI 562 -11533682 164001 acra acriflavin resistance protein acra precursor (cl:lipoyl/biotin-binding homology) (db:pir2.dat) A36938 A36938 Escherichia coli 562 -11533682 238442 acra acriflavine resistance protein (fn:resistance to acriflavine, hydrophobic) (sr:escherichia coli (strain k-12) (library: clarke-carbon) dna) (db:genpept-bct1) (de:e. coli acriflavine resistance proteins (acra and acrb) genes,complete cds.) (le:329) (re:1522) (di:direct) ECOACRAB M94248 g290405 Escherichia coli 562 -11533682 240238 acra 42 kda protein (fn:an is2 insertional mutation in e. coli strain) (db:genpept-bct1) (de:escherichia coli acra, acrb, and acrr genes, complete cds.) (le:1096) (re:2289) (di:direct) ECU00734 U00734 g532310 Escherichia coli 562 -11533682 7500876372 acra lipoprotein acra precursor (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:63874) (re:65067) (di:complement) ECU82664 U82664 g1773145 Escherichia coli 562 -11533682 233715 acra acridine efflux pump (fn:transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 42 of 400 of the completegenome.) (nt:f397; 100 pct identical to acra_ecoli sw: p31223) (le:7840) (re:9033) (di:complement) AE000152 AE000152 g1786668 Escherichia coli 562 -11533682 5000690906 (de:(ecoli_446) (pn:acridine efflux pump) (gn:acra) (gtcfc:11.1) (ec:) (acra_ecoli) (keggfc:11.2) (rileyfc:3.3.1) (db:gtc-escherichia coli)) ECOLI_446 ECOLI_446 Escherichia coli 562 10001071</p>				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835085	8936	31092	417	138

Description

6500729825 ompt:b0565 protease vii precursor:omptin:outer membrane protein 3b:protease a (gtcfc:10.11:11.1) (ec:3.4.21.87) (keggfc:14.1) (rileyfc:3.3.1) (db:gtc-escherichia coli) b0565 b0565 Escherichia coli 562 -11533683 235569 ompt (ec:3.4.21.87) (de:3b) (protease a)) (db:swissprot) OMPT\_ECOLI P09169 ESCHERICHIA COLI 562 -11533683 142254 ompt omptin:precursor:outer membrane protein 3b:outer membrane proteinase ompt:protease a:proteinase vii (cl:escherichia coli proteinase vii) (ec:3.4.21.87) (db:pir2.dat) A31387 A31387 Escherichia coli 562 -11533683 5000690907 (db:genpept-bct1) (de:e. coli ompt gene for outer membrane protease.) (nt:outer membrane preprotease (aa -20 to 297)) (le:460) (re:1413) (di:direct) ECOMPT1 X06903 g42166 Escherichia coli 562 -11533683 240074 protease (sr:escherichia coli (sub\_strain w3110, strain k-12) dna) (db:genpept-bct1) (de:escherichia coli protease vii gene, complete cds.) (le:451) (re:1404) (di:direct) ECOPROVII M23630 g147377 Escherichia coli 562 -11533683 7500887181 ompt protease vii precursor (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (le:25311) (re:26264) (di:complement) ECU82598 U82598 g1778478 Escherichia coli 562 -11533683 235179 ompt outer membrane protein 3b a:protease vii (fn:enzyme; outer membrane constituents) (db:genpept-bct2) (ec:3.4.21.87) (de:escherichia coli k-12 mg1655 section 51 of 400 of the completegenome.) (nt:f317; 100 pct identical to ompt\_ecoli sw: p09169) (le:7569) (re:8522) (di:complement) AE000161 AE000161 g1786777 Escherichia coli 562 -11533683 87694 ompt (ec:3.4.21.87) (de:3b) (protease a)) (db:swissprot) OMPT\_ECOLI P09169 ESCHERICHIA COLI 562 -11533683

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835086	8937	31093	288	95

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835114	8938	31094	1890	629

Description

6500729826 envy:b0566 porin thermoregulatory protein envy (gtcfc:11.1) (keggfc:14.2) (rileyfc:3.3.1) (db:gtc-escherichia coli) b0566 b0566 Escherichia coli 562 -11533684 70249 envy (de:porin thermoregulatory protein envy) (db:swissprot) ENVY\_ECOLI P10805 ESCHERICHIA COLI 562 -11533684 7000685167 envy transcription regulator envy:porin thermoregulatory protein envy:transcription regulation protein envy (db:pir2.dat) D64789 D64789 Escherichia coli 562 -11533684 223099 envy porin thermoregulatory protein envy (sr:escherichia coli(strain:k12) dna, clone:kohara clone #162) (db:genpept-bct1) (de:escherichia coli genomic dna. (12.6 - 12.9 min).) (le:562) (re:1323) (di:complement) D90699 D90699 g1651235 Escherichia coli 562 -11533684 7500881068 envy porin thermoregulatory protein (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (le:26778) (re:27539) (di:complement) ECU82598 U82598 g1778480 Escherichia coli 562 -11533684 240076 envy envelope protein:thermoregulation of porin (fn:structural component; outer membrane) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 51 of 400 of the completegenome.) (nt:f253; this 253 aa orf is 98 pct identical (2 gaps)) (le:9036) (re:9797) (di:complement) AE000161 AE000161 g1786778 Escherichia coli 562 -11533684 5000690908 envy envy protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #162) (db:genpept) (de:escherichia coli genomic dna. (12.6 - 12.9 min).) (nt:orf\_id:o162#1; similar to pir accession number) (le:562) (re:1323) (di:complement) D90699 D90699 g1651235 Escherichia coli 562 -11533684

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835136	8939	31095	300	99

Description

6500729827 rlpa:b0633 rare lipoprotein a precursor (gtcfc:11.1)  
(keggfc:14.2) (rileyfc:3.3.1) (db:gtc-escherichia coli) b0633 b0633  
Escherichia coli 562 -11533685 95578 rlpa (de:rare lipoprotein a precursor)  
(db:swissprot) RLPA\_ECOLI P10100 ESCHERICHIA COLI 562 -11533685 130873 rlpa  
rare lipoprotein a precursor (cl:rpla lipoprotein) (db:pir1.dat) (mp:15 min)  
LPECRA A28387 Escherichia coli 562 -11533685 223120 rlpa lipoprotein rlpa  
precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #168)  
(db:genpept-bct1) (de:escherichia coli genomic dna. (13.9 - 14.3 min).)  
(le:15165) (re:16253) (di:complement) D90703 D90703 g1651260 Escherichia  
coli 562 -11533685 223124 rlpa lipoprotein rlpa precursor (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #169) (db:genpept-bct1)  
(de:escherichia coli genomic dna. (14.3 - 14.7 min).) (le:350) (re:1438)  
(di:complement) D90704 D90704 g1651265 Escherichia coli 562 -11533685  
240146 (sr:e.coli (strain jml109) dna, clone pit101) (db:genpept-bct1)  
(de:e.coli rlpa gene encoding a 36kd lipoprotein, complete cds, mrdbgene, 3'  
end, and daga gene encoding d-alanine carboxypeptidase, 5'end.) (nt:36kd  
lipoprotein (rlpa) precursor) (le:64) (... ECORLPA M18276 g147660  
Escherichia coli 562 -11533685 7500890391 rlpa rare lipoprotein a precursor  
(db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.)  
(le:104732) (re:105820) (di:complement) ECU82598 U82598 g1778550 Escherichia  
coli 562 -11533685 235836 rlpa a minor lipoprotein (fn:membrane;  
macromolecule synthesis,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655  
section 58 of 400 of the completegenome.) (nt:f362; 100 pct identical to  
rlpa\_ecoli sw: p10100) (le:1837) (re:2925) (di:complement) AE000168 AE000168  
g1786852 Escherichia coli 562 -11533685 5000690909 rlpa lipoprotein rlpa  
precursor. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #168)  
(db:genpept) (de:escherichia coli genomic dna. (14.0 - 14.4 min).)  
(nt:orf\_id:o169#1; similar to pir accession number) (le:15165) (re:16253)  
(di:complement) D90703 D90703 g1651260 Escherichia coli 562 -11533685  
7502851958 rlpa lipoprotein rlpa precursor. (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #169) (db:genpept) (de:escherichia  
coli genomic dna. (14.3 - 14.7 min).) (nt:orf\_id:o169#1; similar to pir  
accession number) (le:350) (re:1438) (di:complement) D90704 D90704 g1651265  
Escherichia coli 562 -11533685

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835153	8940	31096	423	140

Description

GTC ORF with score 118 to: (or:Boreogadus saida) (db:genpept-vrt)  
(de:boreogadus saida antifreeze glycopeptide afgp polyprotein precursorgene,  
complete cds.) (nt:cleavage of polyprotein at conserved spacers r or)  
(le:209:281) (re:211:1801) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835160	8941	31097	1065	355

Description

6500729828 rlpb:b0641 rare lipoprotein b precursor (gtcfc:11.1)  
(keggfc:14.2) (rileyfc:3.3.1) (db:gtc-escherichia coli) b0641 b0641  
Escherichia coli 562 -11533686 95579 rlpb (de:rare lipoprotein b precursor)  
(db:swissprot) RLPB\_ECOLI P10101 ESCHERICHIA COLI 562 -11533686 7000686417  
rlpb lipoprotein rlpb precursor (cl:rlpb lipoprotein) (db:pir1.dat) (mp:15  
min) LPECRB G64798 Escherichia coli 562 -11533686 223127 rlpb lipoprotein  
rlpb precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone  
#169) (db:genpept-bct1) (de:escherichia coli genomic dna. (14.3 - 14.7  
min).) (le:7853) (re:8434) (di:complement) D90704 D90704 g1651268  
Escherichia coli 562 -11533686 7500890392 rlpb lipoprotein b precursor  
(db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.)  
(le:112235) (re:112816) (di:complement) ECU82598 U82598 g1778559 Escherichia  
coli 562 -11533686 240155 rlpb a minor lipoprotein (fn:membrane;  
macromolecule synthesis,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655  
section 58 of 400 of the completegenome.) (nt:f193; 99 pct identical to  
rlpb\_ecoli sw: p10101) (le:9340) (re:9921) (di:complement) AE000168 AE000168  
g1786860 Escherichia coli 562 -11533686 5000690910 rlpb lipoprotein rlpb  
precursor. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #169)  
(db:genpept) (de:escherichia coli genomic dna. (14.3 - 14.7 min).)  
(nt:orf\_id:o169#9; similar to pir accession number) (le:7853) (re:8434)  
(di:complement) D90704 D90704 g1651268 Escherichia coli 562 -11533686

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501835163	8942	31098	504	167

# Description

6500729829 ompf:tolf:cmlb:coa:cry:b0929 outer membrane protein f precursor:outer membrane protein 1a:ia:or b (gtcfc:11.1:12.13) (keggfc:12.1) (rileyfc:3.3.1) (db:gtc-escherichia coli) b0929 b0929 Escherichia coli 562 -11533687 87679 ompf:tolf:cmlb:coa:cry (de:protein 1a, ia, or b)) (db:swissprot) OMPF\_ECOLI P02931 ESCHERICHIA COLI 562 -11533687 130834 ompf:tolf:cmlb:coa:cry outer membrane porin ompf precursor:outer membrane protein 1a:outer membrane protein b (cl:outer membrane protein phoe) (db:pir1.dat) (mp:21 min) MMECF A93449 Escherichia coli 562 -11533687 223285 ompf outer membrane protein f precursor outer (sr:escherichia coli(strain:k12) dna, clone:kohara clone #218) (db:genpept-bct1) (de:escherichia coli genomic dna. (20.8 - 21.2 min).) (le:18248) (re:19336) (di:complement) D90730 D90730 g1651450 Escherichia coli 562 -11533687 223288 ompf outer membrane protein f precursor outer (sr:escherichia coli(strain:k12) dna, clone:kohara clone #219) (db:genpept-bct1) (de:escherichia coli genomic dna. (21.1 - 21.4 min).) (le:3047) (re:4135) (di:complement) D90731 D90731 g1651454 Escherichia coli 562 -11533687 7500887177 ompf (sr:escherichia coli k-12, clone lambda-ompf1 (1),(2)) (db:genpept-bct1) (de:e.coli ompf gene coding for major outer membrane protein ompf.) (nt:pro-ompf outer membrane protein) (le:457) (re:1545) (di:direct) ECOOMPJ J01655 g147010 Escherichia coli 562 -11533687 235278 ompf outer membrane protein 1a ia:b:f (fn:membrane; outer membrane constituents) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 85 of 400 of the completegenome.) (nt:f362; 100 pct identical to ompf\_ecoli sw:p02931) (le:2940) (re:4028) (di:complement) AE000195 AE000195 g1787160 Escherichia coli 562 -11533687 5000690911 cmlb outer membrane protein f precursor outer (sr:escherichia coli(strain:k12) dna, clone:kohara clone #218) (db:genpept) (de:escherichia coli genomic dna. (20.9 - 21.3 min).) (nt:orf\_id:o219#4; similar to swissprot accession) (le:18248) (re:19336) (di:complement) D90730 D90730 g1651450 Escherichia coli 562 -11533687 7502851959 cmlb outer membrane protein f precursor outer (sr:escherichia coli(strain:k12) dna, clone:kohara clone #219) (db:genpept) (de:escherichia coli genomic dna. (21.2 - 21.5 min).) (nt:orf\_id:o219#4; similar to swissprot accession) (le:3047) (re:4135) (di:complement) D90731 D90731 g1651454 Escherichia coli 562 -11533687

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501835167	8943	31099	285	94

# Description

6500729830 ompa:tolg:tut:con:b0957 outer membrane protein a:outer membrane protein a precursor:outer membrane protein ii (gtcfc:11.1) (keggfc:14.2) (rileyfc:3.3.1) (db:gtc-escherichia coli) b0957 b0957 Escherichia coli 562 -11533688 235263 ompa:tolg:tut:con (de:outer membrane protein a precursor (outer membrane protein ii\*)) (db:swissprot) OMPA\_ECOLI P02934 ESCHERICHIA COLI 562 -11533688 130864 ompa:tolg:tut:con outer membrane protein a precursor:outer membrane protein ii\* (cl:outer membrane protein a) (db:pir1.dat) (mp:22 min) MMECA A93707 Escherichia coli 562 -11533688 223298 ompa outer membrane protein a precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #222) (db:genpept-bct1) (de:escherichia coli genomic dna. (21.6 - 22.0 min).) (le:12365) (re:13405) (di:complement) D90733 D90733 g1651465 Escherichia coli 562 -11533688 223301 ompa outer membrane protein a precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #223) (db:genpept-bct1) (de:escherichia coli genomic dna. (21.9 - 22.2 min).) (le:536) (re:1576) (di:complement) D90734 D90734 g1651469 Escherichia coli 562 -11533688 7500887176 ompa ompa protein (db:genpept-bct1) (de:e. coli ompa gene (codes for the outer membrane protein ii\*).) (le:1037) (re:2077) (di:direct) ECOMPA V00307 g42161 Escherichia coli 562 -11533688 5000690912 ompa (sr:e.coli dna: strain k12, clone ptu100 and clone ptu302; and f-facto) (db:genpept-bct1) (de:e.coli sula and ompa genes coding for sula protein (lon suppressor)and outer membrane protein ii.) (nt:outer membrane protein ii) (le:1036) (re:2076) (di:direct) ECOOMPA J01654 g146981 Escherichia coli 562 -11533688 235165 ompa outer membrane protein 3a ii\*:g:d (fn:membrane; outer membrane constituents) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 88 of 400 of the completegenome.) (nt:f346; 100 pct identical to ompa\_ecoli sw: p02934) (le:651) (re:1691) (di:complement) AE000198 AE000198 g1787191 Escherichia coli 562 -11533688 7502851960 con outer membrane protein a precursor outer (sr:escherichia coli(strain:k12) dna, clone:kohara clone #222) (db:genpept) (de:escherichia coli genomic dna. (21.7 - 22.1 min).) (nt:orf\_id:o223#2; similar to swissprot accession) (le:12365) (re:13405) (di:complement) D90733 D90733 g1651465 Escherichia coli 562 -11533688 7502851961 con outer membrane protein a precursor outer (sr:escherichia coli(strain:k12) dna, clone:kohara clone #223) (db:genpept) (de:escherichia coli genomic dna. (22.0 - 22.3 min).) (nt:orf\_id:o223#2; similar to swissprot accession) (le:536) (re:1576) (di:complement) D90734 D90734 g1651469 Escherichia coli 562 -11533688 87660 ompa:tolg:tut:con (de:outer membrane protein a precursor (outer membrane protein ii\*)) (db:swissprot) OMPA\_ECOLI P02934 ESCHERICHIA COLI 562 -11533688

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835180	8944	31100	2145	715

Description

6500729831 ompc:meoa:par:b2215 outer membrane protein c precursor:outer membrane protein 1b (gtcfc:11.1:12.13) (keggfc:12.1) (rileyfc:3.3.1) (db:gtc-escherichia coli) b2215 b2215 Escherichia coli 562 -11533689 87673 ompc:meoa:par (de:protein 1b)) (db:swissprot) OMPC\_ECOLI P06996 ESCHERICHIA COLI 562 -11533689 130836 ompc outer membrane porin ompc precursor (cl:outer membrane protein phoe) (db:pir1.dat) (mp:47 min) MMECP C A20867 Escherichia coli 562 -11533689 224682 ompc:meoa:par outer membrane protein c precursor outer (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #373(49.5-49.9 min.)) (nt:orf\_id:o373#5; similar to (swissprot accession) (le:11164) (re:12267) (di:complement) D90850 D90850 g1736856 Escherichia coli 562 -11533689 301322 ompc outer membrane protein (sr:e.coli k-12 (strain w620) dna, clone pmy111 (1),(2),(3); k-12 dn) (db:genpept-bct1) (de:e.coli ompc and micf genes coding for major outer membrane protein ompc and mrna-interfering complementary rna (micrna).) (le:491) (re:1594) (di:direct) ECOOMP C K00541 g147008 Escherichia coli 562 -11533689 235277 ompc outer membrane protein 1b ib:c (fn:membrane; outer membrane constituents) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 200 of 400 of the complete genome.) (nt:f367; 100 pct identical to ompc\_ecoli sw: p06996) (le:7966) (re:9069) (di:complement) AE000310 AE000310 g1788544 Escherichia coli 562 -11533689 5000690913 (de:(ecoli\_2164) (pn:outer membrane protein 1b:ib;c) (gn:ompc) (gtcfc:11.1) (ec:) (ompc\_ecoli) (keggfc:11.2) (rileyfc:3.3.1) (db:gtc-escherichia coli)) ECOLI\_2164 ECOLI\_2164 Escherichia coli 562 10029816

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835198	8945	31101	234	77

Description

6500729832 smpa:b2617 small protein a (gtcfc:11.1) (keggfc:14.2) (rileyfc:3.3.1) (db:gtc-escherichia coli) b2617 b2617 Escherichia coli 562 -11533690 7000691916 smpa small protein a (db:pir2.dat) D65040 D65040 Escherichia coli 562 -11533690 7500960461 smpa small membrane protein a (fn:orf; inner membrane) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 237 of 400 of the complete genome.) (nt:o50; 100 pct identical to smpa\_ecoli sw:) (le:7516) (re:7668) (di:direct) AE000347 AE000347 g1788970 Escherichia coli 562 -11533690 5000690915 (de:(ecoli\_2553) (pn:small membrane protein) (gn:smpa) (gtcfc:11.1) (ec:) (smpa\_ecoli:) (keggfc:11.2) (rileyfc:3.3.1) (db:gtc-escherichia coli)) ECOLI\_2553 ECOLI\_2553 Escherichia coli 562 10123750

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835201	8946	31102	186	61

Description

6500729833 acre:envc:b3265 acre:acriflavin resistance protein e precursor:envc protein (gtcfc:11.1:13.3) (keggfc:14.2) (rileyfc:3.3.1) (db:gtc-escherichia coli) b3265 b3265 Escherichia coli 562 -11533691 233719 acre:envc (de:acriflavin resistance protein e precursor (envc protein)) (db:swissprot) ACRE\_ECOLI P24180 ESCHERICHIA COLI 562 -11533691 7000684506 acre:envc acriflavin resistance protein acre precursor:envelope protein (cl:lipoyl/biotin-binding homology) (db:pir2.dat) C65119 C65119 Escherichia coli 562 -11533691 5000690917 envc envelope protein (db:genpept-bct1) (de:e.coli envc, envd and envr genes.) (le:2435) (re:3592) (di:direct) ECENVCD X57948 g510829 Escherichia coli 562 -11533691 236505 acre acriflavine resistance protein (fn:resistance to acriflavine, hydrophobic) (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e. coli acriflavine resistant proteins (acre and acrf) genes,complete cds.) (le:202) (re:1359) (di:direct) ECOACREF M96848 g290408 Escherichia coli 562 -11533691 7500876375 acre (fn:acriflavine resistance protein) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:alternate name envc) (le:194610) (re:195767) (di:direct) ECOUW67 U18997 g606206 Escherichia coli 562 -11533691 232770 acre transmembrane protein affects septum formation (fn:membrane; inner membrane) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 295 of 400 of the completegenome.) (nt:o385; alternate name envc; 100 pct identical) (le:3660) (re:4817) (di:direct) AE000405 AE000405 g1789665 Escherichia coli 562 -11533691 58294 acre:envc (de:acriflavin resistance protein e precursor (envc protein)) (db:swissprot) ACRE\_ECOLI P24180 ESCHERICHIA COLI 562 -11533691



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835204	8947	31103	279	92
<u>Description</u>				
6500729834 tolq:fii:b0737 tolq protein (gtcfc:11.1) (keggfc:14.2) (rileyfc:5.2.0) (db:gtc-escherichia coli) b0737 b0737 Escherichia coli 562 -11533692 101764 tolq:fii (de:tolq protein) (db:swissprot) TOLQ_ECOLI P05828 ESCHERICHIA COLI 562 -11533692 131572 tolq:fii biopolymer transport protein tolq (cl:biopolymer transport protein) (db:pir1.dat) (mp:17 min) BVECTQ B25980 Escherichia coli 562 -11533692 223180 tolq tolq protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #178) (db:genpept-bct1) (de:escherichia coli genomic dna. (16.5 - 16.8 min).) (le:8343) (re:9035) (di:direct) D90713 D90713 g1651329 Escherichia coli 562 -11533692 7500893250 (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli tolqra gene cluster dna.) (nt:orf 2; putative) (le:546) (re:1238) (di:direct) ECOTOLQRA M16489 g1128978 Escherichia coli 562 -11533692 236121 tolq inner membrane protein:membrane-spanning (fn:membrane; colicin-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 67 of 400 of the completegenome.) (nt:o230; 100 pct identical to tolq_ecoli sw: p05828;) (le:938) (re:1630) (di:direct) AE000177 AE000177 g1786958 Escherichia coli 562 -11533692 5000691114 fii tolq protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #178) (db:genpept) (de:escherichia coli genomic dna. (16.5 - 16.9 min).) (nt:orf_id:o178#6; similar to pir accession number) (le:8343) (re:9035) (di:direct) D90713 D90713 g1651329 Escherichia coli 562 -11533692				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835205	8948	31104	234	78

Description

6500729835 tolr:b0738 tolr protein (gtcfc:11.1) (keggfc:14.2) (rileyfc:5.2.0) (db:gtc-escherichia coli) b0738 b0738 Escherichia coli 562 -11533693 101767 tolr (de:tolr protein) (db:swissprot) TOLR\_ECOLI P05829 ESCHERICHIA COLI 562 -11533693 131574 tolr tol protein (cl:tolr protein) (db:pir1.dat) (mp:17 min) BVETR C25980 Escherichia coli 562 -11533693 223181 tolr tol protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #178) (db:genpept-bct1) (de:escherichia coli genomic dna.(16.5 - 16.8 min).) (le:9039) (re:9467) (di:direct) D90713 D90713 g1651330 Escherichia coli 562 -11533693 7500893252 (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli tolqra gene cluster dna.) (nt:orf 3; putative) (le:1242) (re:1670) (di:direct) ECOTOLQRA M16489 g1128980 Escherichia coli 562 -11533693 236123 tol putative inner membrane protein:involved in the (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 67 of 400 of the completegenome.) (nt:ol42; 100 pct identical to tolr\_ecoli sw: p05829) (le:1634) (re:2062) (di:direct) AE000177 AE000177 g1786959 Escherichia coli 562 -11533693 5000691115 tol tol protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #178) (db:genpept) (de:escherichia coli genomic dna. (16.5 - 16.9 min).) (nt:orf\_id:ol78#7; similar to pir accession number) (le:9039) (re:9467) (di:direct) D90713 D90713 g1651330 Escherichia coli 562 -11533693

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835218	8949	31105	324	108

Description

6500729836 tola:cim:excc:lky:b0739 protein:tola protein (gtcfc:11.1) (keggfc:14.2) (rileyfc:5.2.0) (db:gtc-escherichia coli) b0739 b0739 Escherichia coli 562 -11533694 101756 tola:cim:excc:lky (de:tola protein) (db:swissprot) TOLA\_ECOLI P19934 ESCHERICHIA COLI 562 -11533694 164691 tola tola protein (db:pir2.dat) (mp:17 min) JV0057 JV0057 Escherichia coli 562 -11533694 223182 tola tola protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #178) (db:genpept-bct1) (de:escherichia coli genomic dna. (16.5 - 16.8 min).) (le:9532) (re:10797) (di:direct) D90713 D90713 g1651331 Escherichia coli 562 -11533694 7500893244 tola (sr:e.coli (strain k12) dna) (db:genpept-bct1) (de:e.coli tolerance to colicins (tolA and tolB) genes, complete cds.) (le:79) (re:1344) (di:direct) ECOTOLAB M28232 g148019 Escherichia coli 562 -11533694 236118 tola membrane spanning protein:required for outer (fn:membrane; colicin-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 67 of 400 of the completegenome.) (nt:o421; 100 pct identical to tola\_ecoli sw: p19934;) (le:2127) (re:3392) (di:direct) AE000177 AE000177 g1786960 Escherichia coli 562 -11533694 5000691116 excc tola protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #178) (db:genpept) (de:escherichia coli genomic dna. (16.5 - 16.9 min).) (nt:orf\_id:ol78#8; similar to swissprot accession) (le:9532) (re:10797) (di:direct) D90713 D90713 g1651331 Escherichia coli 562 -11533694

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835219	8950	31106	837	278

Description

6500729837 tolB:b0740 protein precursor:21 aa signal peptide:tolB protein precursor (gtcfc:11.1) (keggfc:14.2) (rileyfc:5.2.0) (db:gtc-escherichia coli) b0740 b0740 Escherichia coli 562 -11533695 101759 tolB (de:tolB protein precursor) (db:swissprot) TOLB\_ECOLI P19935 ESCHERICHIA COLI 562 -11533695 7000686807 tolB tolB protein precursor (db:pir2.dat) (mp:17 min) C64810 C64810 Escherichia coli 562 -11533695 7500893246 tolB periplasmic protein involved in the (fn:factor; colicin-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 67 of 400 of the completegenome.) (nt:o430; 99.8 pct identical to tolB\_ecoli sw: p19935) (le:3525) (re:4817) (di:direct) AE000177 AE000177 g1786961 Escherichia coli 562 -11533695 5000691117 (de:(ecoli\_714) (pn:periplasmic protein involved in the tonB-independent uptake of group A colicins) (gn:tolB) (gtcfc:12.14) (ec:) (tolB\_ecoli) (keggfc:11.2) (rileyfc:5.2.0) (db:gtc-escherichia coli)) ECOLI\_714 ECOLI\_714 Escherichia coli 562 10043588

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835234	8951	31107	534	177

Description

6500729838 cvpa:dede:b2313 colicin v production protein:dede protein:pur regulon 18 kd protein (gtcfc:11.1) (keggfc:14.2) (rileyfc:5.2.0) (db:gtc-escherichia coli) b2313 b2313 Escherichia coli 562 -11533696 66869 cvpa:dede (de:protein)) (db:swissprot) CVPA\_ECOLI P08550 ESCHERICHIA COLI 562 -11533696 131119 cvpa:dede colicin v production protein (cl:dede protein) (db:pir1.dat) (mp:50 min) XMECED A29803 Escherichia coli 562 -11533696 224846 cvpa dede protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #406(52.2-52.5 min.)) (nt:similar to (pir accession number a29803)) (le:13852) (re:14340) (di:complement) D90862 D90862 g1799694 Escherichia coli 562 -11533696 224854 cvpa dede protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #407(52.4-52.8 min.)) (nt:similar to (pir accession number a29803)) (le:917) (re:1405) (di:complement) D90863 D90863 g1799703 Escherichia coli 562 -11533696 235604 (sr:e.coli (strain k12) dna, clone psi210) (db:genpept-bct1) (de:e.coli histidine (hist, 3' end), deda, dedb (acetyl-coa carboxylasebeta subunit) complete cds, dedc, dedd, dede (complete cds.), andamidophosphoribosyltransferase (purf), segment 1.) (nt:... ECOHISPUR1 M68934 g146367 Escherichia coli 562 -11533696 7500879589 (sr:escherichia coli dna, clones psb5 (1) and psb2 (1), (2)) (db:genpept-bct1) (de:e.coli purf operon: gene coding for protein 17.9 of unknownfunction and purf gene coding for amidophosphoribosyltransferase.) (nt:protein 17.9) (le:353) (re:841) (di:direct) ECOPURF J01666 g147415 Escherichia coli 562 -11533696 234662 cvpa membrane protein required for colicin v (fn:membrane; colicin-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 210 of 400 of the completegenome.) (nt:f162; 100 pct identical to cvpa\_ecoli sw: p08550;) (le:4344) (re:4832) (di:complement) AE000320 AE000320 g1788652 Escherichia coli 562 -11533696 5000691118 (de:(ecoli\_2262) (pn:membrane protein required for colicin v production) (gn:cvpa) (gtcfc:12.14) (ec:) (cvpa\_ecoli) (keggfc:11.2) (rileyfc:5.2.0) (db:gtc-escherichia coli)) ECOLI\_2262 ECOLI\_2262 Escherichia coli 562 10009487

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835243	8952	31108	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835249	8953	31109	459	152

Description

6500729839 rcsf:b0196 rcsf protein (gtcfc:11.2) (keggfc:14.2)  
(rileyfc:3.3.2) (db:gtc-escherichia coli) b0196 b0196 Escherichia coli 562  
-11533697 7000691904 rcsf exopolysaccharide synthesis regulator rcsf  
(db:pir2.dat) D64744 D64744 Escherichia coli 562 -11533697 239823 orf134  
(sr:escherichia coli (sub\_strain w3110, strain k-12) (library: kohara')  
(db:genpept-bct1) (de:e.coli genomic dna, 5'flanking region of rrnh gene.)  
(le:1281) (re:1685) (di:complement) ECORRNHK12 D15061 g303559 Escherichia  
coli 562 -11533697 7500959735 rcsf exopolysaccharide synthesis regulator  
(db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:50666)  
(re:51070) (di:complement) ECU70214 U70214 g1552772 Escherichia coli 562  
-11533697 235930 rcsf regulator in colanic acid synthesis:interacts  
(fn:regulator; surface polysaccharides and) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 18 of 400 of the completegenome.)  
(nt:f134; 97 pct identical (1 gap) to rcsf\_ecoli) (le:9992) (re:10396)  
(di:complement) AE000128 AE000128 g1786394 Escherichia coli 562 -11533697  
5000690919 (de:(ecoli\_196) (pn:regulator in solanic acid synthesis;  
interacts with rcsb) (gn:rcsf) (gtcfc:11.2) (ec:) (rcsf\_ecoli) (keggfc:11.2)  
(rileyfc:3.3.2) (db:gtc-escherichia coli)) ECOLI\_196 ECOLI\_196 Escherichia  
coli 562 10122702

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835253	8954	31110	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835275	8955	31111	582	193

Description

6500729840 rcsa:b1951 colanic acid capsular biosynthesis activation protein a:colanic acid capsular biosynthesis activation protein a (gtcfc:11.2:12.13) (keggfc:12.1) (rileyfc:3.3.2) (db:gtc-escherichia coli) b1951 b1951 Escherichia coli 562 -11533698 93676 rcsa (de:colanic acid capsular biosynthesis activation protein a) (db:swissprot) RCSA\_ECOLI P24210 ESCHERICHIA COLI 562 -11533698 164352 rcsa colanic acid capsular biosynthesis activation protein a:polysaccharide synthesis regulation protein rcsa (db:pir2.dat) A37320 A37320 Escherichia coli 562 -11533698 224459 rcsa polysaccharide synthesis regulation protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #343(43.3-43.6 min.)) (nt:orf\_id:o343#15; similar to (pir accession number) (le:13348) (re:13971) (di:direct) D90834 D90834 g1736617 Escherichia coli 562 -11533698 301105 rcsa polysaccharide synthesis regulation protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #344(43.5-43.9 min.)) (nt:orf\_id:o343#15; similar to (pir accession number) (le:2373) (re:2996) (di:direct) D90835 D90835 g1736624 Escherichia coli 562 -11533698 301099 rcsa (sr:e. coli dna) (db:genpept-bct1) (de:escherichia coli capsular polysaccharide regulator (rcsa) gene,complete cds.) (nt:capsular polysaccharide regulator) (le:211) (re:834) (di:direct) ECORCSA M58003 g147521 Escherichia coli 562 -11533698 235708 rcsa positive regulator for ctr capsule biosynthesis (fn:regulator; surface polysaccharides and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 177 of 400 of the completegenome.) (nt:o207; 100 pct identical to rcsa\_ecoli sw: p24210;) (le:2466) (re:3089) (di:direct) AE000287 AE000287 g1788262 Escherichia coli 562 -11533698 224465 rcsa polysaccharide synthesis regulation protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #344(43.5-43.9 min.)) (nt:orf\_id:o343#15; similar to (pir accession number) (le:2373) (re:2996) (di:direct) D90835 D90835 g1736624 Escherichia coli 562 -11533698 5000690920 (de:(ecoli\_1905) (pn:positive regulator for ctr capsule biosynthesis, positive transcription factor) (gn:rcsa) (gtcfc:11.2) (ec:) (rcsa\_ecoli) (keggfc:11.2) (rileyfc:3.3.2) (db:gtc-escherichia coli)) ECOLI\_1905 ECOLI\_1905 Escherichia coli 562 10035668

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835281	8956	31112	642	213
<u>Description</u>				
6500729841 rfbx:b2037 putative o-antigen transporter (gtcfc:11.2:12.6) (keggfc:14.2) (rileyfc:3.3.2) (db:gtc-escherichia coli) b2037 b2037 Escherichia coli 562 -11533699 7000691895 rfbx o-antigen transporter (cl:o-antigen transporter protein) (db:pir2.dat) D64969 D64969 Escherichia coli 562 -11533699 224562 rfbx putative o-antigen transporter. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #351(45.1-45.5 min.)) (nt:orf_id:o351#13; similar to (swissprot accession) (le:14637) (re:15884) (di:complement) D90841 D90841 g1736727 Escherichia coli 562 -11533699 224574 rfbx putative o-antigen transporter. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #352(45.3-45.7 min.)) (nt:orf_id:o351#13; similar to (swissprot accession) (le:5426) (re:6673) (di:complement) D90842 D90842 g1736740 Escherichia coli 562 -11533699 7000691896 wzx putative o-antigen transporter (db:genpept-bct1) (de:escherichia coli k-12 dtdp-d-glucose 4,6-dehydratase (rmlb),dtdp-6-deoxy-l-mannose-dehydrogenase (rmlc), glucose-1-phosphatethymidylyltransferase (rmla), dtdp-6-deoxy-d-glucose-3,5 epimerase(rmlc), putative o-antigen transporter (... ECU09876 U09876 g2665492 Escherichia coli 562 -11533699 301202 rfbx putative o-antigen transporter (fn:putative transport; surface polysaccharides and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 184 of 400 of the completegenome.) (nt:f415; 99 pct identical to rfbx_ecoli sw: p37746; cg) (le:11094) (re:12341) (di:complement) AE000294 AE000294 g1788349 Escherichia coli 562 -11533699 301214 wzx putative o-antigen transporter (db:genpept-bct1) (de:escherichia coli k-12 dtdp-d-glucose 4,6-dehydratase (rmlb),dtdp-6-deoxy-l-mannose-dehydrogenase (rmlc), glucose-1-phosphatethymidylyltransferase (rmla), dtdp-6-deoxy-d-glucose-3,5 epimerase(rmlc), putative o-antigen transporter (... ECU09876 U09876 g2665492 Escherichia coli 562 -11533699 5000690921 (de:(ecoli_1985) (pn:hydrophobic protein involved in assembly of o antigen) (gn:rfbx) (gtcfc:11.2) (ec:) (rfbx_ecoli) (keggfc:11.2) (rileyfc:3.3.2) (db:gtc-escherichia coli)) ECOLI_1985 ECOLI_1985 Escherichia coli 562 10119968				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835286	8957	31113	276	92
<u>Description</u>				
<p>6500729842 rcsb:b2217 regulator of capsule synthesis b component: capsular synthesis regulator component b (gtcfc:11.2:12.13) (keggfc:12.1) (rileyfc:3.3.2) (db:gtc-escherichia coli) b2217 b2217 Escherichia coli 562 -11533700 93681 rcsb (de: capsular synthesis regulator component b) (db:swissprot) RCSB_ECOLI P14374 ESCHERICHIA COLI 562 -11533700 130890 rcsb colanic acid biosynthesis positive regulator rcsb:regulator of capsule synthesis b component (cl:regulatory protein coma:response regulator homology) (db:pir1.dat) (mp:48 min) BVECCB JV0068 Escherichia coli 562 -11533700 224684 rcsb colanic acid biosynthesis positive regulator (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #373(49.5-49.9 min.)) (nt:orf_id:o373#7; similar to (pir accession number) (le:15700) (re:16350) (di:direct) D90850 D90850 g1736858 Escherichia coli 562 -11533700 301332 rcsb colanic acid biosynthesis positive regulator (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #374(49.8-50.1 min.)) (nt:orf_id:o373#7; similar to (pir accession number) (le:749) (re:1399) (di:direct) D90851 D90851 g1736867 Escherichia coli 562 -11533700 235713 rcsb capsule synthesis regulator component b (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli capsule synthesis regulators b and c (rcsb and rcsc) genes, complete cds.) (le:3681) (re:4331) (di:complement) ECORCSB M28242 g457113 Escherichia coli 562 -11533700 301324 rcsb (fn: capsule synthesis regulator component b) (sr:escherichia coli (strain o9:k30:h12) dna) (db:genpept-bct1) (de:escherichia coli (clone pwq600) rcsc gene, complete cds; rcsb gene, complete cds.) (nt:putative) (le:3227) (re:3877) (di:complement) ECORCSC L11272 g147529 Escherichia coli 562 -11533700 235711 rcsb positive response regulator for colanic capsule (fn:regulator; surface polysaccharides and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 200 of 400 of the complete genome.) (nt:o216; 100 pct identical to rcsb_ecoli sw: p14374) (le:12497) (re:13147) (di:direct) AE000310 AE000310 g1788546 Escherichia coli 562 -11533700 224692 rcsb colanic acid biosynthesis positive regulator (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #374(49.8-50.1 min.)) (nt:orf_id:o373#7; similar to (pir accession number) (le:749) (re:1399) (di:direct) D90851 D90851 g1736867 Escherichia coli 562 -11533700 5000690922 (de:(ecoli_2166) (pn:positive response regulator for ctr capsule biosynthesis, :sensor, rcsc) (gn:rcsb) (gtcfc:11.2) (ec:) (rcsb_ecoli) (keggfc:11.2) (rileyfc:3.3.2) (db:gtc-escherichia coli)) ECOLI_2166 ECOLI_2166 Escherichia coli 562 10035673</p>				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835290	8958	31114	468	155

Description

6500729843 rcsc:b2218 sensor protein rcsc:capsular synthesis regulator component c (gtcfc:11.2:12.13) (ec:2.7.3.-) (keggfc:12.1) (rileyfc:3.3.2) (db:gtc-escherichia coli) b2218 b2218 Escherichia coli 562 -11533701  
7000688977 rcsc sensor protein rcsc::regulatory protein rcsc (cl:rcsc protein:response regulator homology) (ec:2.7.3.-) (db:pir1.dat) (mp:48 min) BVECCC H64991 Escherichia coli 562 -11533701 7500953621 rcsc sensor for ctr capsule biosynthesis:probable (fn:enzyme; surface polysaccharides and antigens) (db:genpept-bct2) (ec:2.7.3.-) (de:escherichia coli k-12 mg1655 section 201 of 400 of the completegenome.) (nt:f949; 99 pct identical rcsc\_ecoli sw: p14376) (le:130) (re:2931) (di:complement) AE000311 AE000311 g1788548 Escherichia coli 562 -11533701 5000690923 (de:(ecoli\_2167) (pn:negative regulator for ctr capsule biosynthesis, probable histidine kinase sensor acting on rcsb) (gn:rcsc) (gtcfc:11.2) (ec:2.7.3.-) (rcsc\_ecoli) (keggfc:11.1) (rileyfc:3.3.2) (db:gtc-escherichia coli))  
ECOLI\_2167 ECOLI\_2167 Escherichia coli 562 10123602

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835291	8959	31115	537	178

Description

6500729844 rfaf:b3620 adp-heptose--lps heptosyltransferase ii (gtcfc:11.2) (keggfc:14.2) (rileyfc:3.3.2) (db:gtc-escherichia coli) b3620 b3620 Escherichia coli 562 -11533702 94120 rfaf (de:adp-heptose--lps heptosyltransferase ii) (db:swissprot) RFAF\_ECOLI P37692 ESCHERICHIA COLI 562 -11533702 164512 rfaf adp-heptose--lps heptosyltransferase ii (cl:adp-heptose--lps heptosyltransferase ii) (db:pir2.dat) S47841 S47841 Escherichia coli 562 -11533702 7500889671 rfaf (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:209193) (re:210239) (di:direct) ECOUW76 U00039 g466758 Escherichia coli 562 -11533702 236857 rfaf adp-heptose--lps heptosyltransferase ii (fn:putative enzyme; macromolecule metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 330 of 400 of the completegenome.) (nt:o348; 100 pct identical amino acid sequence and) (le:2295) (re:3341) (di:direct) AE000440 AE000440 g1790050 Escherichia coli 562 -11533702 5000690924 (de:(ecoli\_3540) (pn:lipopolysaccharide core biosynthesis) (gn:rfaf) (gtcfc:11.2) (ec:) (rfaf\_ecoli) (keggfc:11.2) (rileyfc:3.3.2) (db:gtc-escherichia coli)) ECOLI\_3540 ECOLI\_3540 Escherichia coli 562 10036103

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835292	8960	31116	489	162

Description

6500729845 rfac:rfa-2:b3621 lipopolysaccharide heptosyltransferase-1  
(gtcfc:11.2) (keggfc:14.2) (rileyfc:3.3.2) (db:gtc-escherichia coli) b3621  
b3621 Escherichia coli 562 -11533703 7500889668 rfac:rfa-2  
(de:lipopolysaccharide heptosyltransferase-1) (db:swissprot) RFAC\_ECOLI  
P24173 ESCHERICHIA COLI 562 -11533703 163187 rfac:rfa-2  
heptosyltransferase:i:lipopolysaccharide inner core synthesis protein rfa-2  
(cl:heptosyltransferase i) (ec:2.4.99.-) (db:pir2.dat) (mp:82 min) A40619  
A40619 Escherichia coli 562 -11533703 238048 rfac (sr:escherichia coli  
(sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e.  
coli chromosomal region from 76.0 to 81.5 minutes.) (nt:alternate gene name  
rfa2; cg site no. 300) (le:210243) (re:211202) (di:direct) ECOUW76 U00039  
g466759 Escherichia coli 562 -11533703 5000690925 rfa-2 (db:genpept-bct1)  
(de:e.coli rfa-2 gene.) (le:897) (re:1856) (di:direct) ECRFA2 X62530 g42715  
Escherichia coli 562 -11533703 236858 rfac heptosyl transferase  
i:lipopolysaccharide core (fn:enzyme; macromolecule metabolism:)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 330 of 400 of the  
completegenome.) (nt:o319; 100 pct identical to rfac\_ecoli sw: p24173;)  
(le:3345) (re:4304) (di:direct) AE000440 AE000440 g1790051 Escherichia coli  
562 -11533703 94115 rfac:rfa-2 (de:lipopolysaccharide  
heptosyltransferase-1) (db:swissprot) RFAC\_ECOLI P24173 ESCHERICHIA COLI 562  
-11533703

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835312	8961	31117	423	141

Description

5000690926 rfal (gtcfc:11.2) (keggfc:14.2) (rileyfc:3.3.2)  
(db:gtc-escherichia coli) b3622 b3622 Escherichia coli 562 -11533704 164515  
rfal rfal protein (db:pir2.dat) S47843 S47843 Escherichia coli 562 -11533704  
7500960449 rfal (sr:escherichia coli (sub\_strain mg1655, strain k-12)  
(library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0  
to 81.5 minutes.) (le:211212) (re:212471) (di:direct) ECOUW76 U00039 g466760  
Escherichia coli 562 -11533704 236859 rfal o-antigen  
ligase:lipopolysaccharide core (fn:enzyme; macromolecule metabolism:)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 330 of 400 of the  
completegenome.) (nt:o419; 94 pct identical amino acid sequence and)  
(le:4314) (re:5573) (di:direct) AE000440 AE000440 g1790052 Escherichia coli  
562 -11533704 6500729846 rfal (gtcfc:11.2) (keggfc:14.2) (rileyfc:3.3.2)  
(db:gtc-escherichia coli) b3622 b3622 Escherichia coli 562 -11533704

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835319	8962	31118	1494	498

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835323	8963	31119	1545	514

Description

6500729847 rfak:b3623 lipopolysaccharide  
 1:2-n-acetylglucosaminetransferase:lipopolysaccharide  
 1:2-n-acetylglucosaminetransferase (gtcfc:11.2) (ec:2.4.1.56) (keggfc:14.1)  
 (rileyfc:3.3.2) (db:gtc-escherichia coli) b3623 b3623 Escherichia coli 562  
 -11533705 94129 rfak (ec:2.4.1.56) (de:lipopolysaccharide  
 1,2-n-acetylglucosaminetransferase,) (db:swissprot) RFAK\_ECOLI P27242  
 ESCHERICHIA COLI 562 -11533705 7000686311 rfak lipopolysaccharide  
 1:2-n-acetylglucosaminetransferase::rfak protein (ec:2.4.-.-) (db:pir2.dat)  
 A65163 A65163 Escherichia coli 562 -11533705 7500889677 rfak  
 (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda)  
 (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.)  
 (le:212503) (re:213576) (di:complement) ECOUW76 U00039 g466761 Escherichia  
 coli 562 -11533705 236860 rfak probably hexose  
 transferase:lipopolysaccharide (fn:enzyme; macromolecule metabolism:)  
 (db:genpept-bct2) (ec:2.4.-.-) (de:escherichia coli k-12 mg1655 section 330  
 of 400 of the completegenome.) (nt:f357; 100 pct identical amino acid  
 sequence and) (le:5605) (re:6678) (di:complement) AE000440 AE000440 g1790053  
 Escherichia coli 562 -11533705 5000690927 (de:(ecoli\_3543)  
 (pn:lipopolysaccharide core biosynthesis; probably hexose transferase)  
 (gn:rfak) (gtcfc:11.2) (ec:2.4.1.56) (rfak\_ecoli) (keggfc:11.1)  
 (rileyfc:3.3.2) (db:gtc-escherichia coli)) ECOLI\_3543 ECOLI\_3543 Escherichia  
 coli 562 10036112

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835324	8964	31120	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835333	8965	31121	738	245

Description

6500729848 rfaz:b3624 lipopolysaccharide core biosynthesis protein rfaz (gtcfc:11.2) (keggfc:14.2) (rileyfc:3.3.2) (db:gtc-escherichia coli) b3624 b3624 Escherichia coli 562 -11533706 94140 rfaz (de:lipopolysaccharide core biosynthesis protein rfaz) (db:swissprot) RFAZ\_ECOLI P27241 ESCHERICHIA COLI 562 -11533706 164523 rfaz rfaz protein (db:pir2.dat) S47845 S47845 Escherichia coli 562 -11533706 7500889685 rfaz (fn:lipopolysaccharide core biosynthesis) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:213609) (re:214460) (di:complement) ECOUW76 U00039 g466762 Escherichia coli 562 -11533706 236861 rfaz lipopolysaccharide core biosynthesis (fn:enzyme; macromolecule metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 330 of 400 of the completegenome.) (nt:f283; 100 pct identical amino acid sequence and) (le:6711) (re:7562) (di:complement) AE000440 AE000440 g1790054 Escherichia coli 562 -11533706 5000690928 (de:(ecoli\_3544) (pn:lipopolysaccharide core biosynthesis) (gn:rfaz) (gtcfc:11.2) (ec:) (rfaz\_ecoli) (keggfc:11.2) (rileyfc:3.3.2) (db:gtc-escherichia coli)) ECOLI\_3544 ECOLI\_3544 Escherichia coli 562 10036123

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835355	8966	31122	1248	416

Description

6500729849 rfay:b3625 lipopolysaccharide core biosynthesis protein rfay (gtcfc:11.2) (keggfc:14.2) (rileyfc:3.3.2) (db:gtc-escherichia coli) b3625 b3625 Escherichia coli 562 -11533707 94137 rfay (de:lipopolysaccharide core biosynthesis protein rfay) (db:swissprot) RFAY\_ECOLI P27240 ESCHERICHIA COLI 562 -11533707 164521 rfay rfay protein (db:pir2.dat) S47846 S47846 Escherichia coli 562 -11533707 7500889682 rfay (fn:lipopolysaccharide core biosynthesis) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:214531) (re:215229) (di:complement) ECOUW76 U00039 g466763 Escherichia coli 562 -11533707 236862 rfay lipopolysaccharide core biosynthesis (fn:enzyme; macromolecule metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 330 of 400 of the completegenome.) (nt:f232; 100 pct identical amino acid sequence and) (le:7633) (re:8331) (di:complement) AE000440 AE000440 g1790055 Escherichia coli 562 -11533707 5000690929 (de:(ecoli\_3545) (pn:lipopolysaccharide core biosynthesis) (gn:rfay) (gtcfc:11.2) (ec:) (rfay\_ecoli) (keggfc:11.2) (rileyfc:3.3.2) (db:gtc-escherichia coli)) ECOLI\_3545 ECOLI\_3545 Escherichia coli 562 10036120

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835375	8967	31123	417	138

Description

6500729850 rfaj:b3626 udp-d-glucose galactosyllipopolysaccharide glucosyltransferase:lipopolysaccharide 1:2-glucosyltransferase (gtcfc:11.2:7.2:12.2) (ec:2.4.1.58) (keggfc:14.1) (rileyfc:3.3.2) (db:gtc-escherichia coli) b3626 b3626 Escherichia coli 562 -11533708 94127 rfaj:wwaj (ec:2.4.1.58) (de:lipopolysaccharide 1,2-glucosyltransferase,) (db:swissprot) RFAJ\_ECOLI P27129 ESCHERICHIA COLI 562 -11533708 164800 rfaj lipopolysaccharide glucosyltransferase i (ec:2.4.1.58) (db:pir2.dat) S47847 S47847 Escherichia coli 562 -11533708 7500889676 rfaj udp-d-glucose:galactosyl lipopolysaccharide (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 17611) (le:215247) (re:216263) (di:complement) ECOUW76 U00039 g912479 Escherichia coli 562 -11533708 236863 rfaj udp-d-glucose:galactosyl lipopolysaccharide (fn:enzyme; surface polysaccharides and antigens) (db:genpept-bct2) (ec:2.4.1.58) (de:escherichia coli k-12 mg1655 section 330 of 400 of the completegenome.) (nt:f338; 100 pct identical to rfaj\_ecoli sw: p27129;) (le:8349) (re:9365) (di:complement) AE000440 AE000440 g1790056 Escherichia coli 562 -11533708 5000690930 (de:(ecoli\_3546) (pn:udp-d-glucose:udp-d-glucose,:galactosyllipopolysaccharide glucosyltransferase) (gn:rfaj) (gtcfc:11.2) (ec:2.4.1.58) (rfaj\_ecoli) (keggfc:11.1) (rileyfc:3.3.2) (db:gtc-escherichia coli)) ECOLI\_3546 ECOLI\_3546 Escherichia coli 562 10036110

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835378	8968	31124	558	186

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835380	8969	31125	396	131

Description

6500729851 rfai:b3627 udp-d-galactose::glucosyllipopolysaccharide  
-alpha-1:3-d-galactosyltransferase:lipopolysaccharide  
1:3-galactosyltransferase (gtcfc:11.2:7.2:12.2) (ec:2.4.1.44) (keggfc:14.1)  
(rileyfc:3.3.2) (db:gtc-escherichia coli) b3627 b3627 Escherichia coli 562  
-11533709 94125 rfai:waii (ec:2.4.1.44) (de:lipopolysaccharide  
1,3-galactosyltransferase,) (db:swissprot) RFAI\_ECOLI P27128 ESCHERICHIA  
COLI 562 -11533709 164799 rfai lipopolysaccharide  
3-alpha-galactosyltransferase::lipopolysaccharide core assembly protein  
rfai:udp-d-galactose--glucosyl  
lipopolysaccharide-alpha-1:3-d-galactosyltransferase (ec:2.4.1.44)  
(db:pir2.dat) C42982 C42982 Escherichia coli 562 -11533709 236864 rfai  
lipopolysaccharide core biosynthesis protein (sr:escherichia coli (strain  
k-12) dna) (db:genpept-bct1) (de:escherichia coli lipopolysaccharide core  
biosynthesis proteinoperon (rfaq, rfap, rfag, rfas, rfab, rfai, and rfaj)  
genes,complete cds.) (le:5484) (re:6503) (di:direct) ECOLPOSACR M80599  
g146656 Escherichia coli 562 -11533709 7500889675 rfai  
udp-d-galactose:glucosyl lipopolysaccharide (sr:escherichia coli (sub\_strain  
mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli  
chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 17614)  
(le:216303) (re:217322) (di:complement) ECOUW76 U00039 g466765 Escherichia  
coli 562 -11533709 235011 rfai udp-d-galactose:glucosyl lipopolysaccharide-  
(fn:enzyme; surface polysaccharides and antigens) (db:genpept-bct2)  
(ec:2.4.1.44) (de:escherichia coli k-12 mg1655 section 330 of 400 of the  
completegenome.) (nt:f339; 100 pct identical to rfai\_ecoli sw: p27128;)  
(le:9405) (re:10424) (di:complement) AE000440 AE000440 g1790057 Escherichia  
coli 562 -11533709 5000690931 (de:(ecoli\_3547)  
(pn:udp-d-galactose:udp-d-galactose,:glucosyllipopolysaccharide-alpha-1,3-d-  
galactosyltransferase) (gn:rfai) (gtcfc:11.2) (ec:2.4.1.44) (rfai\_ecoli)  
(keggfc:11.1) (rileyfc:3.3.2) (db:gtc-escherichia coli)) ECOLI\_3547  
ECOLI\_3547 Escherichia coli 562 10036108

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835389	8970	31126	783	260

Description

6500729852 rfas:b3629 lipopolysaccharide core biosynthesis protein rfas (gtcfc:11.2) (keggfc:14.2) (rileyfc:3.3.2) (db:gtc-escherichia coli) b3629 b3629 Escherichia coli 562 -11533710 94136 rfas (de:lipopolysaccharide core biosynthesis protein rfas) (db:swissprot) RFAS\_ECOLI P27126 ESCHERICHIA COLI 562 -11533710 164519 rfas rfas protein (db:pir2.dat) (mp:81 min) A42982 A42982 Escherichia coli 562 -11533710 236866 rfas lipopolysaccharide core biosynthesis protein (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli lipopolysaccharide core biosynthesis proteinoperon (rfaq, rfap, rfag, rfas, rfab, rfai, and rfaj) genes,complete cds.) (le:3426) (re:4361) (di:direct) ECOLPOSACR M80599 g146654 Escherichia coli 562 -11533710 7500889681 rfas (fn:lipopolysaccharide core biosynthesis) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:218445) (re:219380) (di:complement) ECOUW76 U00039 g466767 Escherichia coli 562 -11533710 235009 rfas lipopolysaccharide core biosynthesis (fn:enzyme; macromolecule metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 330 of 400 of the completegenome.) (nt:f311; 100 pct identical amino acid sequence and) (le:11547) (re:12482) (di:complement) AE000440 AE000440 g1790059 Escherichia coli 562 -11533710 5000690932 (de:(ecoli\_3549) (pn:lipopolysaccharide core biosynthesis) (gn:rfas) (gtcfc:11.2) (ec:) (rfas\_ecoli) (keggfc:11.2) (rileyfc:3.3.2) (db:gtc-escherichia coli)) ECOLI\_3549 ECOLI\_3549 Escherichia coli 562 10036119

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835390	8971	31127	627	209

Description

6500729853 rfap:b3630 lipopolysaccharide core biosynthesis protein rfap (gtcfc:11.2) (keggfc:14.2) (rileyfc:3.3.2) (db:gtc-escherichia coli) b3630 b3630 Escherichia coli 562 -11533711 94133 rfap (de:lipopolysaccharide core biosynthesis protein rfap) (db:swissprot) RFAP\_ECOLI P25741 ESCHERICHIA COLI 562 -11533711 164516 rfap rfap protein (db:pir2.dat) (mp:81 min) C42595 C42595 Escherichia coli 562 -11533711 236867 rfap lipopolysaccharide core biosynthesis protein (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli lipopolysaccharide core biosynthesis proteinoperon (rfaq, rfap, rfag, rfas, rfab, rfai, and rfaj) genes,complete cds.) (le:2592) (re:3389) (di:direct) ECOLPOSACR M80599 g146653 Escherichia coli 562 -11533711 7500889679 rfap (fn:lipopolysaccharide core biosynthesis;) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 298) (le:219417) (re:220214) (di:complement) ECOUW76 U00039 g466768 Escherichia coli 562 -11533711 235008 rfap lipopolysaccharide core biosynthesis (fn:enzyme; macromolecule metabolism;) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 330 of 400 of the completegenome.) (nt:f265; 100 pct identical to rfap\_ecoli sw: p25741;) (le:12519) (re:13316) (di:complement) AE000440 AE000440 g1790060 Escherichia coli 562 -11533711 5000690933 (de:(ecoli\_3550) (pn:lipopolysaccharide core biosynthesis; phosphorylation of core heptose; attaches phosphate-containing substrate to lps co) (gn:rfap) (gtcfc:11.2) (ec:) (rfap\_ecoli) (keggfc:11.2) (rileyfc:3.3.2) (db:gtc-esche) ECOLI\_3550 ECOLI\_3550 Escherichia coli 562 10036116

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835415	8972	31128	867	288
<u>Description</u>				
6500729854 rfag:pcsa:b3631 lipopolysaccharide core biosynthesis protein rfag:glucosyltransferase i (gtcfc:11.2) (keggfc:14.2) (rileyfc:3.3.2) (db:gtc-escherichia coli) b3631 b3631 Escherichia coli 562 -11533712 94123 rfag:pcsa (de:(glucosyltransferase i)) (db:swissprot) RFAG_ECOLI P25740 ESCHERICHIA COLI 562 -11533712 163117 rfag glucosyltransferase:i (ec:2.4.1.-) (db:pir2.dat) (mp:82 min) B42595 B42595 Escherichia coli 562 -11533712 236868 rfag lipopolysaccharide core biosynthesis protein (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli lipopolysaccharide core biosynthesis proteinoperon (rfaq, rfap, rfag, rfas, rfab, rfai, and rfaj) genes,complete cds.) (le:1475) (re:2599) (di:direct) ECOLPOSACR M80599 g146652 Escherichia coli 562 -11533712 7500889673 rfag glucosyltransferase i (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 15583) (le:220207) (re:221331) (di:complement) ECOUW76 U00039 g466769 Escherichia coli 562 -11533712 235007 rfag glucosyltransferase i:lipopolysaccharide core (fn:enzyme; macromolecule metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 330 of 400 of the completegenome.) (nt:f374; 100 pct identical to rfag_ecoli sw: p25740;) (le:13309) (re:14433) (di:complement) AE000440 AE000440 g179061 Escherichia coli 562 -11533712 5000690934 (de:(ecoli_3551) (pn:lipopolysaccharide core biosynthesis; glucosyltransferase i) (gn:rfag) (gtcfc:11.2) (ec:) (rfag_ecoli) (keggfc:11.2) (rileyfc:3.3.2) (db:gtc-escherichia coli)) ECOLI_3551 ECOLI_3551 Escherichia coli 562 10036106				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835436	8973	31129	516	171

Description

6500729855 rfaq:b3632 lipopolysaccharide core biosynthesis protein rfaq (gtcfc:11.2) (keggfc:14.2) (rileyfc:3.3.2) (db:gtc-escherichia coli) b3632 b3632 Escherichia coli 562 -11533713 94135 rfaq (de:lipopolysaccharide core biosynthesis protein rfaq) (db:swissprot) RFAQ\_ECOLI P25742 ESCHERICHIA COLI 562 -11533713 164518 rfaq rfaq protein (db:pir2.dat) (mp:82 min) S27560 S27560 Escherichia coli 562 -11533713 235006 rfaq (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli kdtA encodes kdo transferase,3-deoxy-d-manno-octulosonic acid transferase,complete cds.) (le:649) (re:1683) (di:complement) ECOKDORFA M86305 g146542 Escherichia coli 562 -11533713 236869 rfaq lipopolysaccharide core biosynthesis protein (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli lipopolysaccharide core biosynthesis proteinoperon (rfaq, rfap, rfag, rfas, rfab, rfai, and rfaj) genes,complete cds.) (le:444) (re:1478) (di:direct) ECOLPOSACR M80599 g146651 Escherichia coli 562 -11533713 7500889680 rfaq (fn:lipopolysaccharide core biosynthesis) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:221328) (re:222362) (di:complement) ECOUW76 U00039 g466770 Escherichia coli 562 -11533713 234920 rfaq lipopolysaccharide core biosynthesis (fn:enzyme; macromolecule metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 330 of 400 of the completegenome.) (nt:f344; 100 pct identical amino acid sequence and) (le:14430) (re:15464) (di:complement) AE000440 AE000440 g1790062 Escherichia coli 562 -11533713 5000690935 (de:(ecoli\_3552) (pn:lipopolysaccharide core biosynthesis) (gn:rfaq) (gtcfc:11.2) (ec:) (rfaq\_ecoli) (keggfc:11.2) (rileyfc:3.3.2) (db:gtc-escherichia coli)) ECOLI\_3552 ECOLI\_3552 Escherichia coli 562 10036118

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835440	8974	31130	894	297

Description

6500729856 kdtA:b3633 3-deoxy-d-manno-octulosonic-acid transferase:kdo transferase (gtcfc:11.2) (ec:2.-.-.-) (keggfc:14.1) (rileyfc:3.3.2) (db:gtc-escherichia coli) b3633 b3633 Escherichia coli 562 -11533714 80600 kdtA (ec:2.-.-.-) (de:transferase)) (db:swissprot) KDTA\_ECOLI P23282 ESCHERICHIA COLI 562 -11533714 162610 kdtA 3-deoxy-d-manno-octulosonic acid transferase::kdo transferase (ec:2.-.-.-) (db:pir2.dat) (mp:82 min) JU0467 JU0467 Escherichia coli 562 -11533714 234932 kdtA 3-deoxy-d-manno-octulosonic-acid transferase (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli kdtA encodes kdo transferase,3-deoxy-d-manno-octulosonic acid transferase,complete cds.) (le:2124) (re:3401) (di:direct) ECOKDORFA M86305 g146543 Escherichia coli 562 -11533714 236870 kdtA kdo transferase (sr:e.coli k-12 dna) (db:genpept-bct1) (de:escherichia coli kdo transferase (kdtA) gene, complete cds, andformamidopyrimidine-dna glycosylase (fpg) gene, 3' end.) (le:790) (re:2067) (di:direct) ECOKDTA M60670 g146556 Escherichia coli 562 -11533714 7500884575 kdtA kdo transferase (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:222804) (re:224081) (di:direct) ECOUW76 U00039 g466771 Escherichia coli 562 -11533714 234921 kdtA 3-deoxy-d-manno-octulosonic-acid transferase (fn:enzyme; surface polysaccharides and antigens) (db:genpept-bct2) (ec:2.-.-.-) (de:escherichia coli k-12 mg1655 section 331 of 400 of the completegenome.) (nt:o425; 100 pct identical amino acid sequence and) (le:435) (re:1712) (di:direct) AE000441 AE000441 g1790064 Escherichia coli 562 -11533714 5000690936 (de:(ecoli\_3553) (pn:3-deoxy-d-manno-octulosonic-acid transferase:kdo transferase) (gn:kdtA) (gtcfc:11.2) (ec:2.-.-.-) (kdtA\_ecoli) (keggfc:11.1) (rileyfc:3.3.2) (db:gtc-escherichia coli)) ECOLI\_3553 ECOLI\_3553 Escherichia coli 562 10022842

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835453	8975	31131	582	193

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835470	8976	31132	231	76

Description

GTC ORF with score 248 to: (sr:aspergillus saitoi cdna to mrna) (db:genpept-pln1) (ec:3.2.1.113) (de:aspergillus saitoi mrna for alpha-mannosidase, complete cds.) (nt:alpha-mannosidase specific for 1,2-alpha-mannosidic) (le:1) (re:1542) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835480	8977	31133	600	199
<u>Description</u>				
<p>6500729857 kdtb:b3634 lipopolysaccharide core biosynthesis protein kdtb (gtcfc:11.2) (keggfc:14.2) (rileyfc:3.3.2) (db:gtc-escherichia coli) b3634 b3634 Escherichia coli 562 -11533715 80602 kdtb (de:lipopolysaccharide core biosynthesis protein kdtb) (db:swissprot) KDTB_ECOLI P23875 ESCHERICHIA COLI 562 -11533715 163953 kdtb kdtb protein (cl:lipopolysaccharide core biosynthesis protein kdtb) (db:pir2.dat) JU0468 JU0468 Escherichia coli 562 -11533715 234933 18 kd protein (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli kdtb encodes kdo transferase,3-deoxy-d-manno-octulosonic acid transferase,complete cds.) (nt:orf) (le:3409) (re:3888) (di:direct) ECOKDORFA M86305 g146544 Escherichia coli 562 -11533715 236871 18 kd protein (sr:e.coli k-12 dna) (db:genpept-bct1) (de:escherichia coli kdtb transferase (kdtb) gene, complete cds, andformamidopyrimidine-dna glycosylase (fpg) gene, 3' end.) (nt:function unknown) (le:2075) (re:2554) (di:direct) ECOKDTA M60670 g146557 Escherichia coli 562 -11533715 7500884577 kdtb (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:4th start codon) (le:224089) (re:224568) (di:direct) ECOUW76 U00039 g466772 Escherichia coli 562 -11533715 234922 kdtb putative enzyme of lipopolysaccharide synthesis (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 331 of 400 of the completegenome.) (nt:o159) (le:1720) (re:2199) (di:direct) AE000441 AE000441 g1790065 Escherichia coli 562 -11533715 5000690937 (de:(ecoli_3554) (pn:putative enzyme of lipopolysaccharide synthesis) (gn:kdtb) (gtcfc:11.2) (ec:) (kdtb_ecoli) (keggfc:11.2) (rileyfc:3.3.2) (db:gtc-escherichia coli)) ECOLI_3554 ECOLI_3554 Escherichia coli 562 10022844</p>				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501835486	8978	31134	765	254

Description

6500729858 rfah:hlyt:sfrb:b3842 transcriptional activator:transcriptional activator rfah (gtcfc:11.2::10.2) (keggfc:14.2) (rileyfc:3.3.2) (db:gtc-escherichia coli) b3842 b3842 Escherichia coli 562 -11533716 235758 rfah:hlyt:sfrb (de:transcriptional activator rfah) (db:swissprot) RFAH\_ECOLI P26614 ESCHERICHIA COLI 562 -11533716 164477 rfah:hlyt transcription activator rfah:hlyt protein (db:pir2.dat) (mp:87 min) S30732 S30732 Escherichia coli 562 -11533716 5000690938 hlyt transcriptional activator of haemolysin (db:genpept-bct1) (de:e.coli dna sequence of hlyt (rfah, sfrb) locus and orf.) (nt:allelic to rfah and sfrb locus) (le:1971) (re:2459) (di:direct) ECHLYT X65013 g41729 Escherichia coli 562 -11533716 237066 rfah (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e. coli rfah gene, complete cds.) (le:770) (re:1258) (di:direct) ECORFAH M94889 g1209302 Escherichia coli 562 -11533716 7500889674 rfah::cgsc no. 164 (fn:regulator of lipopolysaccharide, sex factor and) (db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (nt:also called sfrb, hlyt) (le:77400) (re:77888) (di:complement) ECOUW85 M87049 g148241 Escherichia coli 562 -11533716 233124 rfah transcriptional activator affecting biosynthesis (fn:regulator; macromolecule metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 349 of 400 of the completegenome.) (nt:f162; 100 pct identical to rfah\_ecoli sw: p26614;) (le:8073) (re:8561) (di:complement) AE000459 AE000459 g1790276 Escherichia coli 562 -11533716 94124 rfah:hlyt:sfrb (de:transcriptional activator rfah) (db:swissprot) RFAH\_ECOLI P26614 ESCHERICHIA COLI 562 -11533716

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501835491	8979	31135	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501835501	8980	31136	708	235

Description

GTC ORF with score 707 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome v cosmids 9379, 9581, andlambda clone 4678.) (nt:similar to mitochondrial phosphate carrier protein) (le:40977) (re:41879) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835505	8981	31137	195	64

Description

GTC ORF with score 155 to: (sr:baker's yeast strain=s288c (ab972))  
(db:genpept-pln1) (de:saccharomyces cerevisiae chromosome v cosmids 9379, 9581, andlambda clone 4678.) (nt:similar to mitochondrial phosphate carrier protein) (le:40977) (re:41879) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835516	8982	31138	579	193

Description

6500729859 ecpg:b0140 chaperone protein ecpg precursor (gtcfc:11.3:12.7)  
(keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b0140 b0140  
Escherichia coli 562 -11533717 69702 ecpg (de:chaperone protein ecpg  
precursor) (db:swissprot) ECPD\_ECOLI P33128 ESCHERICHIA COLI 562 -11533717  
163035 ecpg pili assembly chaperone ecpg precursor:periplasmic:fimbriae  
biogenesis protein homolog (cl:chaperone protein papd) (db:pir2.dat) S45209  
S45209 Escherichia coli 562 -11533717 301610 orf (sr:escherichia coli  
(sub\_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1)  
(de:escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0  
min).) (nt:'fimbriae biogenesis protein mrkb homology') (le:44059)  
(re:44799) (di:comple... ECO82K D26562 g473799 Escherichia coli 562  
-11533717 233672 ecpg probable pilin chaperone similar to papd (fn:putative  
factor; surface structures) (db:genpept-bct2) (de:escherichia coli k-12  
mg1655 section 13 of 400 of the completegenome.) (nt:f246; 98 pct identical  
to ecpg\_ecoli sw: p33128) (le:5833) (re:6573) (di:complement) AE000123  
AE000123 g1786333 Escherichia coli 562 -11533717 5000690939 (de:(ecoli\_140)  
(pn:probable pilin chaperone similar to papd) (gn:ecpg) (gtcfc:11.3) (ec:)  
(ecpg\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli))  
ECOLI\_140 ECOLI\_140 Escherichia coli 562 10086733

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835518	8983	31139	930	309

Description

6500729860 crl:b0240 curlin genes transcriptional activator:curlin genes transcriptional activatory protein (gtcfc:11.3:10.2) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b0240 b0240 Escherichia coli 562 -11533718 7000690865 crl curlin genes transcription activator:crl protein (db:pir2.dat) A64749 A64749 Escherichia coli 562 -11533718 7500959715 crl crl protein (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:88904) (re:89305) (di:direct) ECU70214 U70214 g1552808 Escherichia coli 562 -11533718 239859 crl transcriptional regulator of cryptic csga gene (fn:regulator; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 22 of 400 of the completegenome.) (nt:o133; 98 pct identical to crl\_ecoli sw: p24251) (le:4545) (re:4946) (di:direct) AE000132 AE000132 g1786435 Escherichia coli 562 -11533718 5000690940 (de:(ecoli\_233) (pn:dna-binding protein affecting expression of cryptic csga gene for surface fibers) (gn:crl) (gtcfc:11.3) (ec:) (crl\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_233 ECOLI\_233 Escherichia coli 562 10122717

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835519	8984	31140	201	66

Description

6500729861 sfmd:b0532 hypothetical protein:outer membrane usher protein sfmd precursor (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b0532 b0532 Escherichia coli 562 -11533719 4000707943 sfmd (de:outer membrane usher protein sfmd precursor) (db:swissprot) SFMD\_ECOLI P77468 ESCHERICHIA COLI 562 -11533719 7000686594 smfd outer membrane usher protein sfmd precursor (cl:outer membrane usher protein fimd) (db:pir2.dat) C64785 C64785 Escherichia coli 562 -11533719 7500891570 fimd homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to s. typhimurium fimd) (le:328) (re:2931) (di:direct) ECU82598 U82598 g1778447 Escherichia coli 562 -11533719 240043 sfmd putative outer membrane protein:export (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 49 of 400 of the completegenome.) (nt:o867; residues 25-568 are 69 pct identical (2 gaps)) (le:3120) (re:5723) (di:direct) AE000159 AE000159 g1786744 Escherichia coli 562 -11533719 5000690941 (de:(ecoli\_515) (pn:function not assigned) (gn:fimd\_1) (gtcfc:11.3) (ec:) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_515 ECOLI\_515 Escherichia coli 562 10122882

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835525	8985	31141	585	194

6500729862 fimz:b0535 fimbriae z protein (gtcfc:11.3) (keggfc:14.2)  
(rileyfc:3.3.3) (db:gtc-escherichia coli) b0535 b0535 Escherichia coli 562  
-11533720 71701 fimz (de:fimbriae z protein) (db:swissprot) FIMZ\_ECOLI  
P21502 ESCHERICHIA COLI 562 -11533720 7000685249 fimz fimbriae z protein  
(cl:regulatory protein coma:response regulator homology) (db:pir1.dat)  
(mp:13 min) QQECY5 F64785 Escherichia coli 562 -11533720 7500881470 fimz  
fimbrial z protein:probable signal transducer (fn:putative regulator;  
surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655  
section 49 of 400 of the completegenome.) (nt:f210; 100 pct identical to  
fimz\_ecoli sw: p21502) (le:7271) (re:7903) (di:complement) AE000159 AE000159  
g1786747 Escherichia coli 562 -11533720 5000690942 (de:(ecoli\_518)  
(pn:fimbrial z protein; probable signal transducer) (gn:fimz) (gtcfc:11.3)  
(ec:) (fimz\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli))  
ECOLI 518 ECOLI 518 Escherichia coli 562 10014259

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835530	8986	31142	279	92

6500729863 csga:b1042 major curlin subunit precursor (gtcfc:11.3)  
(keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1042 b1042  
Escherichia coli 562 -11533721 66628 csga (de:major curlin subunit  
precursor) (db:swissprot) CSGA\_ECOLI P28307 ESCHERICHIA COLI 562 -11533721  
7000684914 csga curlin protein csga precursor:csga protein:major curlin  
protein (db:pir2.dat) (mp:23.15) S70788 S70788 Escherichia coli 562  
-11533721 223336 csga curlin precursor (sr:escherichia coli(strain:k12)  
dna, clone:kohara clone #231) (db:genpept-bct1) (de:escherichia coli genomic  
dna. (23.6 - 23.9 min).) (le:7713) (re:8168) (di:direct) D90741 D90741  
g1651511 Escherichia coli 562 -11533721 7500879452 csga curlin/csga protein  
(db:genpept-bct1) (de:e.coli csfg, csge, csge, csge, csge, csge, and orf  
genes.) (nt:major subunit) (le:3729) (re:4184) (di:direct) ECCSGABDG X90754  
g1147564 Escherichia coli 562 -11533721 232589 csga curlin major  
subunit:coiled surface structures (fn:regulator; surface structures)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 95 of 400 of the  
completegenome.) (nt:o151; 99 pct identical to csga\_ecoli sw: p28307)  
(le:8993) (re:9448) (di:direct) AE000205 AE000205 g1787279 Escherichia coli  
562 -11533721 5000690943 csga major curlin subunit precursor.  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #231) (db:genpept)  
(de:escherichia coli genomic dna. (23.7 - 24.0 min).) (nt:orf\_id:o231#10;  
similar to swissprot accession) (le:7713) (re:8168) (di:direct) D90741  
D90741 g1651511 Escherichia coli 562 -11533721



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835532	8987	31143	228	75

Description

6500729864 flgm:b1071 anti-sigma factor:negative regulator of flagellin synthesis:anti-sigma factor (gtcfc:10.2) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1071 b1071 Escherichia coli 562 -11533722 71934 flgm (de:negative regulator of flagellin synthesis (anti-sigma factor)) (db:swissprot) FLGM\_ECOLI P43532 ESCHERICHIA COLI 562 -11533722 7000685273 flgm transcription factor sigma-28 inhibitor flgm:negative regulator of flagellin synthesis (db:pir2.dat) D64850 D64850 Escherichia coli 562 -11533722 223349 flgm negative regulator of flagellin synthesis (sr:escherichia coli(strain:k12) dna, clone:kohara clone #233) (db:genpept-bct1) (de:escherichia coli genomic dna. (24.0 - 24.4 min).) (le:16201) (re:16494) (di:complement) D90743 D90743 gl651526 Escherichia coli 562 -11533722 7500881563 flgm anti-sigma factor (db:genpept-bct1) (de:escherichia coli anti-sigma factor (flgm), complete cds, and flngene, partial cds.) (le:76) (re:369) (di:direct) ECU19773 U19773 g641928 Escherichia coli 562 -11533722 238759 flgm anti-flia anti-sigma factor:also known as (fn:factor; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 98 of 400 of the completegenome.) (nt:f97; 100 pct identical to flgm\_ecoli sw: p43532) (le:2081) (re:2374) (di:complement) AE000208 AE000208 gl787311 Escherichia coli 562 -11533722 5000690944 flgm negative regulator of flagellin synthesis (sr:escherichia coli(strain:k12) dna, clone:kohara clone #233) (db:genpept) (de:escherichia coli genomic dna. (24.1 - 24.5 min).) (nt:orf\_id:o233#19; similar to swissprot accession) (le:16201) (re:16494) (di:complement) D90743 D90743 gl651526 Escherichia coli 562 -11533722

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835533	8988	31144	450	149

Description

6500729865 flga:b1072 flagellar basal body p-ring protein flga precursor:flagella basal body p-ring formation protein flga precursor (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1072 b1072 Escherichia coli 562 -11533723 118203 flga (de:flagella basal body p-ring formation protein flga precursor) (db:swissprot) FLGA\_ECOLI P75933 ESCHERICHIA COLI 562 -11533723 7000685258 flga flagellar basal body p-ring protein flga precursor (cl:flagellar basal body p-ring protein flga) (db:pir2.dat) E64850 E64850 Escherichia coli 562 -11533723 7500881541 flga flagellar biosynthesis:assembly of basal-body (fn:putative structure; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 98 of 400 of the completegenome.) (nt:f219; 71 pct identical to flga\_salty sw: p40131) (le:2450) (re:3109) (di:complement) AE000208 AE000208 g1787312 Escherichia coli 562 -11533723 5000690945 flga flagella basal body p-ring formation protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #233) (db:genpept) (de:escherichia coli genomic dna. (24.1 - 24.5 min).) (nt:orf\_id:o233#20; similar to swissprot accession) (le:16570) (re:17229) (di:complement) D90743 D90743 g4062649 Escherichia coli 562 -11533723

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835543	8989	31145	303	100

Description

6500729866 flgb:flba:fla\_fii:b1073 putative flagellar basal-body rod protein flgb:proximal rod protein:flagellar basal-body rod protein flgb:putative proximal rod protein (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1073 b1073 Escherichia coli 562 -11533724 7000691893 flgb:flba:fla\_fii flagellar basal body rod protein flgb:proximal rod protein (cl:rod protein flgb) (db:pir2.dat) F64850 F64850 Escherichia coli 562 -11533724 7500955362 flgb flagellar biosynthesis:cell-proximal portion of (fn:structural component; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 98 of 400 of the completegenome.) (nt:o138; 81 pct identical to flgb\_salty sw: p16437 but) (le:3264) (re:3680) (di:direct) AE000208 AE000208 g1787313 Escherichia coli 562 -11533724 5000690946 flgb rod protein flgb. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #233) (db:genpept) (de:escherichia coli genomic dna. (24.1 - 24.5 min).) (nt:orf\_id:o233#21; similar to pir accession number) (le:17384) (re:17800) (di:direct) D90743 D90743 g4062650 Escherichia coli 562 -11533724

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835546	8990	31146	294	97

#### Description

6500729867 flgc:flaw:fla\_fiii:b1074 putative flagellar basal-body rod protein flgc:proximal rod protein:flagellar basal-body rod protein flgc:putative proximal rod protein (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1074 b1074 Escherichia coli 562 -11533725 118213 flgc:flaw:fla::fiii (de:flagellar basal-body rod protein flgc (putative proximal rod protein)) (db:swissprot) FLGC\_ECOLI P75935 ESCHERICHIA COLI 562 -11533725 7000685261 flgc:flaw:fla\_fiii flagellar basal body rod protein flgc (cl:rod protein flgc) (db:pir2.dat) G64850 G64850 Escherichia coli 562 -11533725 7500881550 flgc flagellar biosynthesis:cell-proximal portion of (fn:structural component; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 98 of 400 of the completegenome.) (nt:o134; 93 pct identical to flgc\_salty sw: p16438) (le:3684) (re:4088) (di:direct) AE000208 AE000208 g1787314 Escherichia coli 562 -11533725 5000690947 flgc rod protein flgc (sr:escherichia coli(strain:k12) dna, clone:kohara clone #233) (db:genpept) (de:escherichia coli genomic dna. (24.1 - 24.5 min).) (nt:orf\_id:o233#22; similar to pir accession number) (le:17804) (re:18208) (di:direct) D90743 D90743 g4062651 Escherichia coli 562 -11533725

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835569	8991	31147	468	155

#### Description

6500729868 flgd:flav:fla\_fiv:b1075 flagellar hook formation protein flgd:basal-body rod modification protein flgd (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1075 b1075 Escherichia coli 562 -11533726 118216 flgd:flav:fla::fiv (de:basal-body rod modification protein flgd) (db:swissprot) FLGD\_ECOLI P75936 ESCHERICHIA COLI 562 -11533726 7000685262 flgd:flav:fla\_fiv flagellar hook formation protein flgd (db:pir2.dat) H64850 H64850 Escherichia coli 562 -11533726 7500881551 flgd flagellar biosynthesis:initiation of hook (fn:putative structure; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 98 of 400 of the completegenome.) (nt:o231; 83 pct identical (1 gap) to pir:) (le:4100) (re:4795) (di:direct) AE000208 AE000208 g1787315 Escherichia coli 562 -11533726 5000690948 flgd flgd protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #233) (db:genpept) (de:escherichia coli genomic dna. (24.1 - 24.5 min).) (nt:orf\_id:o233#23; similar to pir accession number) (le:18220) (re:18915) (di:direct) D90743 D90743 g4062652 Escherichia coli 562 -11533726

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835575	8992	31148	792	264

Description

6500729869 flge:flak:fla\_fv:b1076 flagellar hook protein flge (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1076 b1076 Escherichia coli 562 -11533727 7000690880 flge:flak:fla\_fv flagellar hook protein flge (db:pir2.dat) A64851 A64851 Escherichia coli 562 -11533727 7500959740 flge flagellar biosynthesis:hook protein (fn:structural component; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 98 of 400 of the completegenome.) (nt:o402; 86 pct identical (1 gap) to flge\_salty) (le:4820) (re:6028) (di:direct) AE000208 AE000208 g1787316 Escherichia coli 562 -11533727 5000690949 (de:(ecoli\_1038) (pn:flagellar biosynthesis, hook protein) (gn:flge) (gtcfc:11.3) (ec:)) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_1038 ECOLI\_1038 Escherichia coli 562 10123156

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835578	8993	31149	657	219

Description

6500729870 flgf:flax:fla\_fvi:b1077 putative flagellar basal-body rod protein flgf:proximal rod protein:flagellar basal-body rod protein flgf:putative proximal rod protein (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1077 b1077 Escherichia coli 562 -11533728 118221 flgf:flax:fla::fvi (de:flagellar basal-body rod protein flgf (putative proximal rod protein)) (db:swissprot) FLGF\_ECOLI P75938 ESCHERICHIA COLI 562 -11533728 7000685264 flgf:flax:fla\_fvi flagellar basal body rod protein flgf (cl:rod protein flgf) (db:pir2.dat) B64851 B64851 Escherichia coli 562 -11533728 7500881556 flgf flagellar biosynthesis:cell-proximal portion of (fn:structural component; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 98 of 400 of the completegenome.) (nt:o251; 86 pct identical to flgf\_salty sw: p16323) (le:6048) (re:6803) (di:direct) AE000208 AE000208 g1787317 Escherichia coli 562 -11533728 5000690950 flgf rod protein flgf (sr:escherichia coli(strain:k12) dna, clone:kohara clone #234) (db:genpept) (de:escherichia coli genomic dna. (24.5 - 24.8 min).) (nt:orf\_id:o234#1; similar to pir accession number) (le:756) (re:1511) (di:direct) D90744 D90744 g4062655 Escherichia coli 562 -11533728

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835584	8994	31150	588	195

Description

6500729871 flgg:flal:fla\_fvii:b1078 flagellar basal-body rod protein  
flgg:distal rod protein (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3)  
(db:gtc-escherichia coli) b1078 b1078 Escherichia coli 562 -11533729 118223  
flgg:flal:fla::fvii (de:flagellar basal-body rod protein flgg (distal rod  
protein)) (db:swissprot) FLGG\_ECOLI P75939 ESCHERICHIA COLI 562 -11533729  
7000685266 flgg:flal:fla\_fvii flagellar basal body rod protein flgg:distal  
rod protein (cl:rod protein flgf) (db:pir2.dat) C64851 C64851 Escherichia  
coli 562 -11533729 7500881558 flgg flagellar biosynthesis:cell-distal  
portion of (fn:structural component; surface structures) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 98 of 400 of the completegenome.)  
(nt:o260; 99 pct identical to flgg\_salty sw: p16439) (le:6975) (re:7757)  
(di:direct) AE000208 AE000208 g1787318 Escherichia coli 562 -11533729  
5000690951 flgg basal body rod protein flgg (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #234) (db:genpept) (de:escherichia  
coli genomic dna. (24.5 - 24.8 min).) (nt:orf\_id:o234#2; similar to pir  
accession number) (le:1683) (re:2465) (di:direct) D90744 D90744 g4062656  
Escherichia coli 562 -11533729

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835587	8995	31151	339	112

Description

6500729872 flgh:flay:fla\_fviii:b1079 flagellar l-ring protein  
precursor:basal body l-ring protein (gtcfc:11.3) (keggfc:14.2)  
(rileyfc:3.3.3) (db:gtc-escherichia coli) b1079 b1079 Escherichia coli 562  
-11533730 118226 flgh:flay:fla::fviii (de:flagellar l-ring protein  
precursor (basal body l-ring protein)) (db:swissprot) FLGH\_ECOLI P75940  
ESCHERICHIA COLI 562 -11533730 7000685267 flgh:flay:fla\_fviii flagellar  
basal body l-ring protein precursor (db:pir2.dat) D64851 D64851 Escherichia  
coli 562 -11533730 7500881559 flgh flagellar biosynthesis:basal-body  
(fn:structural component; surface structures) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 98 of 400 of the completegenome.)  
(nt:o232; 90 pct identical to flgh\_salty sw: p15929) (le:7810) (re:8508)  
(di:direct) AE000208 AE000208 g1787319 Escherichia coli 562 -11533730  
5000690952 (de:(ecoli\_1041) (pn:flagellar biosynthesis, basal-body  
outer-membrane l:lipopolysaccharide layer ring protein) (gn:flgh)  
(gtcfc:11.3) (ec:) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli))  
ECOLI\_1041 ECOLI\_1041 Escherichia coli 562 10060311

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835589	8996	31152	762	253

Description

6500729873 flgj:flaz:fla\_fx:b1081 flagellar protein flgj (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1081 b1081 Escherichia coli 562 -11533731 118233 flgj:flaz:fla::fx (de:flagellar protein flgj) (db:swissprot) FLGJ\_ECOLI P75942 ESCHERICHIA COLI 562 -11533731 7000685269 flgj:flaz:fla\_fx flagellar protein flgj (db:pir2.dat) F64851 F64851 Escherichia coli 562 -11533731 7500881561 flgj flagellar biosynthesis (fn:putative structure; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 98 of 400 of the completegenome.) (nt:o313; 82 pct identical (3 gaps) to 316 aa) (le:9617) (re:10558) (di:direct) AE000208 AE000208 g1787321 Escherichia coli 562 -11533731 5000690953 lgj flagellar basal body protein flgj (sr:escherichia coli(strain:k12) dna, clone:kohara clone #234) (db:genpept) (de:escherichia coli genomic dna. (24.5 - 24.8 min).) (nt:orf\_id:o234#5; similar to pir accession number) (le:4325) (re:5266) (di:direct) D90744 D90744 g4062659 Escherichia coli 562 -11533731

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835599	8997	31153	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835604	8998	31154	468	156

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835605	8999	31155	300	99

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835609	9000	31156	537	178

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835631	9001	31157	219	72

Description

GTC ORF with score 102 to: (sr:baker's yeast) (db:genpept-pln1)  
(de:saccharomyces cerevisiae multicopy suppressor of mrtg2-5 (nce2) gene,  
nuclear gene encoding mitochondrial protein, complete cds.) (nt:gene also  
called rtg2s2, ypr149w; multicopy) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835634	9002	31158	306	101

Description

6500729874 flgk:flas:flaw:b1082 flagellar hook-associated protein 1:hap1  
(gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1082  
b1082 Escherichia coli 562 -11533732 7000690881 flgk:flas:flaw flagellar  
hook-associated protein 1:hap1 protein (cl:flagellar hook-associated protein  
1) (db:pir2.dat) G64851 G64851 Escherichia coli 562 -11533732 223350 flgk  
flagellar hook-associated protein 1 hap1 (sr:escherichia coli(strain:k12)  
dna, clone:kohara clone #234) (db:genpept-bct1) (de:escherichia coli genomic  
dna. (24.4 - 24.7 min).) (le:5332) (re:6975) (di:direct) D90744 D90744  
g1651528 Escherichia coli 562 -11533732 7500955493 flgk flagellar  
biosynthesis:hook-filament junction (fn:structural component; surface  
structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 99 of  
400 of the complete genome.) (nt:o547; 100 pct identical to fragment  
flgk\_ecoli) (le:63) (re:1706) (di:direct) AE000209 AE000209 g1787323  
Escherichia coli 562 -11533732 5000690954 flas flagellar hook-associated  
protein 1 hap1 . (sr:escherichia coli(strain:k12) dna, clone:kohara clone  
#234) (db:genpept) (de:escherichia coli genomic dna. (24.5 - 24.8 min).)  
(nt:orf\_id:o235#1; similar to pir accession number) (le:5332) (re:6975)  
(di:direct) D90744 D90744 g1651528 Escherichia coli 562 -11533732

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835642	9003	31159	798	265

Description

6500729875 flgl:flat:flau:b1083 flagellar hook-associated protein  
3:hap3:hook-filament junction protein (gtcfc:11.3) (keggfc:14.2)  
(rileyfc:3.3.3) (db:gtc-escherichia coli) b1083 b1083 Escherichia coli 562  
-11533733 71931 flgl:flat:flau (de:protein)) (db:swissprot) FLGL\_ECOLI  
P29744 ESCHERICHIA COLI 562 -11533733 163205 flgl:flat:flau flagellar  
hook-associated protein 3:hap3 protein (db:pir2.dat) S44022 S44022  
Escherichia coli 562 -11533733 223351 flgl flagellar hook-associated  
protein 3 hap3 (sr:escherichia coli(strain:k12) dna, clone:kohara clone  
#234) (db:genpept-bct1) (de:escherichia coli genomic dna. (24.4 - 24.7  
min).) (le:6987) (re:7940) (di:direct) D90744 D90744 g1651529 Escherichia  
coli 562 -11533733 7500881562 flgl hook-associated protein 3  
(db:genpept-bct1) (de:escherichia coli k12 hook-associated protein 1 (flgk)  
gene, partialcds and hook-associated protein 3 (flgl) gene, complete cds.)  
(le:52) (re:1005) (di:direct) ECU02514 U02514 g407679 Escherichia coli 562  
-11533733 238453 flgl flagellar biosynthesis:hook-filament junction  
(fn:structural component; surface structures) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 99 of 400 of the completegenome.)  
(nt:o317; 100 pct identical to flgl\_ecoli sw: p29744) (le:1718) (re:2671)  
(di:direct) AE000209 AE000209 g1787324 Escherichia coli 562 -11533733  
5000690955 flat flagellar hook-associated protein 3 hap3 (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #234) (db:genpept) (de:escherichia  
coli genomic dna. (24.5 - 24.8 min).) (nt:orf\_id:o235#2; similar to  
swissprot accession) (le:6987) (re:7940) (di:direct) D90744 D90744 g1651529  
Escherichia coli 562 -11533733



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835665	9004	31160	2109	702

#### Description

6500729876 dsbb:roxb:bl185 disulfide bond formation protein b:disulfide oxidoreductase (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) bl185 bl185 Escherichia coli 562 -11533734 69307 dsbb:roxb (de:disulfide bond formation protein b (disulfide oxidoreductase)) (db:swissprot) DSBB\_ECOLI P30018 ESCHERICHIA COLI 562 -11533734 7000685099 dsbb:roxb protein-disulfide oxidoreductase:b:disulfide bond formation protein b (cl:protein-disulfide oxidoreductase dsbb) (ec:1.8.4.-) (db:pir2.dat) (mp:25.5 min) F64864 F64864 Escherichia coli 562 -11533734 7500880668 dsbb reoxidizes dsba protein following formation of (fn:enzyme; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 106 of 400 of the completegenome.) (nt:f176; 100 pct identical to dsbb\_ecoli sw: p30018) (le:11367) (re:11897) (di:complement) AE000216 AE000216 g1787433 Escherichia coli 562 -11533734 5000690956 (de:(ecoli\_1147) (pn:reoxidizes dsba protein following formation of disulfide bond in p-ring of flagella) (gn:dsbb) (gtcfc:11.3) (ec:)) (dsbb\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_1147 ECOLI\_1147 Escherichia coli 562 10011890

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835672	9005	31161	213	70

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835681	9006	31162	186	61

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835683	9007	31163	1173	390

Description

6500729877 flha:b1879 flagellar biosynthesis protein flha (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1879 b1879 Escherichia coli 562 -11533735 1500686058 flha (de:flagellar biosynthesis protein flha) (db:swissprot) FLHA\_ECOLI P76298 ESCHERICHIA COLI 562 -11533735 7000685276 flha flagellar biosynthesis protein flha (cl:regulatory protein lcrd) (db:pir2.dat) G64950 G64950 Escherichia coli 562 -11533735 224378 flagellar biosynthesis protein flha. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #338(42.1-42.5 min..)) (nt:orf\_id:o338#1; similar to (swissprot accession) (le:7339) (re:9417) (di:complement) D90830 D90830 g1736532 Escherichia coli 562 -11533735 301018 flha flagellar biosynthesis:possible export of (fn:structural component; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 171 of 400 of the completegenome.) (nt:f692; 95 pct identical to flha\_salty sw: p40729) (le:8507) (re:10585) (di:complement) AE000281 AE000281 g1788187 Escherichia coli 562 -11533735 5000690957 (de:(ecoli\_1836) (pn:flagellar biosynthesis; export of flagellar proteins) (gn:flha) (gtcfc:11.3) (ec:) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_1836 ECOLI\_1836 Escherichia coli 562 10060255

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835693	9008	31164	708	235

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835702	9009	31165	1860	619

Description

GTC ORF with score 172 to: (sr:african clawed frog) (db:genpept-vrt) (de:xenopus laevis middle molecular weight neurofilament proteinnf-m(1) mrna, complete cds.) (nt:neuronal intermediate filament protein; duplicated) (le:11) (re:2704) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835709	9010	31166	438	145

Description

6500729878 flhc:flai:b1891 flagellar transcriptional activator:flagellar transcriptional activator flhc (gtcfc:11.3:10.2) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1891 b1891 Escherichia coli 562 -11533736 71942 flhc:flai (de:flagellar transcriptional activator flhc) (db:swissprot) FLHC\_ECOLI P11165 ESCHERICHIA COLI 562 -11533736 7000685279 flhc:flai flagellar transcription activator flai (cl:activator flai) (db:pir1.dat) (mp:42 min) XMECIF C64952 Escherichia coli 562 -11533736 224395 flhc:flai flagellar transcriptional activator flhc. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #339(42.4-42.8 min..)) (nt:orf\_id:o339#4; similar to (swissprot accession) (le:8583) (re:9161) (di:complement) D90831 D90831 g1736550 Escherichia coli 562 -11533736 301035 flhc regulator of flagellar biosynthesis acting on (fn:regulator; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 173 of 400 of the completegenome.) (nt:f192; 99 pct identical to flhc\_ecoli sw: p11165; cg) (le:94) (re:672) (di:complement) AE000283 AE000283 g1788201 Escherichia coli 562 -11533736 5000690958 (de:(ecoli\_1848) (pn:regulator of flagellar biosynthesis acting on class 2 operons; transcription initiation factor) (gn:flhc) (gtcfc:11.3) (ec:) (flhc\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_1848 ECOLI\_1848 Escherichia coli 562 10119898

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835710	9011	31167	642	213

Description

6500729879 flhd:flbb:b1892 flagellar transcriptional activator flhd (gtcfc:11.3:10.2) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1892 b1892 Escherichia coli 562 -11533737 71943 flhd:flbb (de:flagellar transcriptional activator flhd) (db:swissprot) FLHD\_ECOLI P11164 ESCHERICHIA COLI 562 -11533737 131447 flhd:flbb flagellar transcription activator flbb:flagellar transcriptional activator flhd (cl:activator flbb) (db:pir1.dat) (mp:42 min) XMECFB A27735 Escherichia coli 562 -11533737 224396 flhd:flbb flagellar transcriptional activator flhd. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #339(42.4-42.8 min.)) (nt:orf\_id:o339#5; similar to (swissprot accession) (le:9164) (re:9523) (di:complement) D90831 D90831 g1736551 Escherichia coli 562 -11533737 301036 (sr:e.coli k12 dna, clone ppm61) (db:genpept-bct1) (de:e.coli flbb operon encoding flagellar transcriptional activators flbb and flai.) (nt:flbb protein (gtg start codon)) (le:265) (re:624) (di:direct) ECOFLBA M19439 g145983 Escherichia coli 562 -11533737 234361 flhd regulator of flagellar biosynthesis:acting on (fn:regulator; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 173 of 400 of the complete genome.) (nt:f119; 100 pct identical to flhd\_ecoli sw: p11164;) (le:675) (re:1034) (di:complement) AE000283 AE000283 g1788202 Escherichia coli 562 -11533737 5000690959 (de:(ecoli\_1849) (pn:regulator of flagellar biosynthesis, acting on class 2 operons; transcriptional initiation factor) (gn:flhd) (gtcfc:11.3) (ec:) (flhd\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_1849 ECOLI\_1849 Escherichia coli 562 10014499

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835723	9012	31168	426	141

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835734	9013	31169	555	184

Description

6500729880 flia:flad:b1922 rna polymerase sigma transcription factor for flagellar operon: rna polymerase sigma factor for flagellar operon: sigma-factor: sigma-27: sigma-28 (gtcfc:11.3:10.2) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1922 b1922 Escherichia coli 562 -11533738 71951 flia:flad (de:(sigma-27) (sigma-28)) (db:swissprot) FLIA\_ECOLI P31804 ESCHERICHIA COLI 562 -11533738 163061 flia transcription initiation factor sigma: flagellar-specific: flia protein (cl:transcription initiation factor sigmad:transcription initiation factor sigma katf homology) (db:pir2.dat) JC4346 JC4346 Escherichia coli 562 -11533738 224425 flia:flad rna polymerase sigma factor for flagellar operon (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #341(42.7-43.1 min.)) (nt:orf\_id:o341#19; similar to (swissprot accession) (le:17600) (re:18319) (di:complement) D90832 D90832 g1736581 Escherichia coli 562 -11533738 301072 flia:flad rna polymerase sigma factor for flagellar operon (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #342(43.0-43.4 min.)) (nt:orf\_id:o341#19; similar to (swissprot accession) (le:2813) (re:3532) (di:complement) D90833 D90833 g1736589 Escherichia coli 562 -11533738 234367 flia flagellar biosynthesis: alternative sigma factor (fn:factor; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 175 of 400 of the complete genome.) (nt:f239; 100 pct identical to flia\_ecoli sw: p31804;) (le:671) (re:1390) (di:complement) AE000285 AE000285 g1788231 Escherichia coli 562 -11533738 238739 flia sigma factor 28 (sr:escherichia coli (strain k-12) dna) (db:genpept-bct2) (de:escherichia coli sigma factor 28 (flia) gene, complete cds.) (nt:putative) (le:325) (re:1044) (di:direct) ECOFLIA L36677 g556180 Escherichia coli 562 -11533738 301065 flia sigma f (db:genpept-bct2) (de:escherichia coli flia operon sigma f (flia), fliz (fliz), and fliy (fliy) genes, complete cds.) (nt:member of sigma 28 family of alternative sigma) (le:258) (re:977) (di:direct) ECU18539 U18539 g687650 Escherichia coli 562 -11533738 224432 flia:flad rna polymerase sigma factor for flagellar operon (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #342(43.0-43.4 min.)) (nt:orf\_id:o341#19; similar to (swissprot accession) (le:2813) (re:3532) (di:complement) D90833 D90833 g1736589 Escherichia coli 562 -11533738 5000690960 (de:(ecoli\_1876) (pn:flagellar biosynthesis; regulation of late gene expression: class 3a and 3b operons; sigma factor) (gn:flia) (gtcfc:11.3) (ec:) (flia\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_1876 ECOLI\_1876 Escherichia coli 562 10014507

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835735	9014	31170	474	157

Description

6500729881 flic:flaf:hag:b1923 flagellin (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1923 b1923 Escherichia coli 562 -11533739 131133 flic:hag flagellin (cl:flagellin) (db:pir1.dat) (mp:42 min) FLEC A37249 Escherichia coli 562 -11533739 224434 flic flagellin (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #342(43.0-43.4 min.)) (nt:orf\_id:o342#1; similar to (pir accession number) (le:3853) (re:5349) (di:complement) D90833 D90833 g1736591 Escherichia coli 562 -11533739 301074 hag (sr:e.coli k12 dna, clone lambda-pflah-2) (db:genpept-bct1) (de:e.coli hag gene encoding flagellin, complete cds.) (nt:flagellin) (le:70) (re:1566) (di:direct) ECOHAG M14358 g146312 Escherichia coli 562 -11533739 234614 flic flagellar biosynthesis:flagellin:filament (fn:structural component; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 175 of 400 of the completegenome.) (nt:f498; 100 pct identical to flic\_ecoli sw: p04949;) (le:1711) (re:3207) (di:complement) AE000285 AE000285 g1788232 Escherichia coli 562 -11533739 5000690961 (de:(ecoli\_1877) (pn:flagellar biosynthesis; flagellin, filament structural protein) (gn:flic) (gtcfc:11.3) (ec:) (flic\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_1877 ECOLI\_1877 Escherichia coli 562 10068039

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835766	9015	31171	393	130

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835767	9016	31172	660	219

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835799	9017	31173	1695	564

Description

6500729882 flid:flbc:flav:b1924 flagellar hook associated protein  
 2:flagellar hook-associated protein 2:hap2:filament cap protein (gtcfc:11.3)  
 (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1924 b1924  
 Escherichia coli 562 -11533740 7000690879 flid:flbc flagellar hook  
 associated protein 2 (db:pir2.dat) (mp:42 min) A64956 A64956 Escherichia  
 coli 562 -11533740 7500959739 flid flagellar biosynthesis:filament capping  
 (fn:putative structure; surface structures) (db:genpept-bct2)  
 (de:escherichia coli k-12 mg1655 section 175 of 400 of the completegenome.)  
 (nt:o468; 99 pct to flid\_ecoli sw: p24216; cg site) (le:3473) (re:4879)  
 (di:direct) AE000285 AE000285 g1788233 Escherichia coli 562 -11533740  
 5000690962 (de:(ecoli\_1878) (pn:flagellar biosynthesis; filament capping  
 protein; enables filament assembly) (gn:flid) (gtcfc:11.3) (ec:)  
 (flid\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli))  
 ECOLI\_1878 ECOLI\_1878 Escherichia coli 562 10123509

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835804	9018	31174	978	325

Description

6500729883 flis:b1925 flagellar protein flis (gtcfc:11.3) (keggfc:14.2)  
 (rileyfc:3.3.3) (db:gtc-escherichia coli) b1925 b1925 Escherichia coli 562  
 -11533741 72028 flis (de:flagellar protein flis) (db:swissprot) FLIS\_ECOLI  
 P26608 ESCHERICHIA COLI 562 -11533741 7000685302 flis flagellar protein  
 flis (cl:flagellar protein flis) (db:pir2.dat) B64956 B64956 Escherichia  
 coli 562 -11533741 224436 flis flagellar protein flis. (sr:escherichia coli  
 (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
 (de:e.coli genomic dna, kohara clone #342(43.0-43.4 min.))  
 (nt:orf\_id:o342#4; similar to (swissprot accession) (le:7046) (re:7456)  
 (di:direct) D90833 D90833 g1736593 Escherichia coli 562 -11533741 301076  
 flis flagellar protein (fn:unknown) (sr:escherichia coli (strain ja11) dna)  
 (db:genpept-bct1) (de:escherichia coli flagellar protein (flid) gene,  
 complete cds;flagellar protein (flis) gene, complete cds; flagellar  
 protein(flit) gene, complete cds; orf1, 5' end.) (le:1532) (r... ECOFLGPRO  
 M85240 g145989 Escherichia coli 562 -11533741 234365 flis flagellar  
 biosynthesis:repressor of class 3a (fn:regulator; surface structures)  
 (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 175 of 400 of the  
 completegenome.) (nt:o136; 100 pct identical to flis\_ecoli sw: p26608;)  
 (le:4904) (re:5314) (di:direct) AE000285 AE000285 g1788234 Escherichia coli  
 562 -11533741 5000690963 (de:(ecoli\_1879) (pn:flagellar biosynthesis;  
 repressor of class 3a and 3b operons:rfla activity) (gn:flis) (gtcfc:11.3)  
 (ec:) (flis\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli))  
 ECOLI\_1879 ECOLI\_1879 Escherichia coli 562 10014584

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835811	9019	31175	720	239

Description

6500729884 flit:b1926 flagellar protein flit (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1926 b1926 Escherichia coli 562 -11533742 72031 flit (de:flagellar protein flit) (db:swissprot) FLIT\_ECOLI P26610 ESCHERICHIA COLI 562 -11533742 7000685304 flit flagellar protein flit (db:pir2.dat) C64956 C64956 Escherichia coli 562 -11533742 224437 flit flagellar protein flit. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #342(43.0-43.4 min.)) (nt:orf\_id:o342#5; similar to (swissprot accession) (le:7456) (re:7821) (di:direct) D90833 D90833 g1736594 Escherichia coli 562 -11533742 301077 flit flagellar protein (fn:unknown) (sr:escherichia coli (strain jall) dna) (db:genpept-bct1) (de:escherichia coli flagellar protein (flid) gene, complete cds;flagellar protein (flis) gene, complete cds; flagellar protein(flit) gene, complete cds; orf1, 5' end.) (le:1942) (r... ECOFLGPRO M85240 g145990 Escherichia coli 562 -11533742 234366 flit flagellar biosynthesis:repressor of class 3a (fn:regulator; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 175 of 400 of the completegenome.) (nt:o121; 100 pct identical to flit\_ecoli sw: p26610;) (le:5314) (re:5679) (di:direct) AE000285 AE000285 g1788235 Escherichia coli 562 -11533742 5000690964 (de:(ecoli\_1880) (pn:flagellar biosynthesis; repressor of class 3a and 3b operons:rfla activity) (gn:flit) (gtcfc:11.3) (ec:) (flit\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_1880 ECOLI\_1880 Escherichia coli 562 10014587



ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501835813	9020	31176	747	249

Description

6500729885 flie:flan:fla\_ai:b1937 flagellar hook-basal body complex protein flie (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1937 b1937 Escherichia coli 562 -11533743 163057 flie flagellar hook-basal body 11k protein flie (db:pir2.dat) A42376 A42376 Escherichia coli 562 -11533743 224443 flie flagellar hook-basal body 11k protein flie (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #342(43.0-43.4 min.)) (nt:orf\_id:o342#13; similar to (pir accession number) (le:14443) (re:14757) (di:complement) D90833 D90833 g1736600 Escherichia coli 562 -11533743 301085 flie flagellar hook-basal body 11k protein flie (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #343(43.3-43.6 min.)) (nt:orf\_id:o342#13; similar to (pir accession number) (le:2080) (re:2394) (di:complement) D90834 D90834 g1736603 Escherichia coli 562 -11533743 301083 flie flagellar protein (fn:basal body structural component) (sr:escherichia coli (strain:jall) dna) (db:genpept-bct1) (de:escherichia coli flagellar hook-basal body subunit (flie) gene, complete cds; and flagellar m-ring protein (flif) gene, 5' end.) (le:231) (re:545) (di:dir... ECOFLIE M84992 g146000 Escherichia coli 562 -11533743 234371 flie flagellar biosynthesis:basal-body component (fn:structural component; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 176 of 400 of the completegenome.) (nt:f105; 100 pct identical to flie\_ecoli sw: p25797) (le:2193) (re:2507) (di:complement) AE000286 AE000286 g1788247 Escherichia coli 562 -11533743 224445 flie flagellar hook-basal body 11k protein flie (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #343(43.3-43.6 min.)) (nt:orf\_id:o342#13; similar to (pir accession number) (le:2080) (re:2394) (di:complement) D90834 D90834 g1736603 Escherichia coli 562 -11533743 5000690965 (de:(ecoli\_1891) (pn:flagellar biosynthesis; basal-body component, possibly at:ms-ring-rod junction) (gn:flie) (gtcfc:11.3) (ec:) (flie\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_1891 ECOLI\_1891 Escherichia coli 562 10086746

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835818	9021	31177	612	203
<u>Description</u>				
6500729886 flif:fla_bi:fla_aii:b1938 flagellar basal-body m-ring protein:flagellar m-ring protein (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1938 b1938 Escherichia coli 562 -11533744 71983 flif:fla:fla .1::bi:aii (de:flagellar m-ring protein) (db:swissprot) FLIF_ECOLI P25798 ESCHERICHIA COLI 562 -11533744 7000685285 flif flagellar basal-body m-ring protein:flagellar hook-basal body ms ring protein flif (db:pir2.dat) G64957 G64957 Escherichia coli 562 -11533744 224446 flif flagellar m-ring protein fragments . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #343(43.3-43.6 min.)) (nt:orf_id:o343#1; similar to (swissprot accession) (le:2609) (re:4267) (di:direct) D90834 D90834 g1736604 Escherichia coli 562 -11533744 301086 flif flagellar biosynthesis:basal-body ms membrane (fn:structural component; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 176 of 400 of the completegenome.) (nt:o552; 87 pct identical (5 gaps) to 550 residues) (le:2722) (re:4380) (di:direct) AE000286 AE000286 g1788248 Escherichia coli 562 -11533744 5000690966 (de:(ecoli_1892) (pn:flagellar biosynthesis; basal-body ms:membrane and supramembrane-ring and collar protein) (gn:flif) (gtcfc:11.3) (ec:) (flif_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI_1892 ECOLI_1892 Escherichia coli 562 10119918				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835821	9022	31178	765	254

Description

6500729887 flig:fla\_bii:fla\_aii:b1939 flagellar motor switch protein flig (gtcfc:11.3:12.9) (keggfc:12.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1939 b1939 Escherichia coli 562 -11533745 71988 flig:fla:fla .2::bii:aii (de:flagellar motor switch protein flig) (db:swissprot) FLIG\_ECOLI P31067 ESCHERICHIA COLI 562 -11533745 7000685287 flig flagellar motor switch protein flig (cl:flagellar switch protein flig) (db:pir2.dat) H64957 H64957 Escherichia coli 562 -11533745 224447 flig:fla\_bii:fla\_aii.2 flagellar motor switch protein flig. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #343(43.3-43.6 min.).) (nt:orf\_id:o343#2; similar to (swissprot accession) (le:4260) (re:5255) (di:direct) D90834 D90834 g1736605 Escherichia coli 562 -11533745 301087 flig flig (db:genpept-bct1) (de:escherichia coli flagellar switch protein (flig) gene, completecds.) (nt:allele: wild-type; flagellar motor component,) (le:1) (re:996) (di:direct) ECU46011 U46011 g1184094 Escherichia coli 562 -11533745 239619 flig flagellar biosynthesis:component of motor (fn:structural component; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 176 of 400 of the completegenome.) (nt:o331; 96 pct identical to flig\_salty sw: p15933;) (le:4373) (re:5368) (di:direct) AE000286 AE000286 g1788249 Escherichia coli 562 -11533745 5000690967 (de:(ecoli\_1893) (pn:flagellar biosynthesis, component of motor switching and energizing, enabling rotation and determining its direction) (gn:flig) (gtcfc:11.3) (ec:) (flig\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherich) ECOLI\_1893 ECOLI\_1893 Escherichia coli 562 10014544

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835827	9023	31179	870	290

Description

6500729888 flih:b1940 flagellar assembly protein flih (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1940 b1940 Escherichia coli 562 -11533746 7000690878 flih flagellar assembly protein flih (db:pir2.dat) A64958 A64958 Escherichia coli 562 -11533746 7500959738 flih flagellar biosynthesis:export of flagellar (fn:transport; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 176 of 400 of the completegenome.) (nt:o235; 84 pct identical (7 gaps) to 228 residues) (le:5340) (re:6047) (di:direct) AE000286 AE000286 g1788250 Escherichia coli 562 -11533746 5000690968 (de:(ecoli\_1894) (pn:flagellar biosynthesis; export of flagellar proteins) (gn:flih) (gtcfc:11.3) (ec:) (flih\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_1894 ECOLI\_1894 Escherichia coli 562 10123513

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835831	9024	31180	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835853	9025	31181	357	118

Description

6500729889 flij:flao:flas:b1942 flagellar flij protein (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1942 b1942 Escherichia coli 562 -11533747 71999 flij:flao:flas (de:flagellar flij protein) (db:swissprot) FLIJ\_ECOLI P52613 ESCHERICHIA COLI 562 -11533747 7000685292 flij flagellar flij protein (db:pir2.dat) C64958 C64958 Escherichia coli 562 -11533747 224450 flij:flao:flas flagellar flij protein. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #343(43.3-43.6 min.)) (nt:orf\_id:o343#5; similar to (swissprot accession) (le:7326) (re:7769) (di:direct) D90834 D90834 g1736608 Escherichia coli 562 -11533747 301090 flij flagellar flij protein (fn:structural component; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 176 of 400 of the completegenome.) (nt:o147; 99 pct identical to flij\_ecoli sw: p52613) (le:7439) (re:7882) (di:direct) AE000286 AE000286 g1788252 Escherichia coli 562 -11533747 5000690969 (de:(ecoli\_1896) (pn:flagellar flij protein) (gn:flij) (gtcfc:11.3) (ec:) (flij\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_1896 ECOLI\_1896 Escherichia coli 562 10119921

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835854	9026	31182	681	226

Description

6500729890 flik:flae:flar:b1943 hook-length control protein:flagellar hook-length control protein (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1943 b1943 Escherichia coli 562 -11533748 72002 flik:flae:flar (de:flagellar hook-length control protein) (db:swissprot) FLIK\_ECOLI P52614 ESCHERICHIA COLI 562 -11533748 7000685294 flik hook-length control protein (db:pir2.dat) D64958 D64958 Escherichia coli 562 -11533748 224451 flik:flae:flar flagellar hook-length control protein. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #343(43.3-43.6 min.)) (nt:orf\_id:o343#6; similar to (swissprot accession) (le:7766) (re:8893) (di:direct) D90834 D90834 g1736609 Escherichia coli 562 -11533748 301091 flik (fn:control of length of flagellar hook) (sr:escherichia coli (sub\_strain ks650, strain k-12) dna) (db:genpept-bct1) (de:escherichia coli flj gene, 3' end of cds, flik gene, complete cds, flil gene, 5' end of cds.) (le:102) (re:1229) (di:direct) ECOFLIK L43491 g894083 Escherichia coli 562 -11533748 234378 flik flagellar hook-length control protein (fn:structural component; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 176 of 400 of the completegenome.) (nt:o375; 100 pct identical to flik\_ecoli sw: p52614) (le:7879) (re:9006) (di:direct) AE000286 AE000286 g1788253 Escherichia coli 562 -11533748 5000690970 (de:(ecoli\_1897) (pn:flagellar hook-length control protein) (gn:flik) (gtcfc:11.3) (ec:) (flik\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_1897 ECOLI\_1897 Escherichia coli 562 10014558

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835868	9027	31183	483	160

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835873	9028	31184	201	66

Description

6500729891 flil:fla\_ai:fla\_qi:checl:b1944 flil protein:flagellar flil protein (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1944 b1944 Escherichia coli 562 -11533749 72006 flil:fla:fla:checl::ai:qi (de:flagellar flil protein) (db:swissprot) FLIL\_ECOLI P06973 ESCHERICHIA COLI 562 -11533749 130899 flil:flaai:checl flil protein (cl:flaai protein) (db:pir1.dat) (mp:43 min) XMECF1 A29842 Escherichia coli 562 -11533749 224452 flil:fla\_ai:fla\_qi:checl flagellar flil protein. (sr:escherichia coli (strain:k12) dna, clone lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #343(43.3-43.6 min..)) (nt:orf\_id:o343#8; similar to (swissprot accession) (le:8998) (re:9462) (di:direct) D90834 D90834 g1736610 Escherichia coli 562 -11533749 301092 flaa (sr:e.coli k-12 dna, clone pck210) (db:genpept-bct1) (de:e.coli flaa gene encoding a protein controlling the rotational direction of flagella during chemotaxis, complete cds.) (nt:flaai protein) (le:266) (re:730) (di:direct) ECOFLAA M12784 g145980 Escherichia coli 562 -11533749 234359 flil flagellar biosynthesis (fn:putative structure; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 176 of 400 of the complete genome.) (nt:o154; 100 pct identical to flil\_ecoli sw: p06973;) (le:9111) (re:9575) (di:direct) AE000286 AE000286 g1788254 Escherichia coli 562 -11533749 5000690971 (de:(ecoli\_1898) (pn:flagellar biosynthesis) (gn:flil) (gtcfc:11.3) (ec:) (flil\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_1898 ECOLI\_1898 Escherichia coli 562 10014562

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835874	9029	31185	942	313

Description

6500729892 flim:fla\_aii:fla\_gii:chec2:b1945 cg site no. 774:alternate name  
chec:flaa:flagellar motor switch protein flim (gtcfc:11.3:12.9)  
(keggfc:12.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1945 b1945  
Escherichia coli 562 -11533750 72010 flim:fla:fla:chec2::aii:gii  
(de:flagellar motor switch protein flim) (db:swissprot) FLIM\_ECOLI P06974  
ESCHERICHIA COLI 562 -11533750 130900 flim:flaaii:checii:flaa:chec  
flagellar motor switch protein flim (cl:flagellar motor switch protein flim)  
(db:pir1.dat) (mp:43 min) XMECF2 B29842 Escherichia coli 562 -11533750  
224453 flim:fla\_aii:fla\_gii:chec2 flagellar motor switch protein flim.  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #343(43.3-43.6  
min.)) (nt:orf\_id:o343#9; similar to (swissprot accession) (le:9467)  
(re:10471) (di:direct) D90834 D90834 g1736611 Escherichia coli 562 -11533750  
301093 flaa (sr:e.coli k-12 dna, clone pck210) (db:genpept-bct1) (de:e.coli  
flaa gene encoding a protein controlling the rotational direction of flagella  
during chemotaxis, complete cds.) (nt:flaaii protein) (le:735) (re:1739)  
(di:direct) ECOFLAA M12784 g145981 Escherichia coli 562 -11533750 234360  
flim flagellar biosynthesis:component of motor (fn:structural component;  
surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655  
section 176 of 400 of the complete genome.) (nt:o334; 100 pct to flim\_ecoli  
sw: p06974; cg site) (le:9580) (re:10584) (di:direct) AE000286 AE000286  
g1788255 Escherichia coli 562 -11533750 5000690972 (de:(ecoli\_1899)  
(pn:flagellar biosynthesis, component of motor switch and energizing,  
enabling rotation and determining its direction) (gn:flim) (gtcfc:11.3)  
(ec:) (flim\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia)  
ECOLI\_1899 ECOLI\_1899 Escherichia coli 562 10014566

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835900	9030	31186	1368	455

Description

6500729893 flin:motd:flan:b1946 flagellar motor switch protein flin  
 (gtcfc:11.3:12.9) (keggfc:12.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)  
 b1946 b1946 Escherichia coli 562 -11533751 72013 flin:motd:flan  
 (de:flagellar motor switch protein flin) (db:swissprot) FLIN\_ECOLI P15070  
 ESCHERICHIA COLI 562 -11533751 131449 flin::flaaii flagellar motor switch  
 protein flin:gene flin protein (cl:flagellar motor switch protein)  
 (db:pir1.dat) (mp:43 min) XMECII JS0111 Escherichia coli 562 -11533751  
 224454 flin:motd:flan flagellar motor switch protein flin. (sr:escherichia  
 coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
 (de:e.coli genomic dna, kohara clone #343(43.3-43.6 min.))  
 (nt:orf\_id:o343#10; similar to (swissprot accession) (le:10468) (re:10881)  
 (di:direct) D90834 D90834 g1736612 Escherichia coli 562 -11533751 301094  
 flin flagellar motor switch complex component (sr:escherichia coli dna)  
 (db:genpept-bct1) (de:e. coli flagellar switch flin (motd) gene, complete  
 cds.) (le:24) (re:437) (di:direct) ECOFLIN M26294 g414721 Escherichia coli  
 562 -11533751 234380 flin flagellar biosynthesis:component of motor  
 (fn:structural component; surface structures) (db:genpept-bct2)  
 (de:escherichia coli k-12 mg1655 section 176 of 400 of the completegenome.)  
 (nt:o137; 100 pct identical to flin\_ecoli sw: p15070;) (le:10581) (re:10994)  
 (di:direct) AE000286 AE000286 g1788256 Escherichia coli 562 -11533751  
 5000690973 (de:(ecoli\_1900) (pn:flagellar biosynthesis, component of motor  
 switch and energizing, enabling rotation and determining its direction)  
 (gn:flin) (gtcfc:11.3) (ec:) (flin\_ecoli) (keggfc:11.2) (rileyfc:3.3.3)  
 (db:gtc-escherichia) ECOLI\_1900 ECOLI\_1900 Escherichia coli 562 10014569



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835902	9031	31187	198	65

Description

6500729894 flio:flbd:flap:b1947 flagellar protein flio (gtcfc:11.3)  
(keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1947 b1947  
Escherichia coli 562 -11533752 72015 flio:flbd:flap (de:flagellar protein  
flio) (db:swissprot) FLIO\_ECOLI P22586 ESCHERICHIA COLI 562 -11533752  
163069 flio flagellar protein flio (cl:flagellar protein flio)  
(db:pir2.dat) A36869 A36869 Escherichia coli 562 -11533752 224455  
flio:flbd:flap flagellar protein flio. (sr:escherichia coli (strain:k12)  
dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic  
dna, kohara clone #343(43.3-43.6 min.)) (nt:orf\_id:o343#11; similar to  
(swissprot accession) (le:10944) (re:11249) (di:direct) D90834 D90834  
g1736613 Escherichia coli 562 -11533752 234381 flio flagellar biosynthesis  
(fn:putative structure; surface structures) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 177 of 400 of the completegenome.)  
(nt:o101; 100 pct identical to flio\_ecoli sw: p22586;) (le:62) (re:367)  
(di:direct) AE000287 AE000287 g1788258 Escherichia coli 562 -11533752  
301095 flio (sr:escherichia coli (strain k-12) dna) (db:genpept-bct2)  
(de:e. coli flagellar protein (flio, flip, fliq, and flir) genes,complete  
cds.) (le:66) (re:371) (di:direct) ECOFLIOPQR L22182 g347242 Escherichia  
coli 562 -11533752 5000690974 (de:(ecoli\_1901) (pn:flagellar biosynthesis)  
(gn:flio) (gtcfc:11.3) (ec:) (flio\_ecoli) (keggfc:11.2) (rileyfc:3.3.3)  
(db:gtc-escherichia coli)) ECOLI\_1901 ECOLI\_1901 Escherichia coli 562  
10014571

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835912	9032	31188	465	154
<u>Description</u>				
6500729895 flip:flar:b1948 flagellar biosynthetic protein flip (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1948 b1948 Escherichia coli 562 -11533753 72018 flip:flar (de:flagellar biosynthetic protein flip) (db:swissprot) FLIP_ECOLI P33133 ESCHERICHIA COLI 562 -11533753 163070 flip flagellar biosynthetic protein flip (cl:flagellar biosynthetic protein flip) (db:pir2.dat) B36869 B36869 Escherichia coli 562 -11533753 224456 flip:flar flagellar biosynthetic protein flip. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #343(43.3-43.6 min.)) (nt:orf_id:o343#12; similar to (swissprot accession) (le:11249) (re:11986) (di:direct) D90834 D90834 g1736614 Escherichia coli 562 -11533753 301102 flip:flar flagellar biosynthetic protein flip. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #344(43.5-43.9 min.)) (nt:orf_id:o343#12; similar to (swissprot accession) (le:274) (re:1011) (di:direct) D90835 D90835 g1736621 Escherichia coli 562 -11533753 234382 flip flagellar biosynthesis (fn:putative structure; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 177 of 400 of the completegenome.) (nt:o245; 100 pct identical to flip_ecoli sw: p33133;) (le:367) (re:1104) (di:direct) AE000287 AE000287 g1788259 Escherichia coli 562 -11533753 301096 flip flagellar protein (sr:escherichia coli (strain k-12) dna) (db:genpept-bct2) (de:e. coli flagellar protein (fliO, flip, fliQ, and flir) genes,complete cds.) (le:371) (re:1108) (di:direct) ECOFLIOPQR L22182 g347243 Escherichia coli 562 -11533753 224462 flip:flar flagellar biosynthetic protein flip. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #344(43.5-43.9 min.)) (nt:orf_id:o343#12; similar to (swissprot accession) (le:274) (re:1011) (di:direct) D90835 D90835 g1736621 Escherichia coli 562 -11533753 5000690975 (de:(ecoli_1902) (pn:flagellar biosynthesis) (gn:flip) (gtcfc:11.3) (ec:) (flip_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI_1902 ECOLI_1902 Escherichia coli 562 10014574				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835914	9033	31189	1329	442
<u>Description</u>				
6500729896 fliq:flaq:b1949 flagellar biosynthetic protein fliq (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1949 b1949 Escherichia coli 562 -11533754 72022 fliq:flaq (de:flagellar biosynthetic protein fliq) (db:swissprot) FLIQ_ECOLI P33134 ESCHERICHIA COLI 562 -11533754 163071 fliq flagellar biosynthesis-specific protein fliq (cl:flagellar biosynthesis-specific protein) (db:pir2.dat) C36869 C36869 Escherichia coli 562 -11533754 224457 fliq:flaq flagellar biosynthetic protein fliq. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #343(43.3-43.6 min.)) (nt:orf_id:o343#13; similar to (swissprot accession) (le:11996) (re:12265) (di:direct) D90834 D90834 g1736615 Escherichia coli 562 -11533754 301103 fliq:flaq flagellar biosynthetic protein fliq. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #344(43.5-43.9 min.)) (nt:orf_id:o343#13; similar to (swissprot accession) (le:1021) (re:1290) (di:direct) D90835 D90835 g1736622 Escherichia coli 562 -11533754 234383 fliq flagellar biosynthesis (fn:putative structure; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 177 of 400 of the completegenome.) (nt:o89; 100 pct identical to fliq_ecoli sw: p33134; cg) (le:1114) (re:1383) (di:direct) AE000287 AE000287 g1788260 Escherichia coli 562 -11533754 301097 fliq (sr:escherichia coli (strain k-12) dna) (db:genpept-bct2) (de:e. coli flagellar protein (fliq, flip, fliq, and flir) genes,complete cds.) (le:1118) (re:1387) (di:direct) ECOFLIOPQR L22182 g347244 Escherichia coli 562 -11533754 224463 fliq:flaq flagellar biosynthetic protein fliq. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #344(43.5-43.9 min.)) (nt:orf_id:o343#13; similar to (swissprot accession) (le:1021) (re:1290) (di:direct) D90835 D90835 g1736622 Escherichia coli 562 -11533754 5000690976 (de:(ecoli_1903) (pn:flagellar biosynthesis) (gn:fliq) (gtcfc:11.3) (ec:) (fliq_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI_1903 ECOLI_1903 Escherichia coli 562 10014578				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835916	9034	31190	339	112

Description

6500729897 flir:flap:b1950 flagellar biosynthetic protein flir (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b1950 b1950 Escherichia coli 562 -11533755 72025 flir:flap (de:flagellar biosynthetic protein flir) (db:swissprot) FLIR\_ECOLI P33135 ESCHERICHIA COLI 562 -11533755 7000685300 flir flagellar biosynthetic protein flir (db:pir2.dat) C64959 C64959 Escherichia coli 562 -11533755 224458 flir:flap flagellar biosynthetic protein flir. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #343(43.3-43.6 min.)) (nt:orf\_id:o343#14; similar to (swissprot accession) (le:12273) (re:13058) (di:direct) D90834 D90834 g1736616 Escherichia coli 562 -11533755 301104 flir:flap flagellar biosynthetic protein flir. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #344(43.5-43.9 min.)) (nt:orf\_id:o343#14; similar to (swissprot accession) (le:1298) (re:2083) (di:direct) D90835 D90835 g1736623 Escherichia coli 562 -11533755 301098 flir flagellar biosynthesis (fn:putative enzyme; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 177 of 400 of the completegenome.) (nt:o261; 99 pct identical to flir\_ecoli sw: p33135; cg) (le:1391) (re:2176) (di:direct) AE000287 AE000287 g1788261 Escherichia coli 562 -11533755 224464 flir:flap flagellar biosynthetic protein flir. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #344(43.5-43.9 min.)) (nt:orf\_id:o343#14; similar to (swissprot accession) (le:1298) (re:2083) (di:direct) D90835 D90835 g1736623 Escherichia coli 562 -11533755 5000690977 (de:(ecoli\_1904) (pn:flagellar biosynthesis) (gn:flir) (gtcfc:11.3) (ec:) (flir\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_1904 ECOLI\_1904 Escherichia coli 562 10119922

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835920	9035	31191	822	273

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835921	9036	31192	279	92

Description

6500729898 fimb:b4312 recombinase involved in phase variation:type 1  
fimbriae regulatory protein fimb (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3)  
(db:gtc-escherichia coli) b4312 b4312 Escherichia coli 562 -11533756 71683  
fimb (de:type 1 fimbriae regulatory protein fimb) (db:swissprot) FIMB\_ECOLI  
P04742 ESCHERICHIA COLI 562 -11533756 154805 fimb type 1 fimbriae  
regulatory protein fimb:recombinase fimb involved in phase variation  
(cl:type 1 fimbriae regulatory protein fime) (db:pir1.dat) RGECFF S56537  
Escherichia coli 562 -11533756 7500881460 fimb recombinase involved in  
phase variation (fn:regulatory gene for expression of fima)  
(db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to  
00.1 minutes.) (nt:cg site no. 18355; alternate gene name pil) (le:231789)  
(re:232391) (di:direct) ECOUW93 U14003 g537153 Escherichia coli 562  
-11533756 237517 fimb recombinase involved in phase variation  
(fn:regulator; surface structures) (db:genpept-bct2) (de:escherichia coli  
k-12 mg1655 section 392 of 400 of the completegenome.) (nt:o200; 100 pct  
identical to fimb\_ecoli sw: p04742;) (le:751) (re:1353) (di:direct) AE000502  
AE000502 g1790767 Escherichia coli 562 -11533756 5000690978  
(de:(ecoli\_4195) (pn:regulator for fima) (gn:fimb) (gtcfc:11.3) (ec:)  
(fimb\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli))  
ECOLI\_4195 ECOLI\_4195 Escherichia coli 562 10014241

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501835929	9037	31193	621	206

Description

6500729899 fime:b4313 recombinase involved in phase variation:type 1  
fimbriae regulatory protein fime (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3)  
(db:gtc-escherichia coli) b4313 b4313 Escherichia coli 562 -11533757 237518  
fime (de:type 1 fimbriae regulatory protein fime) (db:swissprot) FIME\_ECOLI  
P04741 ESCHERICHIA COLI 562 -11533757 131524 fime type 1 fimbriae  
regulatory protein fime (cl:type 1 fimbriae regulatory protein fime)  
(db:pir1.dat) (mp:98 min) RGEFCFE B25111 Escherichia coli 562 -11533757  
5000690979 (db:genpept-bct1) (de:e. coli genes fimb, fime and n-terminus  
fima (type 1 fimbriae).) (nt:fime) (le:1960) (re:2556) (di:direct) ECFIMBE  
X03923 g581086 Escherichia coli 562 -11533757 304564 fime recombinase  
involved in phase variation (fn:regulatory gene for expression of fima)  
(db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to  
00.1 minutes.) (nt:cg site no. 18346) (le:232869) (re:233465) (di:direct)  
ECOUW93 U14003 g537154 Escherichia coli 562 -11533757 232870 fime  
recombinase involved in phase variation (fn:regulator; surface structures)  
(db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 392 of 400 of the  
completegenome.) (nt:o198; 100 pct identical to fime\_ecoli sw: p04741;)  
(le:1831) (re:2427) (di:direct) AE000502 AE000502 g1790768 Escherichia coli  
562 -11533757 71690 fime (de:type 1 fimbriae regulatory protein fime)  
(db:swissprot) FIME\_ECOLI P04741 ESCHERICHIA COLI 562 -11533757

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835932	9038	31194	1266	421

Description

6500729900 fima:pila:b4314 type 1 fimbrial subunit:type-1 fimbrial protein:a chain precursor:type-1a pilin (gtcfc:11.3:12.8) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b4314 b4314 Escherichia coli 562 -11533758 72077 fima:pila (de:type-1 fimbrial protein, a chain precursor (type-1a pilin)) (db:swissprot) FM1A\_ECOLI P04128 ESCHERICHIA COLI 562 -11533758 153937 fima type 1 fimbrial protein fima precursor:type 1 pilin (cl:type 1 fimbrial protein) (db:pir1.dat) YQECT1 S56539 Escherichia coli 562 -11533758 7500881643 fima type 1 fimbrial subunit (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 18358; alternate gene names fimd, pila) (le:233947) (re:234495) (di:direct) ECOUW93 U14003 g537155 Escherichia coli 562 -11533758 237519 fima major type 1 subunit fimbrin pilin (fn:structural component; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 392 of 400 of the completegenome.) (nt:ol82; 100 pct identical to fmla\_ecoli sw: p04128;) (le:2909) (re:3457) (di:direct) AE000502 AE000502 g1790769 Escherichia coli 562 -11533758 5000690980 (de:(ecoli\_4197) (pn:major type 1 subunit fimbrin:pilin) (gn:fima) (gtcfc:11.3) (ec:) (fmla\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_4197 ECOLI\_4197 Escherichia coli 562 10014632

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835944	9039	31195	360	119

Description

6500729901 fimc:b4316 chaperone protein involved in biogenesis of type 1 fimbriae:chaperone protein fimc precursor (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b4316 b4316 Escherichia coli 562 -11533759 71686 fimc (de:chaperone protein fimc precursor) (db:swissprot) FIMC\_ECOLI P31697 ESCHERICHIA COLI 562 -11533759 162816 fimc chaperone protein involved in biogenesis of type 1 fimbriae (cl:chaperone protein papd) (db:pir2.dat) S56541 S56541 Escherichia coli 562 -11533759 7500881464 fimc chaperone protein involved in biogenesis of type (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 18352; alternate gene name pil (cg site) (le:235136) (re:235861) (di:direct) ECOUW93 U14003 g537157 Escherichia coli 562 -11533759 237521 fimc periplasmic chaperone:required for type 1 (fn:factor; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 392 of 400 of the completegenome.) (nt:o241; 100 pct identical to fimc\_ecoli sw: p31697;) (le:4098) (re:4823) (di:direct) AE000502 AE000502 g1790771 Escherichia coli 562 -11533759 5000690981 (de:(ecoli\_4199) (pn:periplasmic chaperone, required for type 1 fimbriae) (gn:fimc) (gtcfc:11.3) (ec:) (fimc\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_4199 ECOLI\_4199 Escherichia coli 562 10014244

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835947	9040	31196	1215	404

Description

6500729902 fimd:b4317 outer membrane usher protein fimd precursor (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b4317 b4317 Escherichia coli 562 -11533760 71688 fimd (de:outer membrane usher protein fimd precursor) (db:swissprot) FIMD\_ECOLI P30130 ESCHERICHIA COLI 562 -11533760 163046 fimd outer membrane usher protein fimd precursor (cl:outer membrane usher protein fimd) (db:pir2.dat) S56542 S56542 Escherichia coli 562 -11533760 7500881465 fimd (fn:involved in export and assembly of fima) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 18349) (le:235929) (re:238565) (di:direct) ECOUW93 U14003 g537158 Escherichia coli 562 -11533760 237522 fimd outer membrane protein:export and assembly of (fn:membrane; outer membrane constituents) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 392 of 400 of the completegenome.) (nt:o878; 100 pct identical to fimd\_ecoli sw: p30130;) (le:4891) (re:7527) (di:direct) AE000502 AE000502 g1790772 Escherichia coli 562 -11533760 5000690982 (de:(ecoli\_4200) (pn:outer membrane protein; export and assembly of type 1 fimbriae) (gn:fimd\_2) (gtcfc:11.3) (ec:) (fimd\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_4200 ECOLI\_4200 Escherichia coli 562 10014246



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835961	9041	31197	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835969	9042	31198	522	174

Description

6500729903 fimf:b4318 fimf protein precursor (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b4318 b4318 Escherichia coli 562 -11533761 71691 fimf (de:fimf protein precursor) (db:swissprot) FIMF\_ECOLI P08189 ESCHERICHIA COLI 562 -11533761 163048 fimf fimbrial protein fimf precursor:type 1 (cl:type 1 fimbrial protein) (db:pir2.dat) S56543 S56543 Escherichia coli 562 -11533761 7500881466 fimf (fn:involved in regulation of length and mediation) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 18343) (le:238575) (re:239105) (di:direct) ECOUW93 U14003 g537159 Escherichia coli 562 -11533761 237523 fimf fimbrial morphology (fn:structural component; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 392 of 400 of the completegenome.) (nt:o176; 100 pct identical to fimf\_ecoli sw: p08189;) (le:7537) (re:8067) (di:direct) AE000502 AE000502 g1790773 Escherichia coli 562 -11533761 5000690983 (de:(ecoli\_4201) (pn:fimbrial morphology) (gn:fimf) (gtcfc:11.3) (ec:) (fimf\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_4201 ECOLI\_4201 Escherichia coli 562 10014249

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835972	9043	31199	1068	355

Description

6500729904 fimg:b4319 fimg protein precursor (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b4319 b4319 Escherichia coli 562 -11533762 71693 fimg (de:fimg protein precursor) (db:swissprot) FIMG\_ECOLI P08190 ESCHERICHIA COLI 562 -11533762 163049 fimg fimbrial protein fimg precursor:type 1 (cl:conserved hypothetical protein b1503) (db:pir2.dat) S56544 S56544 Escherichia coli 562 -11533762 7500881467 fimg (fn:involved in regulation of length and mediation) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 18340) (le:239118) (re:239621) (di:direct) ECOUW93 U14003 g537160 Escherichia coli 562 -11533762 237524 fimg fimbrial morphology (fn:structural component; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 392 of 400 of the completegenome.) (nt:o167; 100 pct identical to fimg\_ecoli sw: p08190;) (le:8080) (re:8583) (di:direct) AE000502 AE000502 g1790774 Escherichia coli 562 -11533762 5000690984 (de:(ecoli\_4202) (pn:fimbrial morphology) (gn:fimg) (gtcfc:11.3) (ec:) (fimg\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_4202 ECOLI\_4202 Escherichia coli 562 10014251

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835989	9044	31200	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835992	9045	31201	246	81

Description

6500729905 fimh:b4320 fimh protein precursor (gtcfc:11.3) (keggfc:14.2) (rileyfc:3.3.3) (db:gtc-escherichia coli) b4320 b4320 Escherichia coli 562 -11533763 71694 fimh (de:fimh protein precursor) (db:swissprot) FIMH\_ECOLI P08191 ESCHERICHIA COLI 562 -11533763 163050 fimh fimbrial protein fimh precursor:type 1 (cl:fimbrial protein fimh) (db:pir2.dat) S56545 S56545 Escherichia coli 562 -11533763 7500881468 fimh (fn:involved in regulation of length and mediation) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 18337) (le:239641) (re:240543) (di:direct) ECOUW93 U14003 g537161 Escherichia coli 562 -11533763 237525 fimh minor fimbrial subunit:d-mannose specific (fn:structural component; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 392 of 400 of the completegenome.) (nt:o300; 100 pct identical to fimh\_ecoli sw: p08191;) (le:8603) (re:9505) (di:direct) AE000502 AE000502 g1790775 Escherichia coli 562 -11533763 5000690985 (de:(ecoli\_4203) (pn:minor fimbrial subunit, d-mannose specific adhesin) (gn:fimh) (gtcfc:11.3) (ec:) (fimh\_ecoli) (keggfc:11.2) (rileyfc:3.3.3) (db:gtc-escherichia coli)) ECOLI\_4203 ECOLI\_4203 Escherichia coli 562 10014252

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501835997	9046	31202	900	300

Description

6500729906 mray:murx:b0087  
phospho-n-acetylmuramoyl-pentapeptide-transferase:phospho-n-acetylmuramoyl-p  
entapeptide-transferase (gtcfc:11.4) (ec:2.7.8.13) (keggfc:7.3)  
(rileyfc:3.3.4) (db:gtc-escherichia coli) b0087 b0087 Escherichia coli 562  
-11533764 233611 mray:murx (ec:2.7.8.13) (de:(udp-murnac-pentapeptide  
phosphotransferase)) (db:swissprot) MRAY\_ECOLI P15876 ESCHERICHIA COLI 562  
-11533764 164297 mray phospho-n-acetylmuramoyl-pentapeptide-transferase  
(cl:phospho-n-acetylmuramoyl-pentapeptide-transferase) (ec:2.7.8.13)  
(db:pir2.dat) (mp:2 min) S08395 S08395 Escherichia coli 562 -11533764  
227994 mray mray protein aa 1-360 (db:genpept-bct1) (de:e. coli 2 minute  
region.) (le:12532) (re:13614) (di:direct) EC2MIN X55034 g40855 Escherichia  
coli 562 -11533764 5000691002 (db:genpept-bct1) (de:escherichia coli murd  
gene and orf-y (ec 6.3.2.9).) (nt:orf-y (aa 1-360)) (le:111) (re:1193)  
(di:direct) ECMUROY X51584 g42059 Escherichia coli 562 -11533764 304531  
mray phospho-n-acetylmuramoyl-pentapeptide-transferas (sr:escherichia coli  
(strain:k-12) dna) (db:genpept-bct1) (ec:2.7.8.13) (de:e.coli k12 genome,  
0-2.4min. region.) (le:95656) (re:96738) (di:direct) ECO110K D10483 g216501  
Escherichia coli 562 -11533764 233431 mray  
phospho-n-acetylmuramoyl-pentapeptide (fn:enzyme; murein sacculus,  
peptidoglycan) (db:genpept-bct2) (ec:2.7.8.13) (de:escherichia coli k-12  
mg1655 section 8 of 400 of the completegenome.) (nt:o360; 100 pct identical  
to mray\_ecoli sw: p15876) (le:12457) (re:13539) (di:direct) AE000118  
AE000118 g1786275 Escherichia coli 562 -11533764 84202 mray:murx  
(ec:2.7.8.13) (de:(udp-murnac-pentapeptide phosphotransferase))  
(db:swissprot) MRAY\_ECOLI P15876 ESCHERICHIA COLI 562 -11533764

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836010	9047	31203	207	68

Description

6500729907 amia:b2435 probable n-acetylmuramoyl-l-alanine amidase (gtcfc:11.4) (ec:3.5.1.28) (keggfc:7.3) (rileyfc:3.3.4) (db:gtc-escherichia coli) b2435·b2435 Escherichia coli 562 -11533765 7500876797 amia (ec:3.5.1.28) (de:(ec 3.5.1.28)) (db:swissprot) AMIA\_ECOLI P36548 ESCHERICHIA COLI 562 -11533765 164116 amia n-acetylmuramoyl-l-alanine amidase (ec:3.5.1.28) (db:pir2.dat) A36964 A36964 Escherichia coli 562 -11533765 225006 amia probable n-acetylmuramoyl-l-alanine amidase ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #420(54.9-55.2 min.)) (nt:similar to (swissprot accession number p36548)) (le:6290) (re:7159) (di:direct) D90873 D90873 g1799865 Escherichia coli 562 -11533765 5000691003 (db:genpept-bct1) (de:e.coli orf1, orf3 and hemf gene for coproporphyrinogen iii oxidase.) (nt:orf1) (le:439) (re:1308) (di:direct) ECHEMF X75413 g453968 Escherichia coli 562 -11533765 233080 amia n-acetylmuramoyl-l-alanine amidase i (fn:enzyme; murein sacculus, peptidoglycan) (db:genpept-bct2) (ec:3.5.1.28) (de:escherichia coli k-12 mg1655 section 221 of 400 of the completegenome.) (nt:o289; 100 pct identical to amia\_ecoli sw: p36548) (le:82) (re:951) (di:direct) AE000331 AE000331 g1788776 Escherichia coli 562 -11533765 59308 amia (ec:3.5.1.28) (de:(ec 3.5.1.28)) (db:swissprot) AMIA\_ECOLI P36548 ESCHERICHIA COLI 562 -11533765

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501836011	9048	31204	723	240

#### Description

6500729908 amib:b4169 n-acetylmuramoyl-l-alanine amidase precursor  
(gtcfc:11.4) (ec:3.5.1.28) (keggfc:7.3) (rileyfc:3.3.4) (db:gtc-escherichia coli) b4169 b4169 Escherichia coli 562 -11533766 59311 amib (ec:3.5.1.28) (de:n-acetylmuramoyl-l-alanine amidase amib precursor,) (db:swissprot) AMIB\_ECOLI P26365 ESCHERICHIA COLI 562 -11533766 164115 amib n-acetylmuramoyl-l-alanine amidase:precursor (ec:3.5.1.28) (db:pir2.dat) S41741 S41741 Escherichia coli 562 -11533766 237374 amib n-acetylmuramoyl-l-alanine amidase (fn:cell wall hydrolase) (sr:escherichia coli (strain k-12) (library: clarke-carbon) dna) (db:genpept-bct1) (ec:3.5.1.28) (de:escherichia coli n-acetylmuramoyl-l-alanine amidase (amib) gene,complete cds, dna repair protein (mutl) gene, partial cds, and... ECOMUTL L19346 g304914 Escherichia coli 562 -11533766 7500876798 amib n-acetylmuramoyl-l-alanine amidase (db:genpept-bct1) (ec:3.5.1.28) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:86893) (re:88230) (di:direct) ECOUW93 U14003 g537010 Escherichia coli 562 -11533766 235205 amib n-acetylmuramoyl-l-alanine amidase ii:a murein (fn:enzyme; murein sacculus, peptidoglycan) (db:genpept-bct2) (ec:3.5.1.28) (de:escherichia coli k-12 mg1655 section 379 of 400 of the completegenome.) (nt:o445; 100 pct identical amino acid sequence and) (le:3779) (re:5116) (di:direct) AE000489 AE000489 g1790611 Escherichia coli 562 -11533766 5000691004 (de:(ecoli\_4052) (pn:n-acetylmuramoyl-l-alanine amidase ii; a murein hydrolase) (gn:amib) (gtcfc:11.4) (ec:3.5.1.28) (amib\_ecoli) (keggfc:7.3) (rileyfc:3.3.4) (db:gtc-escherichia coli)) ECOLI\_4052 ECOLI\_4052 Escherichia coli 562 10002049

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501836015	9049	31205	243	80

#### Description

6500729909 mrcb:ponb:pbbf:b0149 peptidoglycan synthetase:penicillin-binding protein 1b:pbb-1b (gtcfc:11.4) (keggfc:14.2) (rileyfc:3.3.4) (db:gtc-escherichia coli) b0149 b0149 Escherichia coli 562 -11533767 7000688970 mrcb:ponb penicillin-binding protein 1b:peptidoglycan synthetase (cl:penicillin-binding protein 1b) (db:pir1.dat) ZPECPB E64738 Escherichia coli 562 -11533767 7500953611 mrcb peptidoglycan synthetase:penicillin-binding (fn:enzyme; murein sacculus, peptidoglycan) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 14 of 400 of the completegenome.) (nt:o844; 99 pct identical to pbbp\_ecoli sw: p02919;) (le:4067) (re:6601) (di:direct) AE000124 AE000124 g1786343 Escherichia coli 562 -11533767 5000690986 (de:(ecoli\_149) (pn:peptidoglycan synthetase; cell wall biosynthesis; penicillin- binding protein 1b) (gn:mrcb) (gtcfc:11.4) (ec:) (pbbp\_ecoli) (keggfc:11.2) (rileyfc:3.3.4) (db:gtc-escherichia coli)) ECOLI\_149 ECOLI\_149 Escherichia coli 562 10122682

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836041	9050	31206	249	82

Description

6500729910 bola:b0435 bola protein (gtcfc:11.4) (keggfc:14.2)  
(rileyfc:3.3.4) (db:gtc-escherichia coli) b0435 b0435 Escherichia coli 562  
-11533768 131371 bola bola protein (cl:bola protein) (db:pir1.dat) BVECBA  
JS0356 Escherichia coli 562 -11533768 232470 (db:genpept-bct1)  
(de:escherichia coli bola gene and associated promoter regions.) (nt:bola  
protein (aa 1-116)) (le:385) (re:735) (di:direct) ECBOLA X17642 g41070  
Escherichia coli 562 -11533768 240212 bola (db:genpept-bct1)  
(de:escherichia coli minutes 9 to 11 genomic sequence.) (le:33889)  
(re:34239) (di:direct) ECU82664 U82664 g1773119 Escherichia coli 562  
-11533768 7500953647 bola possible regulator of murein genes (fn:putative  
regulator; murein sacculus,) (db:genpept-bct2) (de:escherichia coli k-12  
mg1655 section 39 of 400 of the completegenome.) (nt:ol16; 100 pct identical  
to bola\_ecoli sw: p15298) (le:9879) (re:10229) (di:direct) AE000149 AE000149  
g1786638 Escherichia coli 562 -11533768 61926 bola\_ecoli (de:bola protein.)  
P15298 P15298 Escherichia coli 562 -11533768 5000690987 (de:(ecoli\_419)  
(pn:bola protein) (gn:bola) (gtcfc:11.4) (ec:) (bola\_ecoli) (keggfc:11.2)  
(rileyfc:3.3.4) (db:gtc-escherichia coli)) ECOLI\_419 ECOLI\_419 Escherichia  
coli 562 10004630

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836058	9051	31207	522	174

Description

6500729911 data:pfv:b0632 d-alanine carboxypeptidase:penicillin-binding protein 5 precursor:d-alanyl-d-alanine carboxypeptidase fraction a:dd-peptidase:dd-carboxypeptidase:pbp-5 (gtcfc:11.4) (ec:3.4.16.4) (keggfc:14.1) (rileyfc:3.3.4) (db:gtc-escherichia coli) b0632 b0632 Escherichia coli 562 -11533769 7500879965 data:pfv (ec:3.4.16.4) (de:(dd-carboxypeptidase) (pbp-5)) (db:swissprot) DACA\_ECOLI P04287 ESCHERICHIA COLI 562 -11533769 130782 data:pfv serine-type d-ala-d-ala carboxypeptidase:daca precursor:dd-carboxypeptidase:penicillin-binding protein 5 (cl:penicillin-binding protein 5) (ec:3.4.16.4) (db:pir1.dat) (mp:15 min) ZPECP5 A28536 Escherichia coli 562 -11533769 223119 data penicillin-binding protein 5 precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #168) (db:genpept-bct1) (de:escherichia coli genomic dna. (13.9 - 14.3 min).) (le:13815) (re:15026) (di:complement) D90703 D90703 g1651259 Escherichia coli 562 -11533769 5000690988 (db:genpept-bct1) (de:e. coli daca gene for penicillin-binding protein 5.) (nt:precursor) (le:243) (re:1454) (di:direct) ECDACAG X06479 g41212 Escherichia coli 562 -11533769 232631 data d-alanyl-d-alanine carboxypeptidase:fraction a (fn:enzyme; murein sacculus, peptidoglycan) (db:genpept-bct2) (ec:3.4.16.4) (de:escherichia coli k-12 mg1655 section 58 of 400 of the completegenome.) (nt:f403; 100 pct identical to daca\_ecoli sw: p04287) (le:487) (re:1698) (di:complement) AE000168 AE000168 g1786851 Escherichia coli 562 -11533769 7502851962 data penicillin-binding protein 5 precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #168) (db:genpept) (de:escherichia coli genomic dna. (14.0 - 14.4 min).) (nt:orf\_id:ol68#17; similar to swissprot accession) (le:13815) (re:15026) (di:complement) D90703 D90703 g1651259 Escherichia coli 562 -11533769 67826 data:pfv (ec:3.4.16.4) (de:(dd-carboxypeptidase) (pbp-5)) (db:swissprot) DACA\_ECOLI P04287 ESCHERICHIA COLI 562 -11533769

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501836064	9052	31208	855	284

Description

6500729912 mrdb:roda:b0634 rod shape-determining protein roda (gtcfc:11.4) (keggfc:14.2) (rileyfc:3.3.4) (db:gtc-escherichia coli) b0634 b0634 Escherichia coli 562 -11533770 95887 mrdb:roda (de:rod shape-determining protein roda) (db:swissprot) RODA\_ECOLI P15035 ESCHERICHIA COLI 562 -11533770 131642 mrdb:roda rod shape-determining protein mrdb (cl:rod shape-determining protein) (db:pir1.dat) (mp:15 min) BVECRD JT0500 Escherichia coli 562 -11533770 223121 mrdb rod shape-determining protein mrdb (sr:escherichia coli(strain:k12) dna, clone:kohara clone #168) (db:genpept-bct1) (de:escherichia coli genomic dna. (13.9 - 14.3 min).) (le:16264) (re:17376) (di:complement) D90703 D90703 g1651261 Escherichia coli 562 -11533770 240147 roda (sr:e.coli (k12) dna) (db:genpept-bct1) (de:e.coli rod-shape-determining protein (roda) gene, complete cds, 36kd lipoprotein 5' end, and penicillin-binding protein 2, 3' end.) (nt:rod-shape-determining protein) (le:91) (re:1203) (di:direct) ECORODA M22857 g147695 Escherichia coli 562 -11533770 7500890489 roda rod-shape-determining protein (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (le:105831) (re:106943) (di:complement) ECU82598 U82598 g1778551 Escherichia coli 562 -11533770 235864 mrdb rod shape-determining membrane protein (fn:phenotype; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 58 of 400 of the completegenome.) (nt:f370; 100 pct identical to roda\_ecoli sw: p15035;) (le:2936) (re:4048) (di:complement) AE000168 AE000168 g1786853 Escherichia coli 562 -11533770 5000690989 mrdb rod shape-determining protein mrdb. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #168) (db:genpept) (de:escherichia coli genomic dna. (14.0 - 14.4 min).) (nt:orf\_id:o169#2; similar to pir accession number) (le:16264) (re:17376) (di:complement) D90703 D90703 g1651261 Escherichia coli 562 -11533770 7502851963 mrdb rod shape-determining protein mrdb. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #169) (db:genpept) (de:escherichia coli genomic dna. (14.3 - 14.7 min).) (nt:orf\_id:o169#2; similar to pir accession number) (le:1449) (re:2561) (di:complement) D90704 D90704 g4062253 Escherichia coli 562 -11533770

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501836073	9053	31209	270	89

Description

GTC ORF with score 167 to: (de:(yel051w) (pn:vacuolar atp synthase subunit d:v-atpase d subunit:h) (gn:sygp-orf11:vma8) (gtcfc:2.1) (ec:3.6.1.34) (vatd\_yeast) (keggfc:2.1) (sgdfc:1.8.2:7.2.2:7.8.0:8.5.0:9.10.0) (db:gtc-saccharomyces cerevisiae))

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836077	9054	31210	477	158

Description

6500729913 mrda:pbpa:b0635 mrda:penicillin-binding protein 2:pbp-2  
(gtcf:11.4) (keggfc:14.2) (rileyfc:3.3.4) (db:gtc-escherichia coli) b0635  
b0635 Escherichia coli 562 -11533771 240148 mrda:pbpa  
(de:penicillin-binding protein 2 (pbp-2)) (db:swissprot) PBP2\_ECOLI P08150  
ESCHERICHIA COLI 562 -11533771 130781 mrda:pbpa penicillin-binding protein  
2 (cl:penicillin-binding protein 3) (db:pir1.dat) (mp:15 min) ZPECP2 C24995  
Escherichia coli 562 -11533771 223125 mrda penicillin-binding protein 2  
pbp-2 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #169)  
(db:genpept-bct1) (de:escherichia coli genomic dna. (14.3 - 14.7 min).)  
(le:2564) (re:4465) (di:complement) D90704 D90704 g1651266 Escherichia coli  
562 -11533771 5000690990 pbpa penicillin-binding protein 2 pbp2  
(db:genpept-bct1) (de:e. coli pbpa gene for penicillin-binding protein  
(pbp)2.) (le:1035) (re:2936) (di:direct) ECPBPA X04516 g42316 Escherichia  
coli 562 -11533771 7500887693 pbp2 penicillin-binding protein 2  
(db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.)  
(le:106946) (re:108847) (di:complement) ECU82598 U82598 g1778552 Escherichia  
coli 562 -11533771 237726 mrda cell elongation:e phase:peptidoglycan  
(fn:enzyme; cell division) (db:genpept-bct2) (de:escherichia coli k-12  
mg1655 section 58 of 400 of the completegenome.) (nt:f633; 99 pct identical  
to pbp2\_ecoli sw: p08150;) (le:4051) (re:5952) (di:complement) AE000168  
AE000168 g1786854 Escherichia coli 562 -11533771 7502851964 mrda  
penicillin-binding protein 2 pbp-2 . (sr:escherichia coli(strain:k12) dna,  
clone:kohara clone #169) (db:genpept) (de:escherichia coli genomic dna.  
(14.3 - 14.7 min).) (nt:orf\_id:o169#3; similar to swissprot accession)  
(le:2564) (re:4465) (di:complement) D90704 D90704 g1651266 Escherichia coli  
562 -11533771 88723 mrda:pbpa (de:penicillin-binding protein 2 (pbp-2))  
(db:swissprot) PBP2\_ECOLI P08150 ESCHERICHIA COLI 562 -11533771

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836078	9055	31211	414	137

Description

6500729914 pal:excc:b0741 21 aa signal peptide:peptidoglycan-associated lipoprotein precursor (gtcfc:11.4) (keggfc:14.2) (rileyfc:3.3.4) (db:gtc-escherichia coli) b0741 b0741 Escherichia coli 562 -11533772 7500887634 pal:excc (de:peptidoglycan-associated lipoprotein precursor) (db:swissprot) PAL\_ECOLI P07176 ESCHERICHIA COLI 562 -11533772 130867 pal:excc peptidoglycan-associated lipoprotein precursor (cl:outer membrane protein a) (db:pir1.dat) (mp:17 min) LPECPG A27534 Escherichia coli 562 -11533772 223184 pal peptidoglycan-associated lipoprotein precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #178) (db:genpept-bct1) (de:escherichia coli genomic dna.(16.5 - 16.8 min).) (le:12257) (re:12778) (di:direct) D90713 D90713 g1651333 Escherichia coli 562 -11533772 237686 excc peptidoglycan-associated lipoprotein (db:genpept-bct1) (de:e. coli excc gene for peptidoglycan-associated lipoprotein.) (le:74) (re:595) (di:direct) ECEXCCG X65796 g41360 Escherichia coli 562 -11533772 5000690991 (db:genpept-bct1) (de:e. coli pal gene for peptidoglycan-associated lipoprotein.) (nt:precursor polypeptide (aa-21 to -1)) (le:136) (re:657) (di:direct) ECPAL X05123 g42257 Escherichia coli 562 -11533772 232782 pal peptidoglycan-associated lipoprotein (fn:membrane; macromolecule synthesis,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 67 of 400 of the completegenome.) (nt:ol73; 100 pct identical to pal\_ecoli sw: p07176;) (le:4852) (re:5373) (di:direct) AE000177 AE000177 g1786962 Escherichia coli 562 -11533772 7502851965 excc peptidoglycan-associated lipoprotein precursor. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #178) (db:genpept) (de:escherichia coli genomic dna. (16.5 - 16.9 min).) (nt:orf\_id:ol78#10; similar to swissprot accession) (le:12257) (re:12778) (di:direct) D90713 D90713 g1651333 Escherichia coli 562 -11533772 88558 pal:excc (de:peptidoglycan-associated lipoprotein precursor) (db:swissprot) PAL\_ECOLI P07176 ESCHERICHIA COLI 562 -11533772

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836079	9056	31212	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836083	9057	31213	507	168

Description

6500729915 dacc:b0839 penicillin-binding protein 6  
precursor:d-alanyl-d-alanine carboxypeptidase fraction  
c:dd-peptidase:dd-carboxypeptidase:pbp-6 (gtcfc:11.4) (ec:3.4.16.4)  
(keggfc:14.1) (rileyfc:3.3.4) (db:gtc-escherichia coli) b0839 b0839  
Escherichia coli 562 -11533773 67829 dacc (ec:3.4.16.4)  
(de:(dd-carboxypeptidase) (pbp-6)) (db:swissprot) DACC\_ECOLI P08506  
ESCHERICHIA COLI 562 -11533773 7000684976 dacc serine-type d-ala-d-ala  
carboxypeptidase:dacc precursor:penicillin-binding protein 6  
(cl:penicillin-binding protein 5) (ec:3.4.16.4) (db:pir2.dat) G64821 G64821  
Escherichia coli 562 -11533773 223223 dacc penicillin-binding protein 6  
precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #209)  
(db:genpept-bct1) (de:escherichia coli genomic dna.(18.7 - 19.1 min).)  
(le:9827) (re:11029) (di:direct) D90722 D90722 g1651381 Escherichia coli 562  
-11533773 7500879968 dacc d-alanyl-d-alanine carboxypeptidase (fn:enzyme;  
murein sacculus, peptidoglycan) (db:genpept-bct2) (de:escherichia coli k-12  
mg1655 section 76 of 400 of the completegenome.) (nt:o400; 99 pct identical  
to dacc\_ecoli sw: p08506) (le:2616) (re:3818) (di:direct) AE000186 AE000186  
g1787062 Escherichia coli 562 -11533773 5000690992 dacc penicillin-binding  
protein 6 precursor. (sr:escherichia coli(strain:k12) dna, clone:kohara  
clone #209) (db:genpept) (de:escherichia coli genomic dna. (18.8 - 19.2  
min).) (nt:orf\_id:o209#9; similar to pir accession number) (le:9827)  
(re:11029) (di:direct) D90722 D90722 g1651381 Escherichia coli 562 -11533773

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836084	9058	31214	1722	574

Description

6500729916 hipa:b1507 hipa protein (gtcfc:11.4) (keggfc:14.2)  
(rileyfc:3.3.4) (db:gtc-escherichia coli) b1507 b1507 Escherichia coli 562  
-11533774 7000690904 hipa hipa protein (db:pir2.dat) F64904 F64904  
Escherichia coli 562 -11533774 7500959761 hipa persistence to inhibition of  
murein or dna (fn:regulator; murein sacculus, peptidoglycan)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 138 of 400 of the  
completegenome.) (nt:f440; 99 pct identical to hipa\_ecoli sw: p23874; cg)  
(le:787) (re:2109) (di:complement) AE000248 AE000248 g1787785 Escherichia  
coli 562 -11533774 5000690993 (de:(ecoli\_1467) (pn:frequency of persistence  
to inhibition of murein or dna biosynthesis, dna-binding regulator)  
(gn:hipa) (gtcfc:11.4) (ec:) (hipa\_ecoli) (keggfc:11.2) (rileyfc:3.3.4)  
(db:gtc-escherichia coli)) ECOLI\_1467 ECOLI\_1467 Escherichia coli 562  
10123359

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836096	9059	31215	234	77

Description

Hypothetical protein

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836098	9060	31216	213	70

Description

6500729917 hipb:b1508 hipb protein (gtcfc:11.4) (keggfc:14.2)  
(rileyfc:3.3.4) (db:gtc-escherichia coli) b1508 b1508 Escherichia coli 562  
-11533775 76981 hipb (de:hipb protein) (db:swissprot) HIPB\_ECOLI P23873  
ESCHERICHIA COLI 562 -11533775 163193 hipb hipb protein (db:pir2.dat)  
A38112 A38112 Escherichia coli 562 -11533775 223856 hipb hipb protein  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #301(34.0-34.3  
min.)) (nt:orf\_id:o301#11; similar to (pir accession number) (le:13869)  
(re:14135) (di:complement) D90792 D90792 g1742468 Escherichia coli 562  
-11533775 300601 hipb hipb protein (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #302(34.1-34.5 min.)) (nt:orf\_id:o301#11; similar to (pir  
accession number) (le:7913) (re:8179) (di:complement) D90793 D90793 g1742477  
Escherichia coli 562 -11533775 300608 hipb hipb protein (sr:escherichia  
coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #303(34.3-34.6 min.))  
(nt:orf\_id:o301#11; similar to (pir accession number) (le:586) (re:852)  
(di:complement) D90794 D90794 g1742485 Escherichia coli 562 -11533775  
300593 hipb (db:genpept-bct1) (de:escherichia coli hipa gene, complete cds,  
and hipb gene, completecds.) (le:337) (re:603) (di:direct) ECOHIPO M61242  
g146353 Escherichia coli 562 -11533775 234654 hipb persistence to  
inhibition of murein or dna (fn:regulator; murein sacculus, peptidoglycan)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 138 of 400 of the  
completegenome.) (nt:f88; 100 pct identical to hipb\_ecoli sw: p23873; cg)  
(le:2109) (re:2375) (di:complement) AE000248 AE000248 g1787786 Escherichia  
coli 562 -11533775 223864 hipb hipb protein (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #302(34.1-34.5 min.))  
(nt:orf\_id:o301#11; similar to (pir accession number) (le:7913) (re:8179)  
(di:complement) D90793 D90793 g1742477 Escherichia coli 562 -11533775  
223871 hipb hipb protein (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #303(34.3-34.6 min.)) (nt:orf\_id:o301#11; similar to (pir  
accession number) (le:586) (re:852) (di:complement) D90794 D90794 g1742485  
Escherichia coli 562 -11533775 5000690994 (de:(ecoli\_1468) (pn:frequency of  
persistence to inhibition of murein or dna biosynthesis; regulatory protein  
interacts with hipa) (gn:hipb) (gtcfc:11.4) (ec:) (hipb\_ecoli) (keggfc:11.2)  
(rileyfc:3.3.4) (db:gtc-escherichia coli)) ECOLI\_1468 ECOLI\_1468 Escherichia  
coli 562 10019343

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836113	9061	31217	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836123	9062	31218	210	69

Description

6500729918 lpp:mlpa:b1677 major outer membrane lipoprotein  
precursor:murein-lipoprotein (gtcfc:11.4) (keggfc:14.2) (rileyfc:3.3.4)  
(db:gtc-escherichia coli) b1677 b1677 Escherichia coli 562 -11533776 235013  
lpp:mlpa (de:major outer membrane lipoprotein precursor  
(murein-lipoprotein)) (db:swissprot) MULI\_ECOLI P02937 ESCHERICHIA COLI 562  
-11533776 130869 lpp major outer membrane lipoprotein precursor  
(cl:murein-lipoprotein) (db:pir1.dat) (mp:36 min) LPECW A90783 Escherichia  
coli 562 -11533776 224731 lpp major outer membrane lipoprotein precursor  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #319-320gap(37.9-38.0  
min.)) (nt:orf\_id:o319gap#2; similar to (swissprot accession) (le:933)  
(re:1169) (di:direct) D90853 D90853 g1805531 Escherichia coli 562 -11533776  
233323 lipoprotein (db:genpept-bct1) (de:e.coli gene for lipoprotein.)  
(le:55) (re:291) (di:direct) ECLIPXA X68953 g417620 Escherichia coli 562  
-11533776 301371 lpp outer membrane lipoprotein (db:genpept-bct1) (de:e.  
coli lpp gene (codes for an outer membrane protein).) (le:404) (re:640)  
(di:direct) ECLPPX V00302 g41930 Escherichia coli 562 -11533776 5000690995  
lpp lipoprotein (sr:escherichia coli k-12: mrna (1),(3); and strain  
je5519/f'506 dna) (db:genpept-bct1) (de:e.coli lpp structural gene coding  
for outer membrane lipoprotein.) (le:404) (re:640) (di:direct) ECOLPP J01645  
g146659 Escherichia coli 562 -11533776 233320 lpp murein lipoprotein  
(fn:membrane; murein sacculus, peptidoglycan) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 153 of 400 of the completegenome.)  
(nt:o78; 100 pct identical to muli\_ecoli sw: p02937; cg) (le:293) (re:529)  
(di:direct) AE000263 AE000263 g1787967 Escherichia coli 562 -11533776 84676  
lpp:mlpa (de:major outer membrane lipoprotein precursor  
(murein-lipoprotein)) (db:swissprot) MULI\_ECOLI P02937 ESCHERICHIA COLI 562  
-11533776

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836124	9063	31219	651	216
<u>Description</u>				
6500729919 mepa:b2328 penicillin-insensitive murein endopeptidase precursor:d-alanyl-d-alanine-endopeptidase:dd-endopeptidase (gtcfc:11.4) (ec:3.4.99.-) (keggfc:14.1) (rileyfc:3.3.4) (db:gtc-escherichia coli) b2328 b2328 Escherichia coli 562 -11533777 7500885500 mepa (ec:3.4.99.-) (de:(d-alanyl-d-alanine-endopeptidase) (dd-endopeptidase)) (db:swissprot) MEPA_ECOLI P14007 ESCHERICHIA COLI 562 -11533777 164112 mepa penicillin-insensitive murein endopeptidase precursor:a (ec:3.4.99.-) (db:pir2.dat) (mp:50.4 min) S08345 S08345 Escherichia coli 562 -11533777 224871 mepa penicillin-insensitive murein endopeptidase (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #407(52.4-52.8 min.)) (nt:similar to (swissprot accession number p14007)) (le:16202) (re:17026) (di:complement) D90863 D90863 g1799720 Escherichia coli 562 -11533777 5000690996 endopeptidase precursor aa -19 to 255 (db:genpept-bct1) (de:e. coli mepa gene for penicillin-insensitive murein endopeptidase.) (le:117) (re:941) (di:direct) ECMEPAMR X16909 g41993 Escherichia coli 562 -11533777 233370 mepa murein dd-endopeptidase:penicillin-insensitive (fn:enzyme; murein sacculus, peptidoglycan) (db:genpept-bct2) (ec:3.4.99.-) (de:escherichia coli k-12 mg1655 section 211 of 400 of the completegenome.) (nt:f274; 100 pct identical to mepa_ecoli sw: p14007) (le:8908) (re:9732) (di:complement) AE000321 AE000321 g1788668 Escherichia coli 562 -11533777 83459 mepa (ec:3.4.99.-) (de:(d-alanyl-d-alanine-endopeptidase) (dd-endopeptidase)) (db:swissprot) MEPA_ECOLI P14007 ESCHERICHIA COLI 562 -11533777				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836128	9064	31220	279	92

Description

6500729920 dacb:b3182 d-alanyl-d-alanine carboxypeptidase:fraction  
b:penicillin-binding protein 4 precursor:pbp-4:d-alanyl-d-alanine  
carboxypeptidase:dd-peptidase:dd-carboxypeptidase /  
d-alanyl-d-alanine-endopeptidase:dd-endopeptidase (gtcfc:11.4) (keggfc:14.1)  
(rileyfc:3.3.4) (db:gtc-escherichia coli) b3182 b3182 Escherichia coli 562  
-11533778 236419 dacb (ec:3.4.16.4:3.4.99.-)  
(de:d-alanyl-d-alanine-endopeptidase, (dd-endopeptidase)) (db:swissprot)  
PBP4\_ECOLI P24228 ESCHERICHIA COLI 562 -11533778 164605 dacb serine-type  
d-ala-d-ala carboxypeptidase:precursor:penicillin-binding protein 4  
precursor (ec:3.4.16.4) (db:pir2.dat) A54535 A54535 Escherichia coli 562  
-11533778 232654 dacb penicillin-binding protein 4 pbp4 (db:genpept-bct1)  
(de:e.coli dacb gene for penicillin-binding protein 4 (pbp4).) (nt:this  
enzyme is involved as a) (le:140) (re:1573) (di:direct) ECDACB X59460 g41216  
Escherichia coli 562 -11533778 267282 dacb d-alanyl-d-alanine  
carboxypeptidase (db:genpept-bct1) (ec:3.4.16.4) (de:e.coli dacb gene for  
dd-carboxypeptidase.) (le:140) (re:1573) (di:direct) ECDDCP X60038 g41246  
Escherichia coli 562 -11533778 5000690997 dacb d-alanyl-d-alanine  
carboxypeptidase:fraction b (db:genpept-bct1) (ec:3.4.16.4) (de:escherichia  
coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no.  
885; penicillin-binding protein 4) (le:109715) (re:111148) (di:direct)  
ECOUW67 U18997 g606120 Escherichia coli 562 -11533778 7500887696 dacb  
ampicillin-binding protein (db:genpept-bct1) (de:escherichia coli k12  
ampicillin-binding protein (dacb),transcription elongation factor (grea),  
regulatory protein (mrsf),atp-binding protein (mrsc), dihydropteroate  
synthase, regulatoryprotein (mrsc), and membrane protein genes, c... U01376  
U01376 g746398 Escherichia coli 562 -11533778 232632 dacb  
d-alanyl-d-alanine carboxypeptidase:fraction b (fn:enzyme; murein sacculus,  
peptidoglycan) (db:genpept-bct2) (ec:3.4.16.4) (de:escherichia coli k-12  
mg1655 section 289 of 400 of the completegenome.) (nt:o477; cg site no. 885;  
penicillin-binding protein) (le:236) (re:1669) (di:direct) AE000399 AE000399  
g1789573 Escherichia coli 562 -11533778 88734 dacb (ec:3.4.16.4:3.4.99.-)  
(de:d-alanyl-d-alanine-endopeptidase, (dd-endopeptidase)) (db:swissprot)  
PBP4\_ECOLI P24228 ESCHERICHIA COLI 562 -11533778

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836138	9065	31221	636	211

Description

6500729921 mred:b3249 rod shape-determining protein mred (gtcfc:11.4) (keggfc:14.2) (rileyfc:3.3.4) (db:gtc-escherichia coli) b3249 b3249 Escherichia coli 562 -11533779 84211 mred (de:rod shape-determining protein mred) (db:swissprot) MRED\_ECOLI P16927 ESCHERICHIA COLI 562 -11533779 164102 mred rod shape-determining protein mred (db:pir2.dat) (mp:71 min) JV0060 JV0060 Escherichia coli 562 -11533779 236488 (sr:e.coli dna) (db:genpept-bct1) (de:e.coli mreb protein gene, 3' end, mrec protein gene, complete cds,and mred protein gene, complete cds.) (nt:mred protein (gtg start codon)) (le:1204) (re:1692) (di:direct) ECOMERBCD M31792 g146819 Escherichia coli 562 -11533779 7500885867 mred (fn:responsible for formation of shape of) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (le:179132) (re:179620) (di:complement) ECOUW67 U18997 g606189 Escherichia coli 562 -11533779 235114 mred rod shape-determining protein (fn:structural component; murein sacculus,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 294 of 400 of the completegenome.) (nt:f162; 100 pct identical amino acid sequence and) (le:2125) (re:2613) (di:complement) AE000404 AE000404 g1789647 Escherichia coli 562 -11533779 5000690998 (de:(ecoli\_3173) (pn:rod shape-determining protein) (gn:mred) (gtcfc:11.4) (ec:) (mred\_ecoli) (keggfc:11.2) (rileyfc:3.3.4) (db:gtc-escherichia coli)) ECOLI\_3173 ECOLI\_3173 Escherichia coli 562 10026412

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836139	9066	31222	432	144

Description

6500729922 mrec:b3250 rod shape-determining protein mrec (gtcfc:11.4) (keggfc:14.2) (rileyfc:3.3.4) (db:gtc-escherichia coli) b3250 b3250 Escherichia coli 562 -11533780 84208 mrec (de:rod shape-determining protein mrec) (db:swissprot) MREC\_ECOLI P16926 ESCHERICHIA COLI 562 -11533780 131646 mrec rod shape-determining protein mrec (cl:rod shape-determining protein mrec) (db:pir1.dat) (mp:71 min) JV0059 JV0059 Escherichia coli 562 -11533780 236489 (sr:e.coli dna) (db:genpept-bct1) (de:e.coli mrec protein gene, 3' end, mrec protein gene, complete cds, and mred protein gene, complete cds.) (nt:mrec protein) (le:101) (re:1204) (di:direct) ECOMERBCD M31792 g146818 Escherichia coli 562 -11533780 7500885864 mrec (fn:responsible for formation of shape of) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:called mrec in ecomrec; genepplot suggests) (le:179620) (re:180723) (di:complement) ECOUW67 U18997 g606190 Escherichia coli 562 -11533780 235113 mrec rod shape-determining protein (fn:structural component; murein sacculus,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 294 of 400 of the complete genome.) (nt:f367; called mrec in ecomrec; genemark) (le:2613) (re:3716) (di:complement) AE000404 AE000404 g1789648 Escherichia coli 562 -11533780 5000690999 (de:(ecoli\_3174) (pn:rod shape-determining protein) (gn:mrec) (gtcfc:11.4) (ec:) (mrec\_ecoli) (keggfc:11.2) (rileyfc:3.3.4) (db:gtc-escherichia coli)) ECOLI\_3174 ECOLI\_3174 Escherichia coli 562 10026409

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836166	9067	31223	309	102

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836207	9068	31224	1299	432

Description

6500729923 mreB:b3251 rod shape-determining protein mreB (gtcfc:11.4) (keggfc:14.2) (rileyfc:3.3.4) (db:gtc-escherichia coli) b3251 b3251 Escherichia coli 562 -11533781 7000688989 mreB:envB rod shape-determining protein envB (cl:rod shape-determining protein envB) (db:pir1.dat) (mp:71 min) BVECEB E65117 Escherichia coli 562 -11533781 7500953670 mreB (fn:responsible for formation of shape of) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:frameshifts changes start relative to ecomreB) (le:180789) (re:181892) (di:complement) ECOUW67 U18997 g606191 Escherichia coli 562 -11533781 236490 mreB regulator of ftsI:penicillin binding protein 3 (fn:phenotype; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 294 of 400 of the completegenome.) (nt:f367; frameshifts changes start relative to) (le:3782) (re:4885) (di:complement) AE000404 AE000404 g1789649 Escherichia coli 562 -11533781 5000691000 (de:(ecoli\_3175) (pn:rod shape-determining protein) (gn:mreB) (gtcfc:11.4) (ec:) (mreB\_ecoli) (keggfc:11.2) (rileyfc:3.3.4) (db:gtc-escherichia coli)) ECOLI\_3175 ECOLI\_3175 Escherichia coli 562 10123999

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836211	9069	31225	405	135

Description

5000691001 mrca (gtcfc:11.4) (keggfc:14.2) (rileyfc:3.3.4) (db:gtc-escherichia coli) b3396 b3396 Escherichia coli 562 -11533782 7000688969 mrca:pona penicillin-binding protein 1a (cl:penicillin-binding protein) (db:pir1.dat) ZPECPA G65134 Escherichia coli 562 -11533782 7500953610 mrca (fn:peptidoglycan synthetase; cell wall synthesis;) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no.484; alternate name pona) (le:303595) (re:306171) (di:direct) ECOUW67 U18997 g606330 Escherichia coli 562 -11533782 236629 mrca peptidoglycan synthetase:penicillin-binding (fn:enzyme; murein sacculus, peptidoglycan) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 305 of 400 of the completegenome.) (nt:o858; cg site no.484; alternate name pona; 99 pct) (le:65) (re:2641) (di:direct) AE000415 AE000415 g1789799 Escherichia coli 562 -11533782 6500729924 mrca (gtcfc:11.4) (keggfc:14.2) (rileyfc:3.3.4) (db:gtc-escherichia coli) b3396 b3396 Escherichia coli 562 -11533782

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836212	9070	31226	2124	707

Description

6500729925 seca:prld:azi:pea:b0098 preprotein translocase seca subunit (gtcfc:12.10) (keggfc:14.2) (rileyfc:4.5.0) (db:gtc-escherichia coli) b0098 b0098 Escherichia coli 562 -11533783 98292 seca:prld:azi:pea (de:preprotein translocase seca subunit) (db:swissprot) SECA\_ECOLI P10408 ESCHERICHIA COLI 562 -11533783 7000686583 seca preprotein translocase seca (cl:preprotein translocase seca:dead/h box helicase homology) (db:pir1.dat) (mp:2 min) BVECCA B64732 Escherichia coli 562 -11533783 7500891449 seca preprotein translocase:secretion protein (fn:transport; protein, peptide secretion) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 9 of 400 of the completegenome.) (nt:o901; 99 pct identical to seca\_ecoli sw: p10408) (le:3035) (re:5740) (di:direct) AE000119 AE000119 g1786287 Escherichia coli 562 -11533783 5000691005 (de:(ecoli\_98) (pn:protein secretion, atp hydrolysis) (gn:seca) (gtcfc:12.10) (ec:) (seca\_ecoli) (keggfc:11.2) (rileyfc:4.5.0) (db:gtc-escherichia coli)) ECOLI\_98 ECOLI\_98 Escherichia coli 562 10122654

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836235	9071	31227	402	133

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836246	9072	31228	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836253	9073	31229	1659	552

Description

6500729926 secdb0408 protein-export membrane protein secdb (gtcfc:12.10) (keggfc:14.2) (rileyfc:4.5.0) (db:gtc-escherichia coli) b0408 b0408 Escherichia coli 562 -11533784 98305 secdb (de:protein-export membrane protein secdb) (db:swissprot) SECD\_ECOLI P19673 ESCHERICHIA COLI 562 -11533784 7000686584 secdb preprotein translocase chain secdb:protein-export membrane protein secdb:secretion protein secdb (db:pir2.dat) H64769 H64769 Escherichia coli 562 -11533784 7500891471 secdb protein-export membrane protein secdb (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:7097) (re:8944) (di:direct) ECU82664 U82664 g1773092 Escherichia coli 562 -11533784 240185 secdb protein secretion:membrane protein:part of the (fn:transport; protein, peptide secretion) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 37 of 400 of the completegenome.) (nt:o615; 99 pct identical to secdb\_ecoli sw: p19673) (le:5240) (re:7087) (di:direct) AE000147 AE000147 g1786609 Escherichia coli 562 -11533784 5000691006 (de:(ecoli\_392) (pn:protein secretion; inner membrane protein, part of the channel) (gn:secdb) (gtcfc:12.10) (ec:) (secdb\_ecoli) (keggfc:11.2) (rileyfc:4.5.0) (db:gtc-escherichia coli)) ECOLI\_392 ECOLI\_392 Escherichia coli 562 10122819

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836272	9074	31230	414	138

Description

GTC ORF with score 104 to: (db:genpept-inv) (de:litomosoides sigmodontis microfilarial sheath proteins shp3a(shp3a) and shp3 (shp3) genes, complete cds.) (nt:structural protein; similar to shp3 genes from) (le:7991:8260) (re:8047:9219) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836277	9075	31231	933	310

Description

6500729927 secf:b0409 protein-export membrane protein secf (gtcfc:12.10) (keggfc:14.2) (rileyfc:4.5.0) (db:gtc-escherichia coli) b0409 b0409 Escherichia coli 562 -11533785 7500891482 secf (de:protein-export membrane protein secf) (db:swissprot) SECF\_ECOLI P19674 ESCHERICHIA COLI 562 -11533785 164594 secf preprotein translocase chain secf:protein-export membrane protein secf:secretion protein secf (cl:escherichia coli preprotein translocase chain secf) (db:pir2.dat) JQ0697 JQ0697 Escherichia coli 562 -11533785 5000691007 (db:genpept-bct1) (de:escherichia coli secd and secf genes for membrane proteins involved in protein export.) (nt:secf protein) (le:2948) (re:3919) (di:direct) ECSECF X56175 g581231 Escherichia coli 562 -11533785 238228 secf protein secretion:membrane protein (fn:transport; protein, peptide secretion) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 37 of 400 of the complete genome.) (nt:o323; 100 pct identical to secf\_ecoli sw: p19674) (le:7098) (re:8069) (di:direct) AE000147 AE000147 g1786610 Escherichia coli 562 -11533785 98321 secf (de:protein-export membrane protein secf) (db:swissprot) SECF\_ECOLI P19674 ESCHERICHIA COLI 562 -11533785

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836279	9076	31232	261	86

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836281	9077	31233	426	141

Description

6500729928 msyb:b1051 acidic protein msyb:multicopy suppressor of secy:acidic protein msyb (gtcfc:12.10) (keggfc:14.2) (rileyfc:4.5.0) (db:gtc-escherichia coli) b1051 b1051 Escherichia coli 562 -11533786 7000690846 msyb acidic protein msyb:multicopy suppressor of secy (db:pir2.dat) H64847 H64847 Escherichia coli 562 -11533786 7500959670 msyb acidic protein suppresses mutants lacking (fn:phenotype; protein, peptide secretion) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 96 of 400 of the complete genome.) (nt:f125; 100 pct identical to msyb\_ecoli sw: p25738) (le:8065) (re:8442) (di:complement) AE000206 AE000206 g1787289 Escherichia coli 562 -11533786 5000691008 (de:(ecoli\_1013) (pn:acidic protein suppresses mutants lacking function of protein export) (gn:msyb) (gtcfc:12.10) (ec:) (msyb\_ecoli) (keggfc:11.2) (rileyfc:4.5.0) (db:gtc-escherichia coli)) ECOLI\_1013 ECOLI\_1013 Escherichia coli 562 10123146

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836284	9078	31234	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836286	9079	31235	447	148

Description

6500729929 oppa:b1243 periplasmic oligopeptide-binding protein precursor (gtcfc:12.10:12.6) (keggfc:11.1) (rileyfc:4.5.0) (db:gtc-escherichia coli) b1243 b1243 Escherichia coli 562 -11533787 87743 oppa (de:periplasmic oligopeptide-binding protein precursor) (db:swissprot) OPPA\_ECOLI P23843 ESCHERICHIA COLI 562 -11533787 7000686042 oppa oligopeptide-binding protein precursor (cl:dipeptide transport protein) (db:pir2.dat) F64871 F64871 Escherichia coli 562 -11533787 224725 oppa periplasmic oligopeptide-binding protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #251(27.7-28.2 min.)) (nt:orf\_id:o251#4; similar to (swissprot accession) (le:18315) (re:19946) (di:direct) D90852 D90852 g1805524 Escherichia coli 562 -11533787 301365 oppa periplasmic oligopeptide binding protein (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli periplasmic oligopeptide binding protein (oppa)gene, complete cds.) (nt:putative) (le:1095) (re:2726) (di:direct) ECOOPPAA M60918 g304925 Escherichia coli 562 -11533787 235281 oppa oligopeptide transport:periplasmic binding (fn:transport; protein, peptide secretion) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 112 of 400 of the completegenome.) (nt:o543; 100 pct identical to oppa\_ecoli sw: p23843) (le:9817) (re:11448) (di:direct) AE000222 AE000222 g1787495 Escherichia coli 562 -11533787 5000691009 (de:(ecoli\_1203) (pn:oligopeptide transport; periplasmic binding protein) (gn:oppa) (gtcfc:12.10) (ec:) (oppa\_ecoli) (keggfc:11.2) (rileyfc:4.5.0) (db:gtc-escherichia coli)) ECOLI\_1203 ECOLI\_1203 Escherichia coli 562 10029884

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836289	9080	31236	186	61

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836290	9081	31237	288	95

Description

6500729930 oppb:b1244 oligopeptide transport system permease protein oppb (gtcfc:12.1) (keggfc:11.1) (rileyfc:4.5.0) (db:gtc-escherichia coli) b1244 b1244 Escherichia coli 562 -11533788 87748 oppb (de:oligopeptide transport system permease protein oppb) (db:swissprot) OPPB\_ECOLI P31132 ESCHERICHIA COLI 562 -11533788 7000686043 oppb oligopeptide transport system permease protein oppb (cl:oligopeptide permease protein oppb) (db:pir2.dat) B36263 G64871 Escherichia coli 562 -11533788 7500887192 oppb oligopeptide transport permease protein (fn:transport; protein, peptide secretion) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 113 of 400 of the completegenome.) (nt:o306; 96 pct identical to oppb\_salty sw:) (le:73) (re:993) (di:direct) AE000223 AE000223 g1787497 Escherichia coli 562 -11533788 5000691010 (de:(ecoli\_1204) (pn:oligopeptide transport) (gn:oppb) (gtcfc:12.10) (ec:) (oppb\_ecoli) (keggfc:11.2) (rileyfc:4.5.0) (db:gtc-escherichia coli)) ECOLI\_1204 ECOLI\_1204 Escherichia coli 562 10123242

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836306	9082	31238	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836317	9083	31239	1245	414

Description

6500729931 oppc:b1245 oligopeptide transport system permease  
protein:oligopeptide transport system permease protein oppc (gtcfc:12.1)  
(keggfc:11.1) (rileyfc:4.5.0) (db:gtc-escherichia coli) b1245 b1245  
Escherichia coli 562 -11533789 121662 oppc (de:oligopeptide transport  
system permease protein oppc) (db:swissprot) OPPC\_ECOLI P77664 ESCHERICHIA  
COLI 562 -11533789 7000686045 oppc oligopeptide transport system permease  
protein oppc (cl:oligopeptide permease protein oppb) (db:pir2.dat) H64871  
H64871 Escherichia coli 562 -11533789 223451 oligopeptide transport system  
permease protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara  
lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#252(28.1-28.4 min.)) (nt:orf\_id:o252#2; similar to (swissprot accession)  
(le:2155) (re:3063) (di:direct) D90763 D90763 g1742034 Escherichia coli 562  
-11533789 301367 oligopeptide transport system permease protein  
(sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #251(27.7-28.2  
min.)) (nt:orf\_id:o252#2; similar to (swissprot accession) (le:20967)  
(re:21875) (di:direct) D90852 D90852 g1805526 Escherichia coli 562 -11533789  
300254 oppc homolog of salmonella oligopeptide transport (fn:putative  
transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12  
mg1655 section 113 of 400 of the completegenome.) (nt:o302; 96 pct identical  
to oppc\_salty sw: p08006) (le:1008) (re:1916) (di:direct) AE000223 AE000223  
g1787498 Escherichia coli 562 -11533789 224727 oligopeptide transport  
system permease protein (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #251(27.7-28.2 min.)) (nt:orf\_id:o252#2; similar to (swissprot  
accession) (le:20967) (re:21875) (di:direct) D90852 D90852 g1805526  
Escherichia coli 562 -11533789 5000691011 (de:(ecoli\_1205) (pn:oligopeptide  
transport) (gn:oppc) (gtcfc:12.10) (ec:) (keggfc:11.2) (rileyfc:4.5.0)  
(db:gtc-escherichia coli)) ECOLI\_1205 ECOLI\_1205 Escherichia coli 562  
10065104

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836322	9084	31240	1014	337

Description

GTC ORF with score 304 to: (or:Caenorhabditis elegans) (db:genpept-inv)  
(de:caenorhabditis elegans cosmid b0513, complete sequence.) (nt:cdna est  
embl:d67325 comes from this gene; cdna est) (le:18399:19636:19964)  
(re:18611:19836:20168) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836324	9085	31241	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836325	9086	31242	693	230

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836365	9087	31243	822	274

Description

6500729932 oppd:b1246 oligopeptide transport atp-binding protein oppd  
(gtcfc:12.1) (keggfc:11.1) (rileyfc:4.5.0) (db:gtc-escherichia coli) b1246  
b1246 Escherichia coli 562 -11533790 117289 oppd (de:oligopeptide transport  
atp-binding protein oppd) (db:swissprot) OPPD\_ECOLI P76027 ESCHERICHIA COLI  
562 -11533790 7000686046 oppd oligopeptide transport atp-binding protein  
oppd (cl:inner membrane protein malk:atp-binding cassette homology)  
(db:pir2.dat) A64872 A64872 Escherichia coli 562 -11533790 7500887200 oppd  
homolog of salmonella atp-binding protein of (fn:putative transport; not  
classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 113  
of 400 of the completegenome.) (nt:91 pct identical (2 gaps) to oppd\_salty  
sw: p04285) (le:1928) (re:2941) (di:direct) AE000223 AE000223 g1787499  
Escherichia coli 562 -11533790 5000691012 (de:(ecoli\_1206) (pn:oligopeptide  
transport) (gn:oppd) (gtcfc:12.10) (ec:) (keggfc:11.2) (rileyfc:4.5.0)  
(db:gtc-escherichia coli)) ECOLI\_1206 ECOLI\_1206 Escherichia coli 562  
10059040

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836369	9088	31244	1107	368

Description

6500729933 oppf:b1247 oligopeptide transport atp-binding protein oppf (gtcfc:12.1) (keggfc:11.1) (rileyfc:4.5.0) (db:gtc-escherichia coli) b1247 b1247 Escherichia coli 562 -11533791 117291 oppf (de:oligopeptide transport atp-binding protein oppf) (db:swissprot) OPPF\_ECOLI P77737 ESCHERICHIA COLI 562 -11533791 7000686047 oppf oligopeptide transport atp-binding protein oppf (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) B64872 B64872 Escherichia coli 562 -11533791 223453 oligopeptide transport atp-binding protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #252(28.1-28.4 min.)) (nt:orf\_id:o252#4; similar to (swissprot accession) (le:4085) (re:5089) (di:direct) D90763 D90763 g1742036 Escherichia coli 562 -11533791 300256 oppf homolog of salmonella atp-binding protein of (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 113 of 400 of the completegenome.) (nt:o334; 94 pct identical to oppf\_salty sw: p08007) (le:2938) (re:3942) (di:direct) AE000223 AE000223 g1787500 Escherichia coli 562 -11533791 5000691013 (de:(ecoli\_1207) (pn:oligopeptide transport, atp hydrolysis) (gn:oppf) (gtcfc:12.10) (ec:) (keggfc:11.2) (rileyfc:4.5.0) (db:gtc-escherichia coli)) ECOLI\_1207 ECOLI\_1207 Escherichia coli 562 10059042

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836387	9089	31245	498	165

Description

GTC ORF with score 121 to: (fn:processing of pre-ribosomal rna) (sr:baker's yeast) (db:genpept-pln1) (de:s.cerevisiae chromosome xiii cosmid 9959.) (nt:ym9959.11c, unknown, len: 1729, cai: 0.24) (le:16981) (re:22170) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836391	9090	31246	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836400	9091	31247	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836403	9092	31248	1329	442

Description

6500729934 sapf:b1290 peptide transport system atp-binding protein sapf (gtcfc:12.1) (keggfc:11.1) (rileyfc:4.5.0) (db:gtc-escherichia coli) b1290 b1290 Escherichia coli 562 -11533792 97929 sapf (de:peptide transport system atp-binding protein sapf) (db:swissprot) SAPF\_ECOLI P36637 ESCHERICHIA COLI 562 -11533792 7000686560 sapf peptide transport system atp-binding protein sapf (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) E64877 E64877 Escherichia coli 562 -11533792 223517 sapf peptide transport system atp-binding protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #255(28.8-29.2 min.)) (nt:orf\_id:o255#18; similar to (swissprot accession) (le:14096) (re:14902) (di:complement) D90766 D90766 g1742103 Escherichia coli 562 -11533792 223525 sapf peptide transport system atp-binding protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #256(29.0-29.4 min.)) (nt:orf\_id:o255#18; similar to (swissprot accession) (le:7491) (re:8297) (di:complement) D90767 D90767 g1742112 Escherichia coli 562 -11533792 238542 sapf sapf protein (db:genpept-bct1) (de:e.coli sapabcd operon.) (le:4710) (re:5516) (di:direct) ECSAPABCD X97282 g1279404 Escherichia coli 562 -11533792 300320 sapf (db:genpept-bct1) (de:escherichia coli sap operon sapd gene, partial cds, and sapf gene,complete cds.) (nt:shows similarity with atp-binding proteins from) (le:97) (re:903) (di:direct) ECU08190 U08190 g470683 Escherichia coli 562 -11533792 238203 sapf putative atp-binding protein of peptide (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 117 of 400 of the completegenome.) (nt:f268; 100 pct identical to sapf\_ecoli sw: p36637) (le:2912) (re:3718) (di:complement) AE000227 AE000227 g1787547 Escherichia coli 562 -11533792 5000691014 (de:(ecoli\_1250) (pn:peptide transport, abc family of transporters) (gn:sapf) (gtcfc:12.10) (ec:) (sapf\_ecoli) (keggfc:11.2) (rileyfc:4.5.0) (db:gtc-escherichia coli)) ECOLI\_1250 ECOLI\_1250 Escherichia coli 562 10039808

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836424	9093	31249	597	198

Description

6500729935 lepb:b2568 signal peptidase i:spase i:leader peptidase i (gtcfc:11.1) (ec:3.4.21.89) (keggfc:14.1) (rileyfc:4.5.0) (db:gtc-escherichia coli) b2568 b2568 Escherichia coli 562 -11533793 81900 lepb (ec:3.4.21.89) (de:signal peptidase i, (spase i) (leader peptidase i)) (db:swissprot) LEP\_ECOLI P00803 ESCHERICHIA COLI 562 -11533793 7000685731 lepb:lepb signal peptidase i::leader peptidase:spase i (cl:signal peptidase i) (ec:3.4.99.36) (db:pir1.dat) (mp:55 min) ZPECS G65034 Escherichia coli 562 -11533793 7500884932 lepb leader peptidase signal peptidase i (fn:enzyme; protein, peptide secretion) (db:genpept-bct2) (ec:3.4.21.89) (de:escherichia coli k-12 mg1655 section 233 of 400 of the completegenome.) (nt:f324; 98 pct identical (1 gap) to lep\_ecoli) (le:4095) (re:5069) (di:complement) AE000343 AE000343 g1788921 Escherichia coli 562 -11533793 5000691015 (de:(ecoli\_2508) (pn:leader peptidase:signal peptidase i) (gn:lepb) (gtcfc:12.10) (ec:3.4.21.89) (lep\_ecoli) (keggfc:11.1) (rileyfc:4.5.0) (db:gtc-escherichia coli)) ECOLI\_2508 ECOLI\_2508 Escherichia coli 562 10123732

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836433	9094	31250	324	107

Description

6500729936 ffh:b2610 signal recognition particle protein:fifty-four homolog:p48 (gtcfc:12.13) (keggfc:14.2) (rileyfc:4.5.0) (db:gtc-escherichia coli) b2610 b2610 Escherichia coli 562 -11533794 99401 ffh (de:signal recognition particle protein (fifty-four homolog) (p48)) (db:swissprot) SR54\_ECOLI P07019 ESCHERICHIA COLI 562 -11533794 7000686673 ffh signal recognition particle protein (cl:signal recognition particle 54k protein) (db:pir2.dat) (mp:57 min) E65039 E65039 Escherichia coli 562 -11533794 7500892037 ffh gtp-binding export factor binds to signal (fn:transport; protein, peptide secretion) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 237 of 400 of the completegenome.) (nt:f453; 100 pct identical to sr54\_ecoli sw:) (le:155) (re:1516) (di:complement) AE000347 AE000347 g1788963 Escherichia coli 562 -11533794 5000691016 (de:(ecoli\_2546) (pn:gtp-binding export factor binds to signal sequence, gtp and rna) (gn:ffh) (gtcfc:12.10) (ec:) (sr54\_ecoli) (keggfc:11.2) (rileyfc:4.5.0) (db:gtc-escherichia coli)) ECOLI\_2546 ECOLI\_2546 Escherichia coli 562 10041260

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836448	9095	31251	1977	658

Description

6500729937 secg:b3175 preprotein translocase:protein-export membrane protein  
secg:preprotein translocase band 1 subunit:p12 (gtcfc:12.10) (keggfc:14.2)  
(rileyfc:4.5.0) (db:gtc-escherichia coli) b3175 b3175 Escherichia coli 562  
-11533795 98324 secg (de:subunit) (p12)) (db:swissprot) SECG\_ECOLI P33582  
ESCHERICHIA COLI 562 -11533795 164226 secg protein-export protein secg:p12  
protein:preprotein translocase (db:pir2.dat) S40402 S40402 Escherichia coli  
562 -11533795 236412 secg p12 (sr:escherichia coli (strain k12) dna, clone  
519, 520 and 521) (db:genpept-bct1) (de:escherichia coli secg and leu genes  
for p12 and trna-leu2,complete cds.) (le:147) (re:479) (di:direct)  
ECOSECGLU D16463 g431135 Escherichia coli 562 -11533795 267288 secg p12  
(db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to  
76.0 minutes.) (le:102925) (re:103257) (di:complement) ECOUW67 U18997  
g606113 Escherichia coli 562 -11533795 7500891484 membrane protein  
(db:genpept-bct1) (de:escherichia coli k12 ampicillin-binding protein  
(dacb),transcription elongation factor (grea), regulatory protein  
(mrsf),atp-binding protein (mrsc), dihydropteroate synthase,  
regulatoryprotein (mrsc), and membrane protein genes, c... U01376 U01376  
g746404 Escherichia coli 562 -11533795 235966 secg protein export -membrane  
protein (fn:transport; protein, peptide secretion) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 288 of 400 of the completegenome.)  
(nt:f110; 100 pct identical to secg\_ecoli sw: p33582;) (le:4034) (re:4366)  
(di:complement) AE000398 AE000398 g1789565 Escherichia coli 562 -11533795  
5000691017 (de:(ecoli\_3097) (pn:protein export - membrane protein)  
(gn:secg) (gtcfc:12.10) (ec:) (secg\_ecoli) (keggfc:11.2) (rileyfc:4.5.0)  
(db:gtc-escherichia coli)) ECOLI\_3097 ECOLI\_3097 Escherichia coli 562  
10040203

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836451	9096	31252	624	207

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501836459	9097	31253	1221	406

Description

6500729938 dppa:b3544 periplasmic dipeptide transport protein  
precursor:dipeptide-binding protein:dbp (gtcfc:12.1:11.1) (keggfc:11.1:12.2)  
(rileyfc:4.5.0) (db:gtc-escherichia coli) b3544 b3544 Escherichia coli 562  
-11533796 7500880590 dppa (de:protein) (dbp)) (db:swissprot) DPPA\_ECOLI  
P23847 ESCHERICHIA COLI 562 -11533796 162935 dppa periplasmic dipeptide  
transport protein precursor dppa:dipeptide transport protein  
dppa:dipeptide-binding protein dppa (cl:dipeptide transport protein)  
(db:pir2.dat) A39194 A39194 Escherichia coli 562 -11533796 234202 dppa  
dipeptide-binding protein (fn:binds dipeptides containing l-amino acids)  
(sr:escherichia coli (sub\_species mm500, strain k-12) dna) (db:genpept-bct1)  
(de:escherichia coli dpp locus encoding dipeptide transporter, chemotaxis,  
dipeptide-binding protein, transmembrane proteins, and... ECODPP L08399  
g349225 Escherichia coli 562 -11533796 236782 dppa dipeptide transporter  
protein (sr:e.coli (strain k12; isolate e1222) dna, clone lambda-10)  
(db:genpept-bct1) (de:e.coli dipeptide transport protein (fpp) gene,  
complete cds.) (le:147) (re:1754) (di:direct) ECODPPA M35045 g145797  
Escherichia coli 562 -11533796 237865 dppa (fn:dipeptide transporter)  
(sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda)  
(db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.)  
(le:120351) (re:121958) (di:complement) ECOUW76 U00039 g466683 Escherichia  
coli 562 -11533796 5000691018 dppa dipeptide binding protein dbp  
(db:genpept-bct1) (de:e.coli dppa gene for dipeptide binding protein (dbp).)  
(le:147) (re:1754) (di:direct) ECPPA X58051 g42475 Escherichia coli 562  
-11533796 234197 dppa dipeptide transport protein (fn:transport; protein,  
peptide secretion) (db:genpept-bct2) (de:escherichia coli k-12 mg1655  
section 321 of 400 of the completegenome.) (nt:f535; 100 pct identical amino  
acid sequence and) (le:9854) (re:11461) (di:complement) AE000431 AE000431  
g1789966 Escherichia coli 562 -11533796 69227 dppa (de:protein) (dbp))  
(db:swissprot) DPPA\_ECOLI P23847 ESCHERICHIA COLI 562 -11533796



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836468	9098	31254	204	67
<u>Description</u>				
6500729939 secb:b3609 protein-export protein secb (gtcfc:12.10) (keggfc:14.2) (rileyfc:4.5.0) (db:gtc-escherichia coli) b3609 b3609 Escherichia coli 562 -11533797 98303 secb (de:protein-export protein secb) (db:swissprot) SECB_ECOLI P15040 ESCHERICHIA COLI 562 -11533797 131532 secb protein-export protein secb (cl:protein-export protein secb) (db:pir1.dat) VXECS JS0126 Escherichia coli 562 -11533797 236846 secb export protein (sr:escherichia coli (individual_isolate mc4100, strain k-12) (clone) (db:genpept-bct1) (de:e.coli export protein (secb) gene, complete cds.) (le:41) (re:508) (di:direct) ECOSECB M24489 g147797 Escherichia coli 562 -11533797 7500891469 secb (fn:protein export) (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 17896) (le:197911) (re:198378) (di:complement) ECOUW76 U00039 g466747 Escherichia coli 562 -11533797 235961 secb protein export:molecular chaperone:may bind to (fn:transport; protein, peptide secretion) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 329 of 400 of the completgenome.) (nt:f155; cg site no. 17896) (le:1089) (re:1556) (di:complement) AE000439 AE000439 g1790038 Escherichia coli 562 -11533797 5000691019 (de:(ecoli_3529) (pn:protein export; molecular chaperone; may bind to signal sequence) (gn:secb) (gtcfc:12.10) (ec:) (secb_ecoli) (keggfc:11.2) (rileyfc:4.5.0) (db:gtc-escherichia coli)) ECOLI_3529 ECOLI_3529 Escherichia coli 562 10040182				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836477	9099	31255	297	98

#### Description

6500729940 sece:prlg:b3981 preprotein translocase sece subunit (gtcfc:12.10) (keggfc:14.2) (rileyfc:4.5.0) (db:gtc-escherichia coli) b3981 b3981 Escherichia coli 562 -11533798 98310 sece:prlg (de:preprotein translocase sece subunit) (db:swissprot) SECE\_ECOLI P16920 ESCHERICHIA COLI 562 -11533798 131534 sece preprotein translocase sece chain (cl:protein-export protein sece) (db:pir1.dat) (mp:90 min) VXECSA A35139 Escherichia coli 562 -11533798 237191 (sr:e.coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli sece-nusg operon encoding sece and nusg proteins, completecds, tufb rplk genes, partial cds.) (nt:sece protein) (le:240) (re:623) (di:direct) ECOSECE M30610 g147800 Escherichia coli 562 -11533798 235963 sece preprotein translocase (fn:transport; protein, peptide secretion) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 362 of 400 of the completegenome.) (nt:ol27a; 100 pct identical amino acid sequence and) (le:2322) (re:2705) (di:direct) AE000472 AE000472 g1790413 Escherichia coli 562 -11533798 7500891474 sece (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:42600) (re:42983) (di:direct) ECOUW89 U00006 g396320 Escherichia coli 562 -11533798 5000691020 (de:(ecoli\_3871) (pn:protein secretion, inner membrane protein) (gn:sece) (gtcfc:12.10) (ec:)) (sece\_ecoli) (keggfc:11.2) (rileyfc:4.5.0) (db:gtc-escherichia coli)) ECOLI\_3871 ECOLI\_3871 Escherichia coli 562 10040189

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836479	9100	31256	1497	498

#### Description

6500729941 arop:b0112 aromatic amino acid transport protein arop:general aromatic amino acid permease (gtcfc:12.1:11.1) (keggfc:14.2) (rileyfc:4.1.1) (db:gtc-escherichia coli) b0112 b0112 Escherichia coli 562 -11533799 7000688964 arop aromatic amino acid transport protein arop (cl:arginine permease) (db:pir1.dat) (mp:2.6 min) QRECAA H64733 Escherichia coli 562 -11533799 7500953601 arop aromatic amino acid transport protein (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 10 of 400 of the completegenome.) (nt:f457; 98 pct identical (1 gap) to arop\_ecoli) (le:2558) (re:3931) (di:complement) AE000120 AE000120 g1786302 Escherichia coli 562 -11533799 5000691021 (de:(ecoli\_112) (pn:general aromatic amino acid transport) (gn:arop) (gtcfc:12.1) (ec:)) (arop\_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI\_112 ECOLI\_112 Escherichia coli 562 10122664

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836483	9101	31257	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836501	9102	31258	414	137

Description

6500729942 brnq:b0401 branched chain amino acid transport system ii carrier protein:liv-ii (gtcfc:12.1) (keggfc:14.2) (rileyfc:4.1.1) (db:gtc-escherichia coli) b0401 b0401 Escherichia coli 562 -11533800 62034 brnq (de:(liv-ii)) (db:swissprot) BRNQ\_ECOLI P37011 ESCHERICHIA COLI 562 -11533800 7000684729 brnq branched-chain amino acid transport system ii carrier protein brnq (cl:branched-chain amino acid transport system ii carrier protein braz) (db:pir2.dat) A64769 A64769 Escherichia coli 562 -11533800 7500877938 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:similar to s. typhimurium brnq) (le:127181) (re:128500) (di:direct) ECU73857 U73857 g1657597 Escherichia coli 562 -11533800 240018 brnq branched chain amino acid transport system ii (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 36 of 400 of the completegenome.) (nt:o439; 100 pct identical to 70 aa fragment) (le:7077) (re:8396) (di:direct) AE000146 AE000146 g1786601 Escherichia coli 562 -11533800 5000691022 (de:(ecoli\_385) (pn:transport system 1 for isoleucine, leucine, and valine) (gn:brnq) (gtcfc:12.1) (ec:) (brnq\_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI\_385 ECOLI\_385 Escherichia coli 562 10122816

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836504	9103	31259	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836521	9104	31260	1596	531

Description

6500729943 phep:b0576 phenylalanine-specific permease (gtcfc:12.1:5.13) (keggfc:14.2) (rileyfc:4.1.1) (db:gtc-escherichia coli) b0576 b0576 Escherichia coli 562 -11533801 89556 phep (de:phenylalanine-specific permease) (db:swissprot) PHEP\_ECOLI P24207 ESCHERICHIA COLI 562 -11533801 152992 phep phenylalanine transport protein phep:phenylalanine-specific permease (cl:arginine permease) (db:pir2.dat) A39431 A39431 Escherichia coli 562 -11533801 223102 phep phenylalanine-specific permease (sr:escherichia coli(strain:k12) dna, clone:kohara clone #163) (db:genpept-bct1) (de:escherichia coli genomic dna. (12.7 - 13.2 min).) (le:7297) (re:8673) (di:direct) D90700 D90700 g1651239 Escherichia coli 562 -11533801 7500888019 phep permease (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli permease (phep) gene, complete cds.) (nt:associated with the phenylalanine-specific) (le:636) (re:2012) (di:direct) ECOPHEPA M58000 g147188 Escherichia coli 562 -11533801 235414 phep phenylalanine-specific transport system (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 52 of 400 of the completegenome.) (nt:o458; 100 pct identical to phep\_ecoli sw: p24207) (le:8736) (re:10112) (di:direct) AE000162 AE000162 g1786789 Escherichia coli 562 -11533801 5000691023 phep phenylalanine transport protein phep. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #163) (db:genpept) (de:escherichia coli genomic dna. (12.8 - 13.2 min).) (nt:orf\_id:o163#6; similar to pir accession number) (le:7297) (re:8673) (di:direct) D90700 D90700 g1651239 Escherichia coli 562 -11533801

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836524	9105	31261	213	70

Description

6500729944 pote:b0692 putrescine-ornithine antiporter:putrescine transport protein (gtcfc:12.1) (keggfc:14.2) (rileyfc:4.1.1) (db:gtc-escherichia coli) b0692 b0692 Escherichia coli 562 -11533802 90601 pote (de:putrescine-ornithine antiporter (putrescine transport protein)) (db:swissprot) POTE\_ECOLI P24170 ESCHERICHIA COLI 562 -11533802 164443 pote putrescine/ornithine antiporter:putrescine transport protein (cl:l-lysine transport protein) (db:pir2.dat) B40839 B40839 Escherichia coli 562 -11533802 223154 pote putrescine-ornithine antiporter putrescine (sr:escherichia coli(strain:k12) dna, clone:kohara clone #173) (db:genpept-bct1) (de:escherichia coli genomic dna. (15.3 - 15.6 min).) (le:6568) (re:7887) (di:complement) D90708 D90708 g1651299 Escherichia coli 562 -11533802 7500888291 pote putrescine transport protein (sr:e.coli (strain dr112) dna, clone ppt71) (db:genpept-bct1) (de:e.coli ornithine decarboxylase (spef) and putrescine transportprotein (pote) genes, complete cds.) (le:2855) (re:4174) (di:direct) ECOPOTESPE M64495 g147332 Escherichia coli 562 -11533802 235527 pote putrescine transport protein (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 62 of 400 of the completegenome.) (nt:f439; 100 pct identical to pote\_ecoli sw: p24170) (le:8931) (re:10250) (di:complement) AE000172 AE000172 g1786908 Escherichia coli 562 -11533802 5000691024 pote putrescine transport protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #173) (db:genpept) (de:escherichia coli genomic dna. (15.3 - 15.7 min).) (nt:orf\_id:o173#9; similar to pir accession number) (le:6568) (re:7887) (di:complement) D90708 D90708 g1651299 Escherichia coli 562 -11533802

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836539	9106	31262	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836547	9107	31263	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836557	9108	31264	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501836561	9109	31265	423	140

# Description

6500729945 glnq:b0809 glutamine transport atp-binding protein glnq (gtcfc:12.1:11.1:5.1) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b0809 b0809 Escherichia coli 562 -11533803 7500882476 glnq (de:glutamine transport atp-binding protein glnq) (db:swissprot) GLNQ\_ECOLI P10346 ESCHERICHIA COLI 562 -11533803 130728 glnq glutamine transport protein glnq (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir1.dat) (mp:18 min) QRECGQ S03183 Escherichia coli 562 -11533803 223209 glnq glutamine transport protein glnq (sr:escherichia coli(strain:k12) dna, clone:kohara clone #205) (db:genpept-bct1) (de:escherichia coli genomic dna.(18.0 - 18.3 min).) (le:7058) (re:7780) (di:complement) D90718 D90718 g1651363 Escherichia coli 562 -11533803 223214 glnq glutamine transport protein glnq (sr:escherichia coli(strain:k12) dna, clone:kohara clone #206) (db:genpept-bct1) (de:escherichia coli genomic dna.(18.2 - 18.5 min).) (le:273) (re:995) (di:complement) D90719 D90719 g1651369 Escherichia coli 562 -11533803 5000691025 (db:genpept-bct1) (de:escherichia coli glutamine permease glnhpq operon.) (nt:glnq (aa 1-240); gtg start) (le:2214) (re:2936) (di:direct) ECGLNHPQ X14180 g581098 Escherichia coli 562 -11533803 233004 glnq atp-binding component of glutamine high-affinity (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 73 of 400 of the completegenome.) (nt:f240; 100 pct identical to glnq\_ecoli sw: p10346) (le:4108) (re:4830) (di:complement) AE000183 AE000183 g1787029 Escherichia coli 562 -11533803 7502851966 glnq glutamine transport protein glnq. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #205) (db:genpept) (de:escherichia coli genomic dna. (18.1 - 18.4 min).) (nt:orf\_id:o206#1; similar to pir accession number) (le:7058) (re:7780) (di:complement) D90718 D90718 g1651363 Escherichia coli 562 -11533803 7502851967 glnq glutamine transport protein glnq. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #206) (db:genpept) (de:escherichia coli genomic dna. (18.2 - 18.6 min).) (nt:orf\_id:o206#1; similar to pir accession number) (le:273) (re:995) (di:complement) D90719 D90719 g1651369 Escherichia coli 562 -11533803 73994 glnq (de:glutamine transport atp-binding protein glnq) (db:swissprot) GLNQ\_ECOLI P10346 ESCHERICHIA COLI 562 -11533803

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836568	9110	31266	909	303

Description

6500729946 glnp:b0810 glutamine transport system permease protein glnp (gtcfc:12.1:11.1:5.1) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b0810 b0810 Escherichia coli 562 -11533804 7500882475 glnp (de:glutamine transport system permease protein glnp) (db:swissprot) GLNP\_ECOLI P10345 ESCHERICHIA COLI 562 -11533804 130700 glnp glutamine transport system permease protein glnp (cl:histidine permease protein m) (db:pir1.dat) (mp:18 min) QRECGP S03182 Escherichia coli 562 -11533804 223215 glnp glutamine transport protein glnp (sr:escherichia coli(strain:k12) dna, clone:kohara clone #206) (db:genpept-bct1) (de:escherichia coli genomic dna. (18.2 - 18.5 min).) (le:992) (re:1651) (di:complement) D90719 D90719 g1651370 Escherichia coli 562 -11533804 5000691026 (db:genpept-bct1) (de:escherichia coli glutamine permease glnhpq operon.) (nt:glnp (aa 1-219)) (le:1558) (re:2217) (di:direct) ECGLNHPQ X14180 g41572 Escherichia coli 562 -11533804 233003 glnp glutamine high-affinity transport system (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 73 of 400 of the completgenome.) (nt:f219; 100 pct identical to glnp\_ecoli sw: p10345) (le:4827) (re:5486) (di:complement) AE000183 AE000183 g1787030 Escherichia coli 562 -11533804 7502851968 glnp glutamine transport protein glnp. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #205) (db:genpept) (de:escherichia coli genomic dna. (18.1 - 18.4 min).) (nt:orf\_id:o206#2; similar to pir accession number) (le:7777) (re:8436) (di:complement) D90718 D90718 g4062376 Escherichia coli 562 -11533804 7502851969 glnp glutamine transport protein glnp. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #206) (db:genpept) (de:escherichia coli genomic dna. (18.2 - 18.6 min).) (nt:orf\_id:o206#2; similar to pir accession number) (le:992) (re:1651) (di:complement) D90719 D90719 g1651370 Escherichia coli 562 -11533804 73991 glnp (de:glutamine transport system permease protein glnp) (db:swissprot) GLNP\_ECOLI P10345 ESCHERICHIA COLI 562 -11533804

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836575	9111	31267	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836584	9112	31268	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836596	9113	31269	1257	418

Description

GTC ORF with score 103 to: (or:Homo sapiens) (fn:peripheral proteins believed to act as) (sr:human) (db:genpept-pri1) (de:human ankyrin g (ank-3) mrna, complete cds.) (nt:480 kda; antibodies that recognize this sequence) (le:193) (re:13326) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836629	9114	31270	630	210

Description

6500729947 glnh:b0811 glutamine-binding periplasmic protein precursor:glnbp (gtcfc:12.1:11.1:5.1) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b0811 b0811 Escherichia coli 562 -11533805 7500882473 glnh (de:glutamine-binding periplasmic protein precursor (glnbp)) (db:swissprot) GLNH\_ECOLI P10344 ESCHERICHIA COLI 562 -11533805 130690 glnh glutamine-binding periplasmic protein precursor (cl:lysine-arginine-ornithine-binding protein) (db:pir1.dat) (mp:18 min) JKECQ S03181 Escherichia coli 562 -11533805 223211 glnh glutamine-binding protein precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #205) (db:genpept-bct1) (de:escherichia coli genomic dna.(18.0 - 18.3 min).) (le:8575) (re:9321) (di:complement) D90718 D90718 g1651365 Escherichia coli 562 -11533805 223216 glnh glutamine-binding protein precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #206) (db:genpept-bct1) (de:escherichia coli genomic dna.(18.2 - 18.5 min).) (le:1790) (re:2536) (di:complement) D90719 D90719 g1651371 Escherichia coli 562 -11533805 5000691027 (db:genpept-bct1) (de:escherichia coli glutamine permease glnhpq operon.) (nt:glnh precursor (aa -22 to 226)) (le:673) (re:1419) (di:direct) ECGLNHPQ X14180 g41569 Escherichia coli 562 -11533805 233002 glnh periplasmic glutamine-binding protein:permease (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 73 of 400 of the completegenome.) (nt:f248; 100 pct identical to glnh\_ecoli sw: p10344) (le:5625) (re:6371) (di:complement) AE000183 AE000183 g1787031 Escherichia coli 562 -11533805 7502851970 glnh glutamine-binding protein precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #205) (db:genpept) (de:escherichia coli genomic dna.(18.1 - 18.4 min).) (nt:orf\_id:o206#3; similar to pir accession number) (le:8575) (re:9321) (di:complement) D90718 D90718 g1651365 Escherichia coli 562 -11533805 7502851971 glnh glutamine-binding protein precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #206) (db:genpept) (de:escherichia coli genomic dna.(18.2 - 18.6 min).) (nt:orf\_id:o206#3; similar to pir accession number) (le:1790) (re:2536) (di:complement) D90719 D90719 g1651371 Escherichia coli 562 -11533805 73989 glnh (de:glutamine-binding periplasmic protein precursor (glnbp)) (db:swissprot) GLNH\_ECOLI P10344 ESCHERICHIA COLI 562 -11533805



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836630	9115	31271	342	113

Description

6500729948 potf:b0854 putrescine-binding periplasmic protein precursor  
 (gtcfc:12.1:12.6) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli)  
 b0854 b0854 Escherichia coli 562 -11533806 90603 potf  
 (de:putrescine-binding periplasmic protein precursor) (db:swissprot)  
 POTF\_ECOLI P31133 ESCHERICHIA COLI 562 -11533806 7000686159 potf  
 putrescine-binding periplasmic protein potf precursor:putrescine transport  
 protein potf (db:pir2.dat) F64823 F64823 Escherichia coli 562 -11533806  
 223229 potf putrescine transport protein potf (sr:escherichia  
 coli(strain:k12) dna, clone:kohara clone #210) (db:genpept-bct1)  
 (de:escherichia coli genomic dna. (19.0 - 19.3 min).) (le:10468) (re:11580)  
 (di:direct) D90723 D90723 g1651387 Escherichia coli 562 -11533806  
 7500888293 potf periplasmic putrescine-binding protein:permease  
 (fn:transport; transport of small molecules: amino) (db:genpept-bct2)  
 (de:escherichia coli k-12 mg1655 section 77 of 400 of the completegenome.)  
 (nt:o370; 99 pct identical to potf\_ecoli sw: p31133) (le:5768) (re:6880)  
 (di:direct) AE000187 AE000187 g1787078 Escherichia coli 562 -11533806  
 5000691028 potf putrescine transport protein potf. (sr:escherichia  
 coli(strain:k12) dna, clone:kohara clone #210) (db:genpept) (de:escherichia  
 coli genomic dna. (19.1 - 19.4 min).) (nt:orf\_id:o210#12; similar to pir  
 accession number) (le:10468) (re:11580) (di:direct) D90723 D90723 g1651387  
 Escherichia coli 562 -11533806

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836632	9116	31272	486	161
<u>Description</u>				
6500729949 potg:b0855 putrescine transport atp-binding protein potg (gtcfc:12.1:12.6) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b0855 b0855 Escherichia coli 562 -11533807 90604 potg (de:putrescine transport atp-binding protein potg) (db:swissprot) POTG_ECOLI P31134 ESCHERICHIA COLI 562 -11533807 164445 potg putrescine transport protein potg (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) B45313 B45313 Escherichia coli 562 -11533807 223230 potg putrescine transport atp-binding protein potg (sr:escherichia coli(strain:k12) dna, clone:kohara clone #210) (db:genpept-bct1) (de:escherichia coli genomic dna.(19.0 - 19.3 min).) (le:11594) (re:12808) (di:direct) D90723 D90723 g1651388 Escherichia coli 562 -11533807 7500888294 potg nucleotide binding protein (sr:escherichia coli (strain dr112) dna) (db:genpept-bct1) (de:escherichia coli periplasmic putrescine binding protein (potf)gene, complete cds, (potg) gene, transmembrane protein (poth) and(poti) genes, complete cds.) (le:2386) (re:3600) (di:direct) ECOPOTFGHI M93239 g147335 Escherichia coli 562 -11533807 235529 potg atp-binding component of putrescine transport (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 77 of 400 of the completegenome.) (nt:o404; 100 pct identical to potg_ecoli sw: p31134) (le:6894) (re:8108) (di:direct) AE000187 AE000187 g1787079 Escherichia coli 562 -11533807 5000691029 potg putrescine transport protein potg. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #210) (db:genpept) (de:escherichia coli genomic dna. (19.1 - 19.4 min).) (nt:orf_id:o210#13; similar to pir accession number) (le:11594) (re:12808) (di:direct) D90723 D90723 g1651388 Escherichia coli 562 -11533807				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836634	9117	31273	1203	400

Description

6500729950 poth:b0856 putrescine transport system permease protein poth (gtcfc:12.1:12.6) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b0856 b0856 Escherichia coli 562 -11533808 90605 poth (de:putrescine transport system permease protein poth) (db:swissprot) POTH\_ECOLI P31135 ESCHERICHIA COLI 562 -11533808 164446 poth putrescine transport system permease protein poth (cl:spermidine/putrescine transport system permease protein poth) (db:pir2.dat) C45313 C45313 Escherichia coli 562 -11533808 223231 poth putrescine transport system permease protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #210) (db:genpept-bct1) (de:escherichia coli genomic dna. (19.0 - 19.3 min).) (le:12818) (re:13771) (di:direct) D90723 D90723 g1651389 Escherichia coli 562 -11533808 7500888295 poth transmembrane protein (sr:escherichia coli (strain dr112) dna) (db:genpept-bct1) (de:escherichia coli periplasmic putrescine binding protein (potf)gene, complete cds, (potg) gene, transmembrane protein (poth) and(poti) genes, complete cds.) (le:3610) (re:4563) (di:direct) ECOPOTFGHI M93239 g147336 Escherichia coli 562 -11533808 235530 poth putrescine transport protein:permease (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 77 of 400 of the completegenome.) (nt:o317; 100 pct identical to poth\_ecoli sw: p31135) (le:8118) (re:9071) (di:direct) AE000187 AE000187 g1787080 Escherichia coli 562 -11533808 5000691030 poth putrescine transport protein poth. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #210) (db:genpept) (de:escherichia coli genomic dna. (19.1 - 19.4 min).) (nt:orf\_id:o210#14; similar to pir accession number) (le:12818) (re:13771) (di:direct) D90723 D90723 g1651389 Escherichia coli 562 -11533808

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836668	9118	31274	582	193

Description

6500729951 poti:b0857 putrescine transport system permease protein poti (gtcfc:12.1:12.6) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b0857 b0857 Escherichia coli 562 -11533809 90606 poti (de:putrescine transport system permease protein poti) (db:swissprot) POTI\_ECOLI P31136 ESCHERICHIA COLI 562 -11533809 164447 poti putrescine transport system permease protein poti (cl:spermidine/putrescine transport system permease protein poti) (db:pir2.dat) D45313 D45313 Escherichia coli 562 -11533809 223232 poti putrescine transport system permease protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #210) (db:genpept-bct1) (de:escherichia coli genomic dna. (19.0 - 19.3 min).) (le:13768) (re:14613) (di:direct) D90723 D90723 g1651390 Escherichia coli 562 -11533809 7500888296 poti transmembrane protein (sr:escherichia coli (strain dr112) dna) (db:genpept-bct1) (de:escherichia coli periplasmic putrescine binding protein (potf)gene, complete cds, (potg) gene, transmembrane protein (poth) and(poti) genes, complete cds.) (le:4560) (re:5405) (di:direct) ECOPOTFGHI M93239 g147337 Escherichia coli 562 -11533809 235531 poti putrescine transport protein:permease (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 77 of 400 of the completegenome.) (nt:o281; 100 pct identical to poti\_ecoli sw: p31136) (le:9068) (re:9913) (di:direct) AE000187 AE000187 g1787081 Escherichia coli 562 -11533809 5000691031 poti putrescine transport protein poti. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #210) (db:genpept) (de:escherichia coli genomic dna. (19.1 - 19.4 min).) (nt:orf\_id:o210#15; similar to pir accession number) (le:13768) (re:14613) (di:direct) D90723 D90723 g1651390 Escherichia coli 562 -11533809

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836672	9119	31275	927	308

Description

6500729952 artj:b0860 arginine-binding periplasmic protein 2 precursor  
 (gtcfc:12.1:11.1:5.10) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia  
 coli) b0860 b0860 Escherichia coli 562 -11533810 60305 artj  
 (de:arginine-binding periplasmic protein 2 precursor) (db:swissprot)  
 ARTJ\_ECOLI P30860 ESCHERICHIA COLI 562 -11533810 7000684638 artj  
 arginine-binding periplasmic protein 2 precursor  
 (cl:lysine-arginine-ornithine-binding protein) (db:pir2.dat) D64824 D64824  
 Escherichia coli 562 -11533810 223234 artj arginine-binding periplasmic  
 protein 2 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #211)  
 (db:genpept-bct1) (de:escherichia coli genomic dna.(19.3 - 19.7 min).)  
 (le:2123) (re:2854) (di:complement) D90724 D90724 g1651393 Escherichia coli  
 562 -11533810 7500877217 artj arginine 3rd transport system periplasmic  
 (fn:transport; transport of small molecules: amino) (db:genpept-bct2)  
 (de:escherichia coli k-12 mg1655 section 78 of 400 of the completegenome.)  
 (nt:f243; 99 pct identical to artj\_ecoli sw: p30860) (le:130) (re:861)  
 (di:complement) AE000188 AE000188 g1787085 Escherichia coli 562 -11533810  
 5000691032 artj arginine-binding protein artj. (sr:escherichia  
 coli(strain:k12) dna, clone:kohara clone #211) (db:genpept) (de:escherichia  
 coli genomic dna. (19.4 - 19.8 min).) (nt:orf\_id:o211#3; similar to pir  
 accession number) (le:2123) (re:2854) (di:complement) D90724 D90724 g1651393  
 Escherichia coli 562 -11533810

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836684	9120	31276	336	111

Description

6500729953 artm:b0861 arginine transport system permease protein artm (gtcfc:12.1:11.1:5.10) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b0861 b0861 Escherichia coli 562 -11533811 60307 artm (de:arginine transport system permease protein artm) (db:swissprot) ARTM\_ECOLI P30862 ESCHERICHIA COLI 562 -11533811 7000684639 artm arginine transport system permease protein artm (cl:histidine permease protein m) (db:pir2.dat) E64824 E64824 Escherichia coli 562 -11533811 223235 artm arginine transport system permease protein artm (sr:escherichia coli(strain:k12) dna, clone:kohara clone #211) (db:genpept-bct1) (de:escherichia coli genomic dna.(19.3 - 19.7 min).) (le:3145) (re:3813) (di:complement) D90724 D90724 g1651394 Escherichia coli 562 -11533811 7500877218 artm arginine 3rd transport system permease protein (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 78 of 400 of the completengenome.) (nt:f222; 98 pct identical to artm\_ecoli sw: p30862) (le:1152) (re:1820) (di:complement) AE000188 AE000188 g1787086 Escherichia coli 562 -11533811 5000691033 artm arginine transport system protein artm. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #211) (db:genpept) (de:escherichia coli genomic dna. (19.4 - 19.8 min).) (nt:orf\_id:o211#4; similar to pir accession number) (le:3145) (re:3813) (di:complement) D90724 D90724 g1651394 Escherichia coli 562 -11533811

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836688	9121	31277	708	235

Description

GTC ORF with score 102 to: (or:Anolis pulchellus) (fn:precursor of yolk proteins, serum transport) (db:genpept-vrt) (de:anolis pulchellus vitellogenin mrna, partial cds.) (nt:apvtg5; similar to chicken and xenopus phosvitin) (le:<1) (re:546) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836699	9122	31278	417	139

Description

6500729954 artq:b0862 arginine transport system permease protein artq (gtcfc:12.1:11.1:5.10) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b0862 b0862 Escherichia coli 562 -11533812 60311 artq (de:arginine transport system permease protein artq) (db:swissprot) ARTQ\_ECOLI P30861 ESCHERICHIA COLI 562 -11533812 7000684641 artq arginine transport system permease protein artq (cl:histidine permease protein m) (db:pir2.dat) F64824 F64824 Escherichia coli 562 -11533812 223236 artq arginine transport system protein artq (sr:escherichia coli(strain:k12) dna, clone:kohara clone #211) (db:genpept-bct1) (de:escherichia coli genomic dna. (19.3 - 19.7 min).) (le:3813) (re:4529) (di:complement) D90724 D90724 g1651395 Escherichia coli 562 -11533812 7500877222 artq arginine 3rd transport system permease protein (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 78 of 400 of the completegenome.) (nt:f238; 98 pct identical to artq\_ecoli sw: p30861) (le:1820) (re:2536) (di:complement) AE000188 AE000188 g1787087 Escherichia coli 562 -11533812 5000691034 artq arginine transport system protein artq. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #211) (db:genpept) (de:escherichia coli genomic dna. (19.4 - 19.8 min).) (nt:orf\_id:o211#5; similar to pir accession number) (le:3813) (re:4529) (di:complement) D90724 D90724 g1651395 Escherichia coli 562 -11533812

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836705	9123	31279	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836720	9124	31280	570	189

Description

GTC ORF with score 237 to: (de:(ybr011c) (pn:inorganic pyrophosphatase:pyrophosphate phospho-hydrolase:ppase:inorganic pyrophosphatase, cytoplasmic) (gn:ppa1:ppa:ybr0202:ipp1) (gtcfc:2.1) (ec:3.6.1.1) (ipyr\_yeast) (keggfc:2.1) (sgdfc:1.4.1:9.2.0) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836722	9125	31281	192	63
<u>Description</u>				
6500729955 arti:b0863 arginine-binding periplasmic protein 1 precursor (gtcfc:12.1:11.1:5.10) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b0863 b0863 Escherichia coli 562 -11533813 60303 arti (de:arginine-binding periplasmic protein 1 precursor) (db:swissprot) ARTI_ECOLI P30859 ESCHERICHIA COLI 562 -11533813 7000684637 arti arginine-binding periplasmic protein 1 precursor (cl:lysine-arginine-ornithine-binding protein) (db:pir2.dat) G64824 G64824 Escherichia coli 562 -11533813 223237 arti arginine-binding periplasmic protein 1 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #211) (db:genpept-bct1) (de:escherichia coli genomic dna.(19.3 - 19.7 min).) (le:4536) (re:5267) (di:complement) D90724 D90724 g1651396 Escherichia coli 562 -11533813 7500877215 arti arginine 3rd transport system periplasmic (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 78 of 400 of the completegenome.) (nt:f243; this 243 aa orf is 97 pct identical (1 gap)) (le:2543) (re:3274) (di:complement) AE000188 AE000188 g1787088 Escherichia coli 562 -11533813 5000691035 arti arginine binding protein arti (sr:escherichia coli(strain:k12) dna, clone:kohara clone #211) (db:genpept) (de:escherichia coli genomic dna. (19.4 - 19.8 min).) (nt:orf_id:o211#6; similar to pir accession number) (le:4536) (re:5267) (di:complement) D90724 D90724 g1651396 Escherichia coli 562 -11533813				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836723	9126	31282	492	163

Description

6500729956 atp:b0864 arginine transport atp-binding protein atp (gtcfc:12.1:11.1:5.10) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b0864 b0864 Escherichia coli 562 -11533814 60309 atp (de:arginine transport atp-binding protein atp) (db:swissprot) ARTP\_ECOLI P30858 ESCHERICHIA COLI 562 -11533814 7000684640 atp arginine transport protein atp (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) H64824 H64824 Escherichia coli 562 -11533814 223238 atp arginine transport atp-binding protein atp (sr:escherichia coli(strain:k12) dna, clone:kohara clone #211) (db:genpept-bct1) (de:escherichia coli genomic dna.(19.3 - 19.7 min).) (le:5285) (re:6013) (di:complement) D90724 D90724 g1651397 Escherichia coli 562 -11533814 7500877220 atp atp-binding component of 3rd arginine transport (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 78 of 400 of the completegenome.) (nt:f242; 98 pct identical to atp\_ecoli sw: p30858) (le:3292) (re:4020) (di:complement) AE000188 AE000188 g1787089 Escherichia coli 562 -11533814 5000691036 atp periplasmic transport system protein atp. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #211) (db:genpept) (de:escherichia coli genomic dna. (19.4 - 19.8 min).) (nt:orf\_id:o211#7; similar to pir accession number) (le:5285) (re:6013) (di:complement) D90724 D90724 g1651397 Escherichia coli 562 -11533814

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836724	9127	31283	297	98

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836730	9128	31284	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836736	9129	31285	411	136

Description

6500729957 potd:b1123 spermidine/putrescine-binding periplasmic protein precursor:spbp (gtcfc:12.1:12.6) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b1123 b1123 Escherichia coli 562 -11533815 90600 potd (de:spermidine/putrescine-binding periplasmic protein precursor (spbp)) (db:swissprot) POTD\_ECOLI P23861 ESCHERICHIA COLI 562 -11533815 164642 potd spermidine/putrescine-binding protein precursor:spermidine/putrescine transport protein d (db:pir2.dat) D40840 D40840 Escherichia coli 562 -11533815 223369 potd spermidine/putrescine-binding periplasmic (sr:escherichia coli(strain:k12) dna, clone:kohara clone #238) (db:genpept-bct1) (de:escherichia coli genomic dna.(25.1 - 25.5 min).) (le:13470) (re:14516) (di:complement) D90747 D90747 g1651550 Escherichia coli 562 -11533815 235525 potd spermidine/putrescine periplasmic transport (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 102 of 400 of the completegenome.) (nt:f348; 100 pct identical to potd\_ecoli sw: p23861) (le:7785) (re:8831) (di:complement) AE000212 AE000212 g1787367 Escherichia coli 562 -11533815 7500888289 potd transport protein (sr:e.coli (strain dr112) dna, clone ppt104) (db:genpept-bct2) (de:e.coli transport protein (pota, potb, potc and potd) genes,complete cds.) (le:3144) (re:4190) (di:direct) ECOPOTABCD M64519 g147329 Escherichia coli 562 -11533815 5000691037 potd spermidine/putrescine transport protein d (sr:escherichia coli(strain:k12) dna, clone:kohara clone #238) (db:genpept) (de:escherichia coli genomic dna.(25.2 - 25.6 min).) (nt:orf\_id:o238#12; similar to pir accession number) (le:13470) (re:14516) (di:complement) D90747 D90747 g1651550 Escherichia coli 562 -11533815

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836750	9130	31286	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501836751	9131	31287	726	241

# Description

6500729958 potc:b1124 spermidine/putrescine transport system permease protein potc (gtcfc:12.1:12.6) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b1124 b1124 Escherichia coli 562 -11533816 90597 potc (de:spermidine/putrescine transport system permease protein potc) (db:swissprot) POTC\_ECOLI P23859 ESCHERICHIA COLI 562 -11533816 164640 potc spermidine/putrescine transport system permease potc (cl:spermidine/putrescine transport system permease protein poti) (db:pir2.dat) C40840 C40840 Escherichia coli 562 -11533816 223370 potc spermidine/putrescine transport system permease (sr:escherichia coli(strain:k12) dna, clone:kohara clone #238) (db:genpept-bct1) (de:escherichia coli genomic dna. (25.1 - 25.5 min).) (le:14513) (re:15307) (di:complement) D90747 D90747 g1651551 Escherichia coli 562 -11533816 235524 potc spermidine/putrescine transport system permease (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 102 of 400 of the completegenome.) (nt:f264; 100 pct identical to potc\_ecoli sw: p23859) (le:8828) (re:9622) (di:complement) AE000212 AE000212 g1787368 Escherichia coli 562 -11533816 7500888286 potc transport protein (sr:e.coli (strain dr112) dna, clone ppt104) (db:genpept-bct2) (de:e.coli transport protein (pota, potb, potc and potd) genes,complete cds.) (le:2353) (re:3147) (di:direct) ECOPOTABCD M64519 g147328 Escherichia coli 562 -11533816 5000691038 potc spermidine/putrescine transport system permease (sr:escherichia coli(strain:k12) dna, clone:kohara clone #238) (db:genpept) (de:escherichia coli genomic dna. (25.2 - 25.6 min).) (nt:orf\_id:o238#13; similar to swissprot accession) (le:14513) (re:15307) (di:complement) D90747 D90747 g1651551 Escherichia coli 562 -11533816

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501836752	9132	31288	207	68

# Description

6500729959 potb:b1125 spermidine/putrescine transport system permease protein potb (gtcfc:12.1:12.6) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b1125 b1125 Escherichia coli 562 -11533817 90594 potb (de:spermidine/putrescine transport system permease protein potb) (db:swissprot) POTB\_ECOLI P23860 ESCHERICHIA COLI 562 -11533817 164639 potb spermidine/putrescine transport system permease potb (cl:spermidine/putrescine transport system permease protein poth) (db:pir2.dat) B40840 B40840 Escherichia coli 562 -11533817 223371 potb spermidine/putrescine transport system permease (sr:escherichia coli(strain:k12) dna, clone:kohara clone #238) (db:genpept-bct1) (de:escherichia coli genomic dna. (25.1 - 25.5 min).) (le:15304) (re:16131) (di:complement) D90747 D90747 g1651552 Escherichia coli 562 -11533817 235523 potb spermidine/putrescine transport system permease (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 102 of 400 of the completegenome.) (nt:f275; 99 pct identical to potb\_ecoli sw: p23860) (le:9619) (re:10446) (di:complement) AE000212 AE000212 g1787369 Escherichia coli 562 -11533817 7500888282 potb transport protein (sr:e.coli (strain dr112) dna, clone ppt104) (db:genpept-bct2) (de:e.coli transport protein (pota, potb, potc and potd) genes,complete cds.) (le:1529) (re:2356) (di:direct) ECOPOTABCD M64519 g147327 Escherichia coli 562 -11533817 5000691039 potb spermidine/putrescine transport system permease (sr:escherichia coli(strain:k12) dna, clone:kohara clone #238) (db:genpept) (de:escherichia coli genomic dna. (25.2 - 25.6 min).) (nt:orf\_id:o238#14; similar to swissprot accession) (le:15304) (re:16131) (di:complement) D90747 D90747 g1651552 Escherichia coli 562 -11533817

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501836755	9133	31289	1887	628

#### Description

6500729960 pota:b1126 spermidine/putrescine transport atp-binding protein  
pota (gtcfc:12.1:12.6) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia  
coli) b1126 b1126 Escherichia coli 562 -11533818 90590 pota  
(de:spermidine/putrescine transport atp-binding protein pota) (db:swissprot)  
POTA\_ECOLI P23858 ESCHERICHIA COLI 562 -11533818 164641 pota  
spermidine/putrescine transport protein pota (cl:unassigned atp-binding  
cassette proteins:atp-binding cassette homology) (db:pir2.dat) A40840 A40840  
Escherichia coli 562 -11533818 223374 pota spermidine/putrescine transport  
atp-binding (sr:escherichia coli(strain:k12) dna, clone:kohara clone #239)  
(db:genpept-bct1) (de:escherichia coli genomic dna.(25.6 - 26.0 min).)  
(le:692) (re:1828) (di:complement) D90748 D90748 g1651555 Escherichia coli  
562 -11533818 235522 pota atp-binding component of spermidine/putrescine  
(fn:transport; transport of small molecules: amino) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 102 of 400 of the completegenome.)  
(nt:f378; 99 pct identical to pota\_ecoli sw: p23858) (le:10460) (re:11596)  
(di:complement) AE000212 AE000212 g1787370 Escherichia coli 562 -11533818  
7500888279 pota transport protein (sr:e.coli (strain dr112) dna, clone  
ppt104) (db:genpept-bct2) (de:e.coli transport protein (pota, potb, potc and  
potd) genes,complete cds.) (le:379) (re:1515) (di:direct) ECOPOTABCD M64519  
g147326 Escherichia coli 562 -11533818 5000691040 pota  
spermidine/putrescine transport protein a (sr:escherichia coli(strain:k12)  
dna, clone:kohara clone #239) (db:genpept) (de:escherichia coli genomic dna.  
(25.6 - 25.9 min).) (nt:orf\_id:o239#1; similar to pir accession number)  
(le:692) (re:1828) (di:complement) D90748 D90748 g1651555 Escherichia coli  
562 -11533818

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501836757	9134	31290	282	94

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836758	9135	31291	708	235
<u>Description</u>				
6500729961 tyrr:b1323 transcriptional regulatory protein tyrr (gtcfc:10.2:12.1) (keggfc:14.2) (rileyfc:4.1.1) (db:gtc-escherichia coli) b1323 b1323 Escherichia coli 562 -11533819 102929 tyrr (de:transcriptional regulatory protein tyrr) (db:swissprot) TYRR_ECOLI P07604 ESCHERICHIA COLI 562 -11533819 131487 tyrr transcription regulator tyrr (cl:nif-specific regulatory protein:rna polymerase sigma factor interaction domain homology) (db:pir1.dat) (mp:29 min) RGECA Y A47086 Escherichia coli 562 -11533819 223578 tyrr regulatory protein tyrr (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #259(29.6-30.0 min.)) (nt:orf_id:o260#6; similar to (pir accession number) (le:13300) (re:14841) (di:direct) D90770 D90770 g1742168 Escherichia coli 562 -11533819 223589 tyrr regulatory protein tyrr (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #260(29.8-30.2 min.)) (nt:orf_id:o260#6; similar to (pir accession number) (le:5193) (re:6734) (di:direct) D90771 D90771 g1742180 Escherichia coli 562 -11533819 300362 (sr:e.coli k12, clone pmu360) (db:genpept-bct1) (de:e.coli k12 tyrr regulatory gene encoding tyrr protein, completecds.) (nt:tyrr protein) (le:318) (re:1859) (di:direct) ECOTYRR M12114 g148092 Escherichia coli 562 -11533819 236234 tyrr transcriptional regulation of arof:arog:tyra (fn:regulator; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 120 of 400 of the completegenome.) (nt:o513; 100 pct identical to tyrr_ecoli sw: p07604;) (le:4882) (re:6423) (di:direct) AE000230 AE000230 g1787583 Escherichia coli 562 -11533819 5000691041 (de:(ecoli_1283) (pn:regulation of arof, arog, and tyra and aromatic amino acid transport systems) (gn:tyrr) (gtcfc:12.1) (ec:) (tyrr_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI_1283 ECOLI_1283 Escherichia coli 562 10044741				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836783	9136	31292	1431	476

Description

6500729962 tyrp:b1907 tyrosine-specific transport protein:tyrosine permease (gtcfc:12.1:11.1:5.12) (keggfc:14.2) (rileyfc:4.1.1) (db:gtc-escherichia coli) b1907 b1907 Escherichia coli 562 -11533820 102926 tyrp (de:tyrosine-specific transport protein (tyrosine permease)) (db:swissprot) TYRP\_ECOLI P18199 ESCHERICHIA COLI 562 -11533820 7000686841 tyrp tyrosine-specific transport protein:tyrosine permease (cl:tyrosine-specific transport protein) (db:pir1.dat) (mp:42 min) GRECY C64954 Escherichia coli 562 -11533820 224413 tyrp tyrosine-specific transport protein tyrosine (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #341(42.7-43.1 min.)) (nt:orf\_id:o341#7; similar to (swissprot accession) (le:6211) (re:7422) (di:direct) D90832 D90832 g1736569 Escherichia coli 562 -11533820 301053 tyrp tyrosine-specific transport system (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 174 of 400 of the completengenome.) (nt:o403; 99 pct identical to tyrp\_ecoli sw: p18199; cg) (le:1709) (re:2920) (di:direct) AE000284 AE000284 g1788218 Escherichia coli 562 -11533820 5000691042 (de:(ecoli\_1864) (pn:tyrosine-specific transport system) (gn:tyrp) (gtcfc:12.1) (ec:) (tyrp\_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI\_1864 ECOLI\_1864 Escherichia coli 562 10119904

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836807	9137	31293	534	177

Description

6500729963 lysp:cadr:b2156 lysine-specific permease (gtcfc:12.1) (keggfc:14.2) (rileyfc:4.1.1) (db:gtc-escherichia coli) b2156 b2156 Escherichia coli 562 -11533821 7000689359 lysp lysine-specific permease:lysine transport protein (cl:arginine permease) (db:pir2.dat) C64984 C64984 Escherichia coli 562 -11533821 7500955179 lysp lysine specific permease (fn:lysine transport) (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli lysine specific permease (lysp) gene, completeds.) (nt:resistant to lysine analogue thiosine) (le:1517) (re:2986) (di:direct) ECOLYSP M89774 g466778 Escherichia coli 562 -11533821 235032 lysp lysine-specific permease (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 195 of 400 of the completengenome.) (nt:f489; 100 pct identical to lysp\_ecoli sw: p25737;) (le:177) (re:1646) (di:complement) AE000305 AE000305 g1788480 Escherichia coli 562 -11533821 5000691043 (de:(ecoli\_2105) (pn:lysine-specific permease; pleiotropic increase in lysine decarboxylase) (gn:lysp) (gtcfc:12.1) (ec:) (lysp\_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI\_2105 ECOLI\_2105 Escherichia coli 562 10123588

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836813	9138	31294	546	181

Description

6500729964 hisp:b2306 histidine transport atp-binding protein hisp (gtcfc:12.1:5.11) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b2306 b2306 Escherichia coli 562 -11533822 77068 hisp (de:histidine transport atp-binding protein hisp) (db:swissprot) HISP\_ECOLI P07109 ESCHERICHIA COLI 562 -11533822 7000685533 hisp histidine transport protein hisp:histidine permease inner membrane receptor protein p (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) H65002 H65002 Escherichia coli 562 -11533822 224830 histidine transport protein hisp (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #405(52.0-52.3 min.)) (nt:similar to (pir accession number a27835)) (le:13725) (re:14498) (di:complement) D90861 D90861 g1799677 Escherichia coli 562 -11533822 224839 histidine transport protein hisp (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #406(52.2-52.5 min.)) (nt:similar to (pir accession number a27835)) (le:7313) (re:8086) (di:complement) D90862 D90862 g1799687 Escherichia coli 562 -11533822 7500883337 hisp atp-binding component of histidine transport (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 209 of 400 of the completgenome.) (nt:f257; 99 pct identical to hisp\_ecoli sw: p07109) (le:9057) (re:9830) (di:complement) AE000319 AE000319 g1788644 Escherichia coli 562 -11533822 5000691044 (de:(ecoli\_2255) (pn:histidine transport, inner membrane receptor protein p) (gn:hisp) (gtcfc:12.1) (ec:) (hisp\_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI\_2255 ECOLI\_2255 Escherichia coli 562 10120102

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836820	9139	31295	309	102

Description

GTC ORF with score 125 to: (fn:catalyzes conversion of 4-sulfobenzyl alcohol) (db:genpept-bct2) (de:comamonas testosteroni tsar (tsar), toluenesulfonatemethyl-monooxygenase oxygenase component (tsam), toluenesulfonatemethyl-monooxygenase reductase ...



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836821	9140	31296	2241	747

Description

6500729965 hism:b2307 histidine transport system permease protein hism (gtcfc:12.1:11.1:5.11) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b2307 b2307 Escherichia coli 562 -11533823 77066 hism (de:histidine transport system permease protein hism) (db:swissprot) HISM\_ECOLI P20091 ESCHERICHIA COLI 562 -11533823 7000685532 hism histidine permease operon protein m (cl:histidine permease protein m) (db:pir2.dat) B27835 A65003 Escherichia coli 562 -11533823 224840 hism histidine transport system permease protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #406(52.2-52.5 min.)) (nt:similar to (swissprot accession number p20091)) (le:8094) (re:8810) (di:complement) D90862 D90862 g1799688 Escherichia coli 562 -11533823 7500883336 hism histidine transport:membrane protein m (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 209 of 400 of the completegenome.) (nt:f238; residues 1-93 are 100 pct identical to) (le:9838) (re:10554) (di:complement) AE000319 AE000319 g1788645 Escherichia coli 562 -11533823 5000691045 (de:(ecoli\_2256) (pn:histidine transport, membrane protein m) (gn:hism) (gtcfc:12.1) (ec:) (hism\_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI\_2256 ECOLI\_2256 Escherichia coli 562 10019428

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836827	9141	31297	1797	598
<u>Description</u>				
6500729966 hisj:b2309 histidine-binding periplasmic protein hisj:histidine-binding periplasmic protein precursor:hbp (gtcfc:12.1:11.1:5.11) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b2309 b2309 Escherichia coli 562 -11533824 77064 hisj (de:histidine-binding periplasmic protein precursor (hbp)) (db:swissprot) HISJ_ECOLI P39182 ESCHERICHIA COLI 562 -11533824 7000685531 hisj histidine-binding periplasmic protein hisj (cl:lysine-arginine-ornithine-binding protein) (db:pir2.dat) C65003 C65003 Escherichia coli 562 -11533824 224842 hisj histidine-binding periplasmic protein precursor (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #406(52.2-52.5 min.)) (nt:similar to (swissprot accession number p39182)) (le:9583) (re:10365) (di:complement) D90862 D90862 g1799690 Escherichia coli 562 -11533824 7500883335 hisj histidine-binding periplasmic protein of (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 210 of 400 of the completegenome.) (nt:f260; 99 pct identical to hisj_ecoli sw: p39182) (le:75) (re:857) (di:complement) AE000320 AE000320 g1788648 Escherichia coli 562 -11533824 5000691046 (de:(ecoli_2258) (pn:histidine-binding protein of high-affinity histidine transport system) (gn:hisj) (gtcfc:12.1) (ec:) (hisj_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI_2258 ECOLI_2258 Escherichia coli 562 10120106				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836829	9142	31298	420	139
<u>Description</u>				
6500729967 argt:b2310 lysine-arginine-ornithine-binding periplasmic protein precursor:lao-binding protein (gtcfc:12.1:11.1:5.8:5.10) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b2310 b2310 Escherichia coli 562 -11533825 7500877145 argt (de:(lao-binding protein)) (db:swissprot) ARGT_ECOLI P09551 ESCHERICHIA COLI 562 -11533825 7000688963 argt lysine-arginine-ornithine-binding periplasmic protein precursor (cl:lysine-arginine-ornithine-binding protein) (db:pir1.dat) (mp:50 min) JKECT D65003 Escherichia coli 562 -11533825 224843 argt lysine-arginine-ornithine-binding periplasmic (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #406(52.2-52.5 min.).) (nt:similar to (swissprot accession number p09551)) (le:10586) (re:11368) (di:complement) D90862 D90862 g1799691 Escherichia coli 562 -11533825 7500877148 argt lysine-:arginine-:ornithine-binding (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 210 of 400 of the completegenome.) (nt:f260; 97 pct identical to fragment argt_ecoli) (le:1078) (re:1860) (di:complement) AE000320 AE000320 g1788649 Escherichia coli 562 -11533825 5000691047 (de:(ecoli_2259) (pn:lysine-, arginine-, ornithine-binding protein) (gn:argt) (gtcfc:12.1) (ec:) (argt_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI_2259 ECOLI_2259 Escherichia coli 562 10120107				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836830	9143	31299	720	240
<u>Description</u>				
6500729968 prov:b2677 glycine betaine/l-proline transport atp-binding protein prov (gtcfc:12.1:5.3) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b2677 b2677 Escherichia coli 562 -11533826 91217 prov (de:glycine betaine/l-proline transport atp-binding protein prov) (db:swissprot) PROV_ECOLI P14175 ESCHERICHIA COLI 562 -11533826 130731 prov glycine betaine/l-proline transport atp-binding protein prov:nucleotide-binding protein prov (cl:glycine betaine/proline transport protein prov:atp-binding cassette homology:cbs homology) (db:pir1.dat) (mp:57 min) BVECPV JS0128 Escherichia coli 562 -11533826 225232 prov glycine betaine/l-proline transport atp-binding (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #445(60.2-60.6 min.)) (nt:similar to (swissprot accession number p14175)) (le:8287) (re:9489) (di:direct) D90891 D90891 g1800065 Escherichia coli 562 -11533826 7500888560 (sr:e.coli (k12) dna) (db:genpept-bct1) (de:e.coli prov, prow and prox genes (prou operon), complete cds.) (nt:prov peptide) (le:688) (re:1890) (di:direct) ECOPROU M24856 g147373 Escherichia coli 562 -11533826 235566 prov atp-binding component of transport system for (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 242 of 400 of the completegenome.) (nt:o400; cg site no. 18022; 100 pct identical) (le:6016) (re:7218) (di:direct) AE000352 AE000352 g1789032 Escherichia coli 562 -11533826 5000691048 (de:(ecoli_2610) (pn:high-affinity transport system; glycine-betaine-binding protein) (gn:prov) (gtcfc:12.1) (ec:) (prov_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI_2610 ECOLI_2610 Escherichia coli 562 10033316				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836839	9144	31300	777	258

Description

6500729969 prow:b2678 glycine betaine/l-proline transport system permease protein p:glycine betaine/l-proline transport system permease protein prow (gtcfc:12.1:5.3) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b2678 b2678 Escherichia coli 562 -11533827 91219 prow (de:glycine betaine/l-proline transport system permease protein prow) (db:swissprot) PROW\_ECOLI P14176 ESCHERICHIA COLI 562 -11533827 131354 prow glycine betaine/l-proline transport system permease protein p (cl:phot protein) (db:pir1.dat) MMECPW JS0129 Escherichia coli 562 -11533827 225233 prow glycine betaine/proline transport system protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #445(60.2-60.6 min.)) (nt:similar to (pir accession number js0129)) (le:9482) (re:10546) (di:direct) D90891 D90891 g1800066 Escherichia coli 562 -11533827 7500888561 (sr:e.coli (k12) dna) (db:genpept-bct1) (de:e.coli prov, prow and prox genes (prou operon), complete cds.) (nt:prow peptide) (le:1883) (re:2947) (di:direct) ECOPROU M24856 g147374 Escherichia coli 562 -11533827 235567 prow high-affinity transport system for glycine (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 242 of 400 of the completegenome.) (nt:o354; cg site no. 18019; 100 pct identical) (le:7211) (re:8275) (di:direct) AE000352 AE000352 g1789033 Escherichia coli 562 -11533827 5000691049 (de:(ecoli\_2611) (pn:high-affinity transport system for glycine betaine and proline) (gn:prow) (gtcfc:12.1) (ec:) (prow\_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI\_2611 ECOLI\_2611 Escherichia coli 562 10033318

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836854	9145	31301	1719	572

Description

6500729970 sdac:b2796 putative serine transporter:serine transporter  
(gtcfc:12.1:5.3) (keggfc:14.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)  
b2796 b2796 Escherichia coli 562 -11533828 98234 sdac (de:serine  
transporter) (db:swissprot) SDAC\_ECOLI P36559 ESCHERICHIA COLI 562 -11533828  
154712 sdac serine transport protein sdac (cl:threonine-serine permease)  
(db:pir2.dat) S45633 S45633 Escherichia coli 562 -11533828 239370 sdac  
putative serine transporter (db:genpept-bct1) (de:escherichia coli k-12  
putative serine transporter (sdac) gene,complete cds.) (le:803) (re:2092)  
(di:direct) ECU01233 U01233 g402256 Escherichia coli 562 -11533828  
7500891413 sdac putative serine transporter (db:genpept-bct1)  
(de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:cg  
site no. 33329; orf\_o429) (le:9784) (re:11073) (di:direct) ECU29581 U29581  
g882691 Escherichia coli 562 -11533828 238446 sdac probable serine  
transporter (fn:putative transport; transport of small) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 253 of 400 of the completegenome.)  
(nt:o429; 100 pct identical to sdac\_ecoli sw: p36559;) (le:5942) (re:7231)  
(di:direct) AE000363 AE000363 g1789160 Escherichia coli 562 -11533828  
5000691050 (de:(ecoli\_2727) (pn:probable serine transporter) (gn:sdac)  
(gtcfc:12.1) (ec:) (sdac\_ecoli) (keggfc:11.2) (rileyfc:4.1.1)  
(db:gtc-escherichia coli)) ECOLI\_2727 ECOLI\_2727 Escherichia coli 562  
10040113

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836861	9146	31302	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836868	9147	31303	219	72

Description

GTC ORF with score 129 to: (db:genpept-pln2) (de:emerella nidulans  
sterigmatocystin biosynthetic gene cluster:(stca), (stcb), (stcc), (stce),  
(aflr), (stcf), (stci), (stcj), (stck), (stcl), (stco), (stcq), (stcs),  
(stct), (stcu), (stcv) and(stcw) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836869	9148	31304	315	105

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836897	9149	31305	666	221
<u>Description</u>				
6500729971 tdcc:b3116 threonine-serine permease:threonine transporter (gtcfc:12.1:11.1:5.3) (keggfc:14.2) (rileyfc:4.1.1) (db:gtc-escherichia coli) b3116 b3116 Escherichia coli 562 -11533829 100939 tdcc (de:threonine/serine transporter) (db:swissprot) TDCC_ECOLI P11867 ESCHERICHIA COLI 562 -11533829 7000686773 tdcc threonine-serine permease (cl:threonine-serine permease) (db:pir1.dat) (mp:67 min) BVECTC A65101 Escherichia coli 562 -11533829 7500892861 tdcc threonine-serine permease (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 29709; differences from database) (le:44440) (re:45771) (di:complement) ECOUW67 U18997 g606057 Escherichia coli 562 -11533829 236356 tdcc anaerobically inducible l-threonine:l-serine (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 283 of 400 of the completegenome.) (nt:f443; cg site no. 29709; differences from database) (le:4542) (re:5873) (di:complement) AE000393 AE000393 g1789504 Escherichia coli 562 -11533829 5000691051 (de:(ecoli_3041) (pn:anaerobically inducible l-threonine, l-serine permease) (gn:tdcc) (gtcfc:12.1) (ec:) (tdcc_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI_3041 ECOLI_3041 Escherichia coli 562 10042783				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836898	9150	31306	381	126
<u>Description</u>				
6500729972 mtr:b3161 tryptophan-specific permease:tryptophan-specific transport protein:tryptophan permease (gtcfc:12.1:11.1:5.14) (keggfc:14.2) (rileyfc:4.1.1) (db:gtc-escherichia coli) b3161 b3161 Escherichia coli 562 -11533830 84592 mtr (de:tryptophan-specific transport protein (tryptophan permease)) (db:swissprot) MTR_ECOLI P22306 ESCHERICHIA COLI 562 -11533830 164782 mtr tryptophan-specific permease (db:pir2.dat) (mp:69 min) A39187 A39187 Escherichia coli 562 -11533830 235192 mtr tryptophan-specific permease (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli tryptophan-specific permease (mtr) gene, complete cds.) (le:473) (re:1717) (di:direct) ECOMTR M59862 g146894 Escherichia coli 562 -11533830 236400 mtr tryptophan-specific permease (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli mtr tryptophan-specific permease (mtr) gene,complete cds.) (le:694) (re:1938) (di:direct) ECOMTRA M58338 g146896 Escherichia coli 562 -11533830 7500886059 mtr tryptophan-specific permease (fn:5-methyltryptophan resistance) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 478) (le:85325) (re:86569) (di:complement) ECOUW67 U18997 g606101 Escherichia coli 562 -11533830 235191 mtr tryptophan-specific transport protein (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 287 of 400 of the completegenome.) (nt:f414; cg site no. 478; 100 pct identical amino) (le:1196) (re:2440) (di:complement) AE000397 AE000397 g1789552 Escherichia coli 562 -11533830 5000691052 (de:(ecoli_3085) (pn:tryptophan-specific transport protein) (gn:mtr) (gtcfc:12.1) (ec:) (mtr_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI_3085 ECOLI_3085 Escherichia coli 562 10026788				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836921	9151	31307	633	210

Description

6500729973 bfr:b3336 bacterioferritin:bfr:cytochrome b-1:cytochrome b-557 (gtcfc:12.1) (keggfc:14.2) (rileyfc:4.1.1) (db:gtc-escherichia coli) b3336 b3336 Escherichia coli 562 -11533831 61608 bfr (de:bacterioferritin (bfr) (cytochrome b-1) (cytochrome b-557)) (db:swissprot) BFR\_ECOLI P11056 ESCHERICHIA COLI 562 -11533831 130375 bfr bacterioferritin:cytochrome b1 (cl:bacterioferritin) (db:pir1.dat) (mp:73 min) FREC JV0032 Escherichia coli 562 -11533831 236569 bfr bacterioferritin (db:genpept-bct1) (de:e. coli (clones lambda-(g206,9h3), subclones pgs-(275,277,280,281)) glycoprotein 24' (gen24) gene, 3' end; glycoprotein 64(gen64) and bacterioferritin (bfr) genes, complete cds; type 4prepilin-like protein specific leader peptidas... ECOBFR M27176 g145409 Escherichia coli 562 -11533831 7500877778 bfr bacterioferritin (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (le:246997) (re:247473) (di:complement) ECOUW67 U18997 g606270 Escherichia coli 562 -11533831 233898 bfr bacterioferritin:an iron storage homoprotein (fn:carrier; transport of small molecules: cations) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 299 of 400 of the completegenome.) (nt:f158; 100 pct identical amino acid sequence and) (le:12890) (re:13366) (di:complement) AE000409 AE000409 g1789733 Escherichia coli 562 -11533831 5000691053 (de:(ecoli\_3254) (pn:bacterioferri, an iron storage homoprotein) (gn:bfr) (gtcfc:12.1) (ec:) (bfr\_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI\_3254 ECOLI\_3254 Escherichia coli 562 10004317

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836931	9152	31308	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836937	9153	31309	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836938	9154	31310	387	128

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836941	9155	31311	930	310

Description

6500729974 livf:b3454 high-affinity branched-chain amino acid transport atp-binding:high-affinity branched-chain amino acid transport atp-binding protein livf:liv-i protein f (gtcfc:12.1) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b3454 b3454 Escherichia coli 562 -11533832 163991 livf leucine transport protein livf (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) S47673 S47673 Escherichia coli 562 -11533832 7500955229 livf (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:6986) (re:7711) (di:complement) ECOUW76 U00039 g912456 Escherichia coli 562 -11533832 236689 livf atp-binding component of leucine transport (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 311 of 400 of the completegenome.) (nt:f241; 100 pct identical to 237 amino acids) (le:8277) (re:9002) (di:complement) AE000421 AE000421 g1789863 Escherichia coli 562 -11533832 5000691054 (de:(ecoli\_3372) (pn:leucine transport protein) (gn:livf) (gtcfc:12.1) (ec: (livf\_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI\_3372 ECOLI\_3372 Escherichia coli 562 10087120

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836951	9156	31312	912	303

Description

6500729975 livg:b3455 high-affinity branched-chain amino acid transport atp-binding protein livg:liv-i protein g (gtcfc:12.1) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b3455 b3455 Escherichia coli 562 -11533833 82243 livg (de:livg (liv-i protein g)) (db:swissprot) LIVG\_ECOLI P22730 ESCHERICHIA COLI 562 -11533833 236690 livg (fn:high-affinity branched chain amino acid) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 553; membrane component) (le:7701) (re:846... ECOUW76 U00039 g466591 Escherichia coli 562 -11533833 7500885072 livg atp-binding component of high-affinity (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 311 of 400 of the completegenome.) (nt:f255; 100 pct identical to livg\_ecoli sw: p22730;) (le:8992) (re:9759) (di:complement) AE000421 AE000421 g1789864 Escherichia coli 562 -11533833 164005 (de:livg protein - escherichia coli) S47674 S47674 Escherichia coli 562 -11533833 5000691055 (de:(ecoli\_3373) (pn:high-affinity branched-chain amino acid transport system) (gn:livg) (gtcfc:12.1) (ec: (livg\_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI\_3373 ECOLI\_3373 Escherichia coli 562 10024473

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836954	9157	31313	1293	430

#### Description

6500729976 livm:b3456 high-affinity branched-chain amino acid transport permease protein livm:liv-i protein m (gtcfc:12.1) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b3456 b3456 Escherichia coli 562 -11533834 82252 livm (de:livm (liv-i protein m)) (db:swissprot) LIVM\_ECOLI P22729 ESCHERICHIA COLI 562 -11533834 164006 livm leucine transport protein livm (db:pir2.dat) S47675 S47675 Escherichia coli 562 -11533834 7500885076 livm (fn:high-affinity branched chain amino acid) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 18190) (le:8465) (re:9742) (di:complement) ECOUW76 U00039 g466592 Escherichia coli 562 -11533834 236691 livm high-affinity branched-chain amino acid (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 311 of 400 of the completegenome.) (nt:f425; 100 pct identical to livm\_ecoli sw: p22729;) (le:9756) (re:11033) (di:complement) AE000421 AE000421 g1789865 Escherichia coli 562 -11533834 5000691056 (de:(ecoli\_3374) (pn:high-affinity branched-chain amino acid transport) (gn:livm) (gtcfc:12.1) (ec:) (livm\_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI\_3374 ECOLI\_3374 Escherichia coli 562 10024482

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836965	9158	31314	318	105

#### Description

6500729977 livh:b3457 high-affinity branched-chain amino acid transport permease protein livh:liv-i protein h (gtcfc:12.1:11.1) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b3457 b3457 Escherichia coli 562 -11533835 154814 livh leucine transport protein livh (cl:leucine transport protein livh) (db:pir1.dat) (mp:76 min) QRECLH S47676 Escherichia coli 562 -11533835 7500953666 livh (fn:high-affinity branched chain amino acid) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 552; membrane component) (le:9739) (re:106... ECOUW76 U00039 g466593 Escherichia coli 562 -11533835 236692 livh high-affinity branched-chain amino acid (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 311 of 400 of the completegenome.) (nt:f308; 99 pct identical amino acid sequence and) (le:11030) (re:11956) (di:complement) AE000421 AE000421 g1789866 Escherichia coli 562 -11533835 5000691057 (de:(ecoli\_3375) (pn:high-affinity branched-chain amino acid transport system; membrane component) (gn:livh) (gtcfc:12.1) (ec:) (livh\_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI\_3375 ECOLI\_3375 Escherichia coli 562 10081718

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836972	9159	31315	756	251

#### Description

6500729978 livk:b3458 leucine-specific binding protein precursor:ls-bp:l-bp (gtcfc:12.1:12.6) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b3458 b3458 Escherichia coli 562 -11533836 7000688968 livk leucine-specific binding protein precursor:ls-binding protein precursor (cl:liv-binding protein) (db:pir1.dat) (mp:76 min) BLECL E65142 Escherichia coli 562 -11533836 7500953609 livk (fn:transport system) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 550; leucine-specific periplasmic) (le:10713) (re:11822) (di:comp... ECOUW76 U00039 g466594 Escherichia coli 562 -11533836 236693 livk high-affinity leucine-specific transport system (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 311 of 400 of the completengenome.) (nt:f369; 99 pct identical amino acid sequence and) (le:12004) (re:13113) (di:complement) AE000421 AE000421 g1789867 Escherichia coli 562 -11533836 5000691058 (de:(ecoli\_3376) (pn:high-affinity leucine-specific transport system; periplasmic binding protein) (gn:livk) (gtcfc:12.1) (ec:) (livk\_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI\_3376 ECOLI\_3376 Escherichia coli 562 10124036

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836973	9160	31316	324	107

#### Description

6500729979 livj:b3460 leu/ile/val-binding protein precursor (gtcfc:12.1:12.6) (keggfc:11.1) (rileyfc:4.1.1) (db:gtc-escherichia coli) b3460 b3460 Escherichia coli 562 -11533837 7000688967 livj leucine/isoleucine/valine-binding protein precursor:leucine transport protein livj precursor:liv-binding protein (cl:liv-binding protein) (db:pir1.dat) (mp:76 min) BLEC G65142 Escherichia coli 562 -11533837 7500953608 livj (fn:transport system) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 551; periplasmic binding protein for) (le:12817) (re:13977) (di:c... ECOUW76 U00039 g912457 Escherichia coli 562 -11533837 236695 livj high-affinity amino acid transport system (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 312 of 400 of the completengenome.) (nt:f386; 99 pct identical to 367 amino acids) (le:675) (re:1835) (di:complement) AE000422 AE000422 g1789870 Escherichia coli 562 -11533837 5000691059 (de:(ecoli\_3378) (pn:high-affinity amino acid transport system; periplasmic binding protein) (gn:livj) (gtcfc:12.1) (ec:) (livj\_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI\_3378 ECOLI\_3378 Escherichia coli 562 10124037

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501836975	9161	31317	423	140
<u>Description</u>				
6500729980 glts:gltc:b3653 sodium/glutamate symport carrier protein:glutamate permease (gtcfc:12.1) (keggfc:14.2) (rileyfc:4.1.1) (db:gtc-escherichia coli) b3653 b3653 Escherichia coli 562 -11533838 233016 glts:gltc (de:sodium/glutamate symport carrier protein (glutamate permease)) (db:swissprot) GLTS_ECOLI P19933 ESCHERICHIA COLI 562 -11533838 153004 glts sodium--glutamate symport carrier protein:glutamate permease (cl:sodium--glutamate symport carrier protein) (db:pir1.dat) (mp:82 min) YOECNQ G65166 Escherichia coli 562 -11533838 5000691060 glts glts protein (db:genpept-bct1) (de:e. coli glts gene.) (le:300) (re:1505) (di:direct) ECGLTS X17499 g41593 Escherichia coli 562 -11533838 236891 glts::cg site no. 681 glutamate permease (sr:escherichia coli k12 strain mg1655; lambda clones ecl4-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:16852) (re:18057) (di:complement) ECOUW82 L10328 g290503 Escherichia coli 562 -11533838 7500882564 glts glutamate transport (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 332 of 400 of the completegenome.) (nt:f401; 100 pct identical amino acid sequence and) (le:8851) (re:10056) (di:complement) AE000442 AE000442 g1790085 Escherichia coli 562 -11533838 7502851972 glts glutamate permease (db:genpept) (de:pga(+)) positive selection cloning vector glts gene.) (le:852) (re:2057) (di:direct) ASAJ5325 AJ005325 g4028983 synthetic construct 32630 -11533838 7502851973 glts glutamate permease (db:genpept) (de:pga(-)) positive selection cloning vector glts gene.) (le:1150) (re:2355) (di:complement) ASAJ5328 AJ005328 g4028989 synthetic construct 32630 -11533838 7502851974 glts glutamate permease (db:genpept) (de:pcpl(-)) positive selection cloning vector glts gene.) (le:386) (re:1591) (di:direct) PPA005339 AJ005339 g4029313 synthetic construct 32630 -11533838 74131 glts:gltc (de:sodium/glutamate symport carrier protein (glutamate permease)) (db:swissprot) GLTS_ECOLI P19933 ESCHERICHIA COLI 562 -11533838 7000685429 glts sodium--glutamate symport carrier protein:glutamate permease (cl:sodium--glutamate symport carrier protein) (db:pir) (mp:82 min) YOECNQ A36524 Escherichia coli 562 -11533838				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836997	9162	31318	693	230
<u>Description</u>				
6500729981 ttab:trpp:b3709 low affinity tryptophan permease (gtcfc:12.1) (keggfc:14.2) (rileyfc:4.1.1) (db:gtc-escherichia coli) b3709 b3709 Escherichia coli 562 -11533839 101682 ttab:trpp (de:low affinity tryptophan permease) (db:swissprot) TNAB_ECOLI P23173 ESCHERICHIA COLI 562 -11533839 164783 ttab tryptophan transport protein ttab:low affinity tryptophan permease (db:pir2.dat) A39412 A39412 Escherichia coli 562 -11533839 236945 tnab low affinity tryptophan permease (sr:e.coli dna) (db:genpept-bct1) (de:e.coli low affinity tryptophan permease (tnab) gene, complete cds.) (le:1) (re:1248) (di:direct) ECOTNAB M59914 g148003 Escherichia coli 562 -11533839 7500893231 ttab low affinity tryptophan permease (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:alternate gene name trpp) (le:79633) (re:80880) (di:direct) ECOUW82 L10328 g290557 Escherichia coli 562 -11533839 236111 ttab low affinity tryptophan permease (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 338 of 400 of the completegenome.) (nt:o415; 100 pct identical to ttab_ecoli sw: p23173;) (le:1953) (re:3200) (di:direct) AE000448 AE000448 g1790145 Escherichia coli 562 -11533839 5000691061 (de:(ecoli_3627) (pn:low affinity tryptophan permease) (gn:tnab) (gtcfc:12.1) (ec:) (tnab_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI_3627 ECOLI_3627 Escherichia coli 562 10043514				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836998	9163	31319	351	116

Description

6500729982 gltp:b4077 glutamate-aspartate carrier:proton glutamate symport protein:glutamate-aspartate carrier protein (gtcfc:12.1) (keggfc:14.2) (rileyfc:4.1.1) (db:gtc-escherichia coli) b4077 b4077 Escherichia coli 562 -11533840 74129 gltp (de:protein)) (db:swissprot) GLTP\_ECOLI P21345 ESCHERICHIA COLI 562 -11533840 163126 gltp glutamate-aspartate carrier protein:proton glutamate symport protein (db:pir2.dat) A42384 Escherichia coli 562 -11533840 237283 gltp proton-glutamate (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli proton glutamate (gltp) protein, complete cds.) (le:151) (re:1464) (di:direct) ECOPG M84805 g147160 Escherichia coli 562 -11533840 235395 gltp glutamate-aspartate symport protein (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 371 of 400 of the completegenome.) (nt:o437; 100 pct identical amino acid sequence and) (le:3039) (re:4352) (di:direct) AE000481 AE000481 g1790514 Escherichia coli 562 -11533840 7500882563 gltp (fn:glutamate and aspartate carrier) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:159721) (re:161034) (di:direct) ECOUW89 U00006 g396412 Escherichia coli 562 -11533840 5000691062 gltp glutamate-aspartate symport protein (fn:transport; transport of small molecules: amino) (db:genpept) (de:escherichia coli k-12 mg1655 section 371 of 400 of the completegenome.) (nt:o437; 100 pct identical amino acid sequence and) (le:3039) (re:4352) (di:direct) AE000481 AE000481 g1790514 Escherichia coli 562 -11533840

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501836999	9164	31320	714	237
<u>Description</u>				
6500729983 prop:b4111 proline/betaine transporter:proline porter ii:ppii (gtcfc:12.1:5.10) (keggfc:14.2) (rileyfc:4.1.1) (db:gtc-escherichia coli) b4111 b4111 Escherichia coli 562 -11533841 91211 prop (de:proline/betaine transporter (proline porter ii) (ppii)) (db:swissprot) PROP_ECOLI P30848 ESCHERICHIA COLI 562 -11533841 154876 prop proline/betaine transport protein:proline permease ii:proline porter ii (cl:citrate utilization determinant) (db:pir2.dat) (mp:93 min) S32331 S32331 Escherichia coli 562 -11533841 237319 prop a proline/betaine transporter (fn:active uptake of proline or betaine) (db:genpept-bct1) (de:e. coli proline/betaine transporter (prop) gene, complete cds.) (nt:evidence that this open reading frame encodes a) (le:433) (re:1935) (di:direct) ECOPROBETT M83089 g147357 Escherichia coli 562 -11533841 7500888558 prop (fn:active uptake of proline or betaine) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 361) (le:21331) (re:22833) (di:direct) ECOUW93 U14003 g536955 Escherichia coli 562 -11533841 235557 prop low-affinity transport system:proline permease (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 373 of 400 of the completegenome.) (nt:o500; 100 pct identical to prop_ecoli sw: p30848;) (le:5301) (re:6803) (di:direct) AE000483 AE000483 g1790550 Escherichia coli 562 -11533841 5000691063 (de:(ecoli_3997) (pn:low-affinity transport system; proline permease ii) (gn:prop) (gtcfc:12.1) (ec:) (prop_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI_3997 ECOLI_3997 Escherichia coli 562 10033310				



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837000	9165	31321	846	282

Description

6500729984 cadb:b4132 probable cadaverine/lysine antiporter (gtcfc:12.1) (keggfc:14.2) (rileyfc:4.1.1) (db:gtc-escherichia coli) b4132 b4132  
Escherichia coli 562 -11533842 62416 cadb (de:probable cadaverine/lysine antiporter) (db:swissprot) CADB\_ECOLI P23891 ESCHERICHIA COLI 562 -11533842 164016 cadb lysine/cadaverine antiporter membrane protein cadb (cl:l-lysine transport protein) (db:pir2.dat) A41842 A41842 Escherichia coli 562 -11533842 233932 cadb (sr:e.coli k-12 dna, clones lambda-(5g7, 21h11)) (db:genpept-bct1) (de:escherichia coli lysine decarboxylase (cadb, and cadc, completecds, and cada, 5' end) genes.) (le:2775) (re:4109) (di:direct) ECOCADAB M67452 g145453 Escherichia coli 562 -11533842 237341 cadb (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli cada gene, 5' cds and cadb and cadc genes, complete cds.) (le:499) (re:1833) (di:direct) ECOCADABC M76411 g145457 Escherichia coli 562 -11533842 7500878079 cadb (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:49525) (re:50859) (di:complement) ECOUW93 U14003 g536977 Escherichia coli 562 -11533842 233929 cadb transport of lysine/cadaverine (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 376 of 400 of the completegenome.) (nt:f444; 100 pct identical to cadb\_ecoli sw: p23891) (le:70) (re:1404) (di:complement) AE000486 AE000486 g1790575 Escherichia coli 562 -11533842 5000691064 (de:(ecoli\_4019) (pn:transport of lysine) (gn:cadb) (gtcfc:12.1) (ec:) (cadb\_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI\_4019 ECOLI\_4019 Escherichia coli 562 10005114

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837001	9166	31322	390	129
<u>Description</u>				
6500729985 cyca:daga:b4208 d-serine/d-alanine/glycine transporter (gtcfc:12.1:5.2:5.3) (keggfc:14.2) (rileyfc:4.1.1) (db:gtc-escherichia coli) b4208 b4208 Escherichia coli 562 -11533843 67345 cyca:daga (de:d-serine/d-alanine/glycine transporter) (db:swissprot) CYCA_ECOLI P39312 ESCHERICHIA COLI 562 -11533843 163846 cyca d-serine/d-alanine/glycine transporter (cl:arginine permease) (db:pir2.dat) S56433 S56433 Escherichia coli 562 -11533843 7500879822 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o470) (le:120696) (re:122108) (di:direct) ECOUW93 U14003 g537049 Escherichia coli 562 -11533843 237413 cyca transport of d-alanine:d-serine:and glycine (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 382 of 400 of the completegenome.) (nt:o470; 100 pct identical amino acid sequence and) (le:2436) (re:3848) (di:direct) AE000492 AE000492 g1790653 Escherichia coli 562 -11533843 5000691065 (de:(ecoli_4091) (pn:transport of d-alanine, d-serine, and glycine) (gn:cyca) (gtcfc:12.1) (ec:) (cyca_ecoli) (keggfc:11.2) (rileyfc:4.1.1) (db:gtc-escherichia coli)) ECOLI_4091 ECOLI_4091 Escherichia coli 562 10009955				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837016	9167	31323	1149	383
<u>Description</u>				
6500729986 beti:b0313 regulatory protein beti (gtcfc:12.11) (keggfc:14.2) (rileyfc:4.6.0) (db:gtc-escherichia coli) b0313 b0313 Escherichia coli 562 -11533844 7500877761 beti (de:regulatory protein beti) (db:swissprot) BETI_ECOLI P17446 ESCHERICHIA COLI 562 -11533844 162786 beti regulatory protein beti (db:pir2.dat) (mp:7.5 min) S10899 S15180 Escherichia coli 562 -11533844 5000691066 (db:genpept-bct1) (de:escherichia coli bett, beti, betb and beta genes.) (nt:beti gene product (aa 1-195)) (le:3416) (re:4003) (di:direct) ECBET X52905 g48717 Escherichia coli 562 -11533844 232446 beti probably transcriptional repressor of bet genes (fn:putative regulator; osmotic adaptation) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 28 of 400 of the completegenome.) (nt:f195; 100 pct identical to beti_ecoli sw: p17446) (le:4119) (re:4706) (di:complement) AE000138 AE000138 g1786505 Escherichia coli 562 -11533844 61588 beti (de:regulatory protein beti) (db:swissprot) BETI_ECOLI P17446 ESCHERICHIA COLI 562 -11533844				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837045	9168	31324	612	204
<u>Description</u>				
6500729987 mdog:b1048 periplasmic glucans biosynthesis protein mdog precursor (gtcfc:12.11) (keggfc:14.2) (rileyfc:4.6.0) (db:gtc-escherichia coli) b1048 b1048 Escherichia coli 562 -11533845 7500885443 mdog (de:periplasmic glucans biosynthesis protein mdog precursor) (db:swissprot) MDOG_ECOLI P33136 ESCHERICHIA COLI 562 -11533845 164053 mdog glucans biosynthesis protein g precursor:periplasmic (cl:periplasmic glucans biosynthesis protein mdog) (db:pir2.dat) S35417 S35417 Escherichia coli 562 -11533845 223339 mdog mdog protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #232) (db:genpept-bct1) (de:escherichia coli genomic dna. (23.7 - 24.1 min).) (le:5955) (re:7490) (di:direct) D90742 D90742 g1651515 Escherichia coli 562 -11533845 5000691067 mdog (db:genpept-bct1) (de:e.coli mdogh gene.) (le:423) (re:1958) (di:direct) ECMDOGH X64197 g396490 Escherichia coli 562 -11533845 233365 mdog periplasmic glucans biosynthesis protein (fn:enzyme; osmotic adaptation) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 96 of 400 of the completegenome.) (nt:o511; 100 pct identical to mdog_ecoli sw: p33136) (le:3593) (re:5128) (di:direct) AE000206 AE000206 g1787286 Escherichia coli 562 -11533845 7502851975 mdog mdog protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #232) (db:genpept) (de:escherichia coli genomic dna. (23.8 - 24.2 min).) (nt:orf_id:o232#6; similar to pir accession number) (le:5955) (re:7490) (di:direct) D90742 D90742 g1651515 Escherichia coli 562 -11533845 83349 mdog (de:periplasmic glucans biosynthesis protein mdog precursor) (db:swissprot) MDOG_ECOLI P33136 ESCHERICHIA COLI 562 -11533845				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837048	9169	31325	276	91

Description

6500729988 mdoh:b1049 periplasmic glucans biosynthesis protein mdoh (gtcfc:12.11) (keggfc:14.2) (rileyfc:4.6.0) (db:gtc-escherichia coli) b1049 b1049 Escherichia coli 562 -11533846 83350 mdoh (de:periplasmic glucans biosynthesis protein mdoh) (db:swissprot) MDOH\_ECOLI P33137 ESCHERICHIA COLI 562 -11533846 7000685809 mdoh glucan biosynthesis protein h (db:pir2.dat) F64847 F64847 Escherichia coli 562 -11533846 223340 mdoh mdoh protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #232) (db:genpept-bct1) (de:escherichia coli genomic dna. (23.7 - 24.1 min).) (le:7483) (re:10026) (di:direct) D90742 D90742 g1651516 Escherichia coli 562 -11533846 7500885444 mdoh membrane glycosyltransferase:synthesis of (fn:enzyme; osmotic adaptation) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 96 of 400 of the completegenome.) (nt:o847; 99 pct identical to mdoh\_ecoli sw: p33137) (le:5121) (re:7664) (di:direct) AE000206 AE000206 g1787287 Escherichia coli 562 -11533846 5000691068 mdoh mdoh protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #232) (db:genpept) (de:escherichia coli genomic dna. (23.8 - 24.2 min).) (nt:orf\_id:o232#8; similar to pir accession number) (le:7483) (re:10026) (di:direct) D90742 D90742 g1651516 Escherichia coli 562 -11533846

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837063	9170	31326	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837067	9171	31327	288	95

Description

6500729989 osmb:b1283 osmotically inducible lipoprotein b precursor  
(gtcf:12.11:11.1) (keggfc:14.2) (rileyfc:4.6.0) (db:gtc-escherichia coli)  
b1283 b1283 Escherichia coli 562 -11533847 87909 osmb (de:osmotically  
inducible lipoprotein b precursor) (db:swissprot) OSMB\_ECOLI P17873  
ESCHERICHIA COLI 562 -11533847 130875 osmb lipoprotein b  
precursor:osmotically inducible (cl:osmotically inducible lipoprotein omsb)  
(db:pir1.dat) (mp:28 min) LPECOB A32255 Escherichia coli 562 -11533847  
223511 osmb lipoprotein osmb precursor:osmotically (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #255(28.8-29.2 min.))  
(nt:orf\_id:o255#8; similar to (pir accession number) (le:5375) (re:5593)  
(di:complement) D90766 D90766 g1742097 Escherichia coli 562 -11533847  
300314 osmb (sr:e.coli (strain k12; mph2) dna, clones ptz(18u,19u))  
(db:genpept-bct1) (de:e.coli osmb gene encoding osmb protein, complete cds.)  
(le:304) (re:522) (di:direct) ECOOSMB M22859 g147040 Escherichia coli 562  
-11533847 235314 osmb osmotically inducible lipoprotein (fn:putative  
membrane; osmotic adaptation) (db:genpept-bct2) (de:escherichia coli k-12  
mg1655 section 116 of 400 of the completegenome.) (nt:f72; 100 pct identical  
to osmb\_ecoli sw: p17873; cg) (le:4602) (re:4820) (di:complement) AE000226  
AE000226 g1787539 Escherichia coli 562 -11533847 5000691069  
(de:(ecoli\_1243) (pn:osmotically inducible lipoprotein) (gn:osmb)  
(gtcf:12.11) (ec:) (osmb\_ecoli) (keggfc:11.2) (rileyfc:4.6.0)  
(db:gtc-escherichia coli)) ECOLI\_1243 ECOLI\_1243 Escherichia coli 562  
10030050

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837070	9172	31328	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501837073	9173	31329	255	84

# Description

6500729990 osmc:b1482 osmotically inducible protein c (gtcfc:12.11) (keggfc:14.2) (rileyfc:4.6.0) (db:gtc-escherichia coli) b1482 b1482 Escherichia coli 562 -11533848 7000686061 osmc protein c:osmotically inducible (cl:hypothetical protein ykla) (db:pir2.dat) E64901 E64901 Escherichia coli 562 -11533848 223804 osmc osmc protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #277(33.2-33.6 min.)) (nt:orf\_id:o277#12; similar to (pir accession number) (le:14429) (re:14860) (di:direct) D90788 D90788 g1742412 Escherichia coli 562 -11533848 223813 osmc osmc protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #278(33.3-33.7 min.)) (nt:orf\_id:o277#12; similar to (pir accession number) (le:10805) (re:11236) (di:direct) D90789 D90789 g1742422 Escherichia coli 562 -11533848 300560 osmc osmc protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #279(33.5-33.9 min.)) (nt:orf\_id:o277#12; similar to (pir accession number) (le:2908) (re:3339) (di:direct) D90790 D90790 g1742433 Escherichia coli 562 -11533848 300556 osmc osmotically inducible protein (fn:phenotype; osmotic adaptation) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 135 of 400 of the completegenome.) (nt:ol43; 100 pct identical to osmc\_ecoli sw:) (le:3861) (re:4292) (di:direct) AE000245 AE000245 g1787757 Escherichia coli 562 -11533848 87911 osmc (de:osmotically inducible protein c) (db:swissprot) OSMC\_ECOLI P23929 ESCHERICHIA COLI 562 -11533848 223823 osmc osmc protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #279(33.5-33.9 min.)) (nt:orf\_id:o277#12; similar to (pir accession number) (le:2908) (re:3339) (di:direct) D90790 D90790 g1742433 Escherichia coli 562 -11533848 5000691070 (de:(ecoli\_1442) (pn:osmotically inducible protein) (gn:osmc) (gtcfc:12.11) (ec:) (osmc\_ecoli) (keggfc:11.2) (rileyfc:4.6.0) (db:gtc-escherichia coli)) ECOLI\_1442 ECOLI\_1442 Escherichia coli 562 10119636

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837075	9174	31330	483	160
<u>Description</u>				
6500729991 prox:prou:b2679 glycine betaine-binding periplasmic protein precursor (gtcfc:12.11:12.6) (keggfc:11.1) (rileyfc:4.6.0) (db:gtc-escherichia coli) b2679 b2679 Escherichia coli 562 -11533849 91221 prox:prou (de:glycine betaine-binding periplasmic protein precursor) (db:swissprot) PROX_ECOLI P14177 ESCHERICHIA COLI 562 -11533849 130777 prox glycine betaine/proline transport system binding protein prox precursor (cl:glycine betaine and proline transport system binding protein prox) (db:pir1.dat) BLECGP JS0130 Escherichia coli 562 -11533849 225234 prou glycine betaine-binding periplasmic protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #445(60.2-60.6 min.)) (nt:similar to (swissprot accession number p14177)) (le:10604) (re:11596) (di:direct) D90891 D90891 g1800067 Escherichia coli 562 -11533849 7500888562 (sr:e.coli (k12) dna) (db:genpept-bct1) (de:e.coli prov, prow and prox genes (prou operon), complete cds.) (nt:prox peptide precursor) (le:3005) (re:3997) (di:direct) ECOPROU M24856 g147375 Escherichia coli 562 -11533849 235568 prox high-affinity transport system for glycine (fn:transport; osmotic adaptation) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 242 of 400 of the completegenome.) (nt:o330; 100 pct identical to prox_ecoli sw: p14177;) (le:8333) (re:9325) (di:direct) AE000352 AE000352 g1789034 Escherichia coli 562 -11533849 5000691071 (de:(ecoli_2612) (pn:high-affinity transport system for glycine betaine and proline) (gn:prox) (gtcfc:12.11) (ec:) (prox_ecoli) (keggfc:11.2) (rileyfc:4.6.0) (db:gtc-escherichia coli)) ECOLI_2612 ECOLI_2612 Escherichia coli 562 10033320				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837076	9175	31331	1038	345

Description

6500729992 trer:b4241 trehalose operon repressor (gtcfc:12.11) (keggfc:14.2) (rileyfc:4.6.0) (db:gtc-escherichia coli) b4241 b4241 Escherichia coli 562 -11533850 102168 trer (de:trehalose operon repressor) (db:swissprot) TRER\_ECOLI P36673 ESCHERICHIA COLI 562 -11533850 164478 trer regulatory protein trer:trehalose operon repressor (db:pir2.dat) S56467 S56467 Escherichia coli 562 -11533850 295126 trer repressor protein (db:genpept-bct1) (de:escherichia coli k12 repressor protein (trer) gene, complete cds.) (le:155) (re:1102) (di:direct) ECOTRER U07790 g1843456 Escherichia coli 562 -11533850 7500893382 trer (fn:regulatory gene for trebc operon) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:157128) (re:158075) (di:complement) ECOUW93 U14003 g537083 Escherichia coli 562 -11533850 237447 trer repressor of trea:b:c (fn:regulator; osmotic adaptation) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 385 of 400 of the completegenome.) (nt:f315; 100 pct identical amino acid sequence and) (le:6941) (re:7888) (di:complement) AE000495 AE000495 g1790689 Escherichia coli 562 -11533850 5000691072 (de:(ecoli\_4124) (pn:repressor of trea,b,c) (gn:trer) (gtcfc:12.11) (ec:) (trer\_ecoli) (keggfc:11.2) (rileyfc:4.6.0) (db:gtc-escherichia coli)) ECOLI\_4124 ECOLI\_4124 Escherichia coli 562 10043988

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837080	9176	31332	471	157

Description

6500729993 osmy:b4376 periplasmic protein:osmotically inducible protein y precursor (gtcfc:12.11:11.1) (keggfc:14.2) (rileyfc:4.6.0) (db:gtc-escherichia coli) b4376 b4376 Escherichia coli 562 -11533851 87914 osmy (de:osmotically inducible protein y precursor) (db:swissprot) OSMY\_ECOLI P27291 ESCHERICHIA COLI 562 -11533851 163228 osmy hyperosmotically inducible periplasmic protein osmy:csi-5 (db:pir2.dat) A41899 A41899 Escherichia coli 562 -11533851 237581 periplasmic protein (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli k-12 periplasmic protein gene, complete cds.) (nt:hyperosmotically induced periplasmic protein with) (le:366) (re:971) (di:direct) ECOOPERPLAS M89635 g147148 Escherichia coli 562 -11533851 7500887375 osmy periplasmic protein (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:302227) (re:302832) (di:direct) ECOUW93 U14003 g537216 Escherichia coli 562 -11533851 235389 osmy hyperosmotically inducible periplasmic protein (fn:phenotype; osmotic adaptation) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 398 of 400 of the completegenome.) (nt:o201; 100 pct identical amino acid sequence and) (le:2044) (re:2649) (di:direct) AE000508 AE000508 g1790836 Escherichia coli 562 -11533851 5000691074 (de:(ecoli\_4258) (pn:hyperosmotically inducible periplasmic protein) (gn:osmy) (gtcfc:12.11) (ec:) (osmy\_ecoli) (keggfc:11.2) (rileyfc:4.6.0) (db:gtc-escherichia coli)) ECOLI\_4258 ECOLI\_4258 Escherichia coli 562 10030055

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501837082	9177	31333	498	165

# Description

6500729994 ahpc:b0605 alkyl hydroperoxide reductase c22  
protein:scrp-23:sulfate starvation-induced protein 8:ssi8 (gtcfc:12.12)  
(ec:1.6.4.-) (keggfc:14.1) (rileyfc:4.7.0) (db:gtc-escherichia coli) b0605  
b0605 Escherichia coli 562 -11533852 7000689041 ahpc alkyl hydroperoxide  
reductase:c22 protein:sulfate starvation-induced protein ssi8 (cl:alkyl  
hydroperoxide reductase c22 protein:alkyl hydroperoxidase c22 protein  
homology) (ec:1.6.4.-) (db:pir2.dat) JN0289 C64794 Escherichia coli 562  
-11533852 240119 ahpc alkyl hydroperoxide reductase small subunit  
(sr:escherichia coli (sub\_strain w3110, strain k-12) (library: kohara')  
(db:genpept-bct1) (de:escherichia coli genes for alkyl hydroperoxide  
reductase smallsubunit and large subunit, complete and partial cds.)  
(le:195) (re:758) (di:direct) ECOAHPF D13187 g216543 Escherichia coli 562  
-11533852 7500953895 ahpc alkyl hydroperoxide reductase c22  
(db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.)  
(le:79576) (re:80139) (di:direct) ECU82598 U82598 g1778523 Escherichia coli  
562 -11533852 233751 ahpc alkyl hydroperoxide reductase:c22 subunit  
(fn:enzyme; detoxification) (db:genpept-bct2) (ec:1.6.4.-) (de:escherichia  
coli k-12 mg1655 section 56 of 400 of the completegenome.) (nt:ol87; 100 pct  
identical to ahpc\_ecoli sw: p26427) (le:2333) (re:2896) (di:direct) AE000166  
AE000166 g1786822 Escherichia coli 562 -11533852 5000691075 ahpc alkyl  
hydroperoxide reductase c22 protein ec (sr:escherichia coli(strain:k12) dna,  
clone:kohara clone #166) (db:genpept) (de:escherichia coli genomic dna.  
(13.6 - 14.0 min).) (nt:orf\_id:ol67#1; similar to swissprot accession)  
(le:8702) (re:9265) (di:direct) D90701 D90701 g4062222 Escherichia coli 562  
-11533852 7502851976 ahpc alkyl hydroperoxide reductase c22 protein ec  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #167) (db:genpept)  
(de:escherichia coli genomic dna. (13.7 - 14.1 min).) (nt:orf\_id:ol67#1;  
similar to swissprot accession) (le:886) (re:1449) (di:direct) D90702 D90702  
g4062228 Escherichia coli 562 -11533852

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837084	9178	31334	507	168

Description

6500729995 ahpf:b0606 alkyl hydroperoxide reductase f52a protein (gtcfc:12.12) (ec:1.6.4.-) (keggfc:14.1) (rileyfc:4.7.0) (db:gtc-escherichia coli) b0606 b0606 Escherichia coli 562 -11533853 7000690854 ahpf alkyl hydroperoxide reductase:f52a protein (cl:nadh oxidase (hydrogen peroxide-forming):thioredoxin reductase homology) (ec:1.6.4.-) (db:pir2.dat) D64794 D64794 Escherichia coli 562 -11533853 7500953893 ahpf homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to s. typhimurium ahpf) (le:80353) (re:81948) (di:direct) ECU82598 U82598 g1778524 Escherichia coli 562 -11533853 240120 ahpf alkyl hydroperoxide reductase:f52a subunit (fn:enzyme; detoxification) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 56 of 400 of the completegenome.) (nt:o531; 100 pct identical to fragment ahpf\_ecoli) (le:3111) (re:4706) (di:direct) AE000166 AE000166 g1786823 Escherichia coli 562 -11533853 5000691076 (de:(ecoli\_587) (pn:alkyl hydroperoxide reductase, f52a subunit; detoxification of hydroperoxides) (gn:ahpf) (gtcfc:12.12) (ec:1.6.4.-) (ahpf\_ecoli) (keggfc:11.1) (rileyfc:4.7.0) (db:gtc-escherichia coli)) ECOLI\_587 ECOLI\_587 Escherichia coli 562 10122925

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837085	9179	31335	462	153

Description

6500729996 sodb:b1656 superoxide dismutase:fe (gtcfc:12.12) (ec:1.15.1.1) (keggfc:14.1) (rileyfc:4.7.0) (db:gtc-escherichia coli) b1656 b1656 Escherichia coli 562 -11533854 123150 sodb:fe-sod superoxide dismutase:fe (cl:superoxide dismutase (mn)) (ec:1.15.1.1) (db:pir1.dat) (mp:36 min) DSECF A29940 Escherichia coli 562 -11533854 224100 sodb:fe:sod superoxide dismutase ec 1.15.1.1 fe (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #318(37.2-37.6 min.)) (nt:orf\_id:o317#12; similar to (pir accession number) (le:6970) (re:7551) (di:direct) D90809 D90809 g1742729 Escherichia coli 562 -11533854 7500953218 (sr:e.coli k12 (strain n99) dna, clones phs1-(6,8)) (db:genpept-bct1) (de:e.coli sodb gene encoding superoxide dismutase, complete cds.) (nt:superoxide dismutase (sodb)) (le:177) (re:758) (di:direct) ECOSODB J03511 g147842 Escherichia coli 562 -11533854 236008 sodb superoxide dismutase:iron (fn:enzyme; detoxification) (db:genpept-bct2) (ec:1.15.1.1) (de:escherichia coli k-12 mg1655 section 151 of 400 of the completegenome.) (nt:o193; 100 pct identical to sodf\_ecoli sw: p09157) (le:94) (re:675) (di:direct) AE000261 AE000261 g1787946 Escherichia coli 562 -11533854 5000691077 (de:(ecoli\_1615) (pn:superoxide dismutase, iron) (gn:sodb) (gtcfc:12.12) (ec:1.15.1.1) (sodf\_ecoli) (keggfc:11.1) (rileyfc:4.7.0) (db:gtc-escherichia coli)) ECOLI\_1615 ECOLI\_1615 Escherichia coli 562 10065738

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837098	9180	31336	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837113	9181	31337	816	271

Description

GTC ORF with score 229 to: (fn:base excision repair) (sr:fission yeast) (db:genpept-pln2) (de:schizosaccharomyces pombe 3-methyladenine dna glycosylase (mag1)mRNA, complete cds.) (nt:mag1; homolog to s. cerevisiae mag and e. coli) (le:109) (re:795) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837115	9182	31338	237	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837122	9183	31339	945	314

Description

6500729997 thdf:trme:b3706 50 kd protein:thiophene and furan oxidation protein:thiophene and furan oxidation protein thdf (gtcfc:12.12) (keggfc:14.2) (rileyfc:4.7.0) (db:gtc-escherichia coli) b3706 b3706 Escherichia coli 562 -11533855 7500893021 thdf:trme (de:thiophene and furan oxidation protein thdf) (db:swissprot) THDF\_ECOLI P25522 ESCHERICHIA COLI 562 -11533855 7000691921 thdf thiophene and furan oxidation 50 kd protein thdf (cl:thiophen / furan oxidation protein:translation elongation factor tu homology) (db:pir2.dat) C65173 C65173 Escherichia coli 562 -11533855 7500893023 thdf gtp-binding protein in thiophene and furan (fn:putative enzyme; detoxification) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 337 of 400 of the completegenome.) (nt:o454; 100 pct identical to thdf\_ecoli sw:) (le:9842) (re:11206) (di:direct) AE000447 AE000447 g2367268 Escherichia coli 562 -11533855

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837123	9184	31340	807	268

Description

6500729998 soda:b3908 manganese superoxide dismutase:superoxide dismutase:mn (gtcfc:12.12) (ec:1.15.1.1) (keggfc:14.1) (rileyfc:4.7.0) (db:gtc-escherichia coli) b3908 b3908 Escherichia coli 562 -11533856 123147 soda:mn-sod superoxide dismutase:mn (cl:superoxide dismutase (mn)) (ec:1.15.1.1) (db:pir1.dat) (mp:87.5 min) DSECN A24141 Escherichia coli 562 -11533856 238278 soda manganese superoxide dismutase (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 17593) (le:62443) (re:63063) (di:direct) ECOUW87 L19201 g305012 Escherichia coli 562 -11533856 7500953217 (db:genpept-bct1) (de:e. coli mn-superoxide dismutase gene.) (nt:mn-sod (aa 1-206)) (le:141) (re:761) (di:direct) ECSOD X03951 g42973 Escherichia coli 562 -11533856 237126 soda superoxide dismutase:manganese (fn:enzyme; detoxification) (db:genpept-bct2) (ec:1.15.1.1) (de:escherichia coli k-12 mg1655 section 355 of 400 of the completegenome.) (nt:o206; 100 pct identical to sodm\_ecoli sw: p00448;) (le:14988) (re:15608) (di:direct) AE000465 AE000465 g1790342 Escherichia coli 562 -11533856 5000691079 (de:(ecoli\_3807) (pn:superoxide dismutase, manganese) (gn:soda) (gtcfc:12.12) (ec:1.15.1.1) (sodm\_ecoli) (keggfc:11.1) (rileyfc:4.7.0) (db:gtc-escherichia coli)) ECOLI\_3807 ECOLI\_3807 Escherichia coli 562 10065736

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837135	9185	31341	249	82

Description

6500729999 gefl:b0018 gef leader and gef protein (gtcfc:12.12) (keggfc:14.2) (rileyfc:4.8.0) (db:gtc-escherichia coli) b0018 b0018 Escherichia coli 562 -11533857 154869 gefl:gef gef protein (cl:flma protein) (db:pir2.dat) (mp:0.4) S40540 S16473 Escherichia coli 562 -11533857 7500955515 gef gef protein interferes with membrane function (fn:membrane; cell killing) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 2 of 400 of the completegenome.) (nt:f69; residues 1-19 are 100 pct identical) (le:6213) (re:6422) (di:complement) AE000112 AE000112 g1786200 Escherichia coli 562 -11533857 5000691119 (de:(ecoli\_18) (pn:leader peptide of gef) (gn:gefl) (gtcfc:12.14) (ec:) (lpge\_ecoli) (keggfc:11.2) (rileyfc:4.8.0) (db:gtc-escherichia coli)) ECOLI\_18 ECOLI\_18 Escherichia coli 562 10081739

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837136	9186	31342	591	196

#### Description

6500730000 relf:b1562 relf protein (gtcfc:12.12) (keggfc:14.2) (rileyfc:4.8.0) (db:gtc-escherichia coli) b1562 b1562 Escherichia coli 562 -11533858 93890 relf (de:relf protein) (db:swissprot) RELF\_ECOLI P07009 ESCHERICHIA COLI 562 -11533858 7000686296 relf relf protein (cl:flma protein) (db:pir1.dat) (mp:34 min) QQECR5 E64911 Escherichia coli 562 -11533858 223939 relf (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #307(35.1-35.5 min.)) (nt:orf\_id:o308#18; similar to (pir accession number) (le:17113) (re:17268) (di:complement) D90798 D90798 g1742557 Escherichia coli 562 -11533858 300668 relf (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #308(35.3-35.7 min.)) (nt:orf\_id:o308#18; similar to (pir accession number) (le:7086) (re:7241) (di:complement) D90799 D90799 g1742568 Escherichia coli 562 -11533858 300690 relf (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #309(35.4-35.7 min.)) (nt:orf\_id:o308#18; similar to (pir accession number) (le:3862) (re:4017) (di:complement) D90800 D90800 g1742591 Escherichia coli 562 -11533858 300658 relf polypeptide destructive to membrane potential (fn:factor; cell killing) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 143 of 400 of the completgenome.) (nt:f51; 98 pct identical to relf\_ecoli sw:) (le:2871) (re:3026) (di:complement) AE000253 AE000253 g1787845 Escherichia coli 562 -11533858 223949 relf (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #308(35.3-35.7 min.)) (nt:orf\_id:o308#18; similar to (pir accession number) (le:7086) (re:7241) (di:complement) D90799 D90799 g1742568 Escherichia coli 562 -11533858 223971 relf (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #309(35.4-35.7 min.)) (nt:orf\_id:o308#18; similar to (pir accession number) (le:3862) (re:4017) (di:complement) D90800 D90800 g1742591 Escherichia coli 562 -11533858 5000691120 (de:(ecoli\_1522) (pn:polypeptide destructive to membrane potential) (gn:relf) (gtcfc:12.14) (ec:) (relf\_ecoli) (keggfc:11.2) (rileyfc:4.8.0) (db:gtc-escherichia coli)) ECOLI\_1522 ECOLI\_1522 Escherichia coli 562 10119704

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837137	9187	31343	309	102

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837150	9188	31344	324	107

Description

6500730001 ftsz:sfib:sulb:b0095 cell division protein ftsz  
 (gtcfc:12.13:12.8) (keggfc:12.1) (rileyfc:4.3.0) (db:gtc-escherichia coli)  
 b0095 b0095 Escherichia coli 562 -11533859 7000688980 ftsz cell division  
 protein ftsz (cl:cell division protein ftsz) (db:pir1.dat) (mp:2 min) CEECZ  
 G64731 Escherichia coli 562 -11533859 7500953639 ftsz cell division:forms  
 circumferential ring (fn:enzyme; cell division) (db:genpept-bct2)  
 (de:escherichia coli k-12 mg1655 section 9 of 400 of the completegenome.)  
 (nt:o383; 99 pct identical to ftsz\_ecoli sw: p06138) (le:61) (re:1212)  
 (di:direct) AE000119 AE000119 g1786284 Escherichia coli 562 -11533859  
 5000691268 (de:(ecoli\_95) (pn:cell division; forms circumferential ring;  
 gtp-binding protein and gtpase) (gn:fts) (gtcfc:12.8) (ec:) (fts\_ecoli)  
 (keggfc:11.2) (rileyfc:4.3.0) (db:gtc-escherichia coli)) ECOLI\_95 ECOLI\_95  
 Escherichia coli 562 10122652

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837157	9189	31345	432	143

Description

6500730002 kdpc:b0696 potassium-transporting atpase:c chain:atp phosphohydrolase (gtcfc:12.5:12.13) (ec:3.6.1.36) (keggfc:12.1) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_):cell processes-metabolic regulators signal transduction--two component system sensory second messenger) b0696 b0696 Escherichia coli 562 -11533860 60549 kdpc (ec:3.6.1.36) (de:phosphohydrolase (potassium-transporting) c chain)) (db:swissprot) ATKC\_ECOLI P03961 ESCHERICHIA COLI 562 -11533860 125247 kdpc h+/k+-exchanging atpase:chain c:atp phosphohydrolase potassium-transporting chain c:h+/k+-transporting atpase chain c:potassium-transporting atpase chain c (cl:h+/k+-transporting atpase chain c) (ec:3.6.1.36) (db:pir1.dat) (mp:16 min) PWECK A01073 Escherichia coli 562 -11533860 223158 kdpc potassium-transporting atpase:c chain (sr:escherichia coli(strain:k12) dna, clone:kohara clone #173) (db:genpept-bct1) (de:escherichia coli genomic dna. (15.3 - 15.6 min).) (le:14029) (re:14601) (di:complement) D90708 D90708 g1651303 Escherichia coli 562 -11533860 7500877321 kdpc (db:genpept-bct1) (de:escherichia coli kdpabc operon coding for kdp-atpase proteinskdpa,-b,-c.) (le:3889) (re:4461) (di:direct) ECOKDPABC K02670 g146549 Escherichia coli 562 -11533860 234926 kdpc high-affinity potassium transport system (fn:enzyme; transport of small molecules: cations) (db:genpept-bct2) (ec:3.6.1.36) (de:escherichia coli k-12 mg1655 section 63 of 400 of the completgenome.) (nt:f190; 100 pct identical to atkc\_ecoli sw: p03961) (le:3679) (re:4251) (di:complement) AE000173 AE000173 g1786913 Escherichia coli 562 -11533860 5000691205 kdpc potassium-transporting atpase ec 3.6.1.36:c (sr:escherichia coli(strain:k12) dna, clone:kohara clone #173) (db:genpept) (de:escherichia coli genomic dna. (15.3 - 15.7 min).) (nt:orf\_id:o173#14; similar to swissprot accession) (le:14029) (re:14601) (di:complement) D90708 D90708 g1651303 Escherichia coli 562 -11533860



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837160	9190	31346	1173	390

Description

6500730003 kdpb:b0697 potassium-transporting atpase:b chain:atp phosphohydrolase (gtcfc:12.5:12.13) (ec:3.6.1.36) (keggfc:12.1) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_):cell processes-metabolic regulators signal transduction--two component system sensory second messenger) b0697 b0697 Escherichia coli 562 -11533861 60547 kdpb (ec:3.6.1.36) (de:phosphohydrolase (potassium-transporting) b chain)) (db:swissprot) ATKB\_ECOLI P03960 ESCHERICHIA COLI 562 -11533861 7000684655 kdpb h+/k+-exchanging atpase:chain b:atp phosphohydrolase potassium-transporting chain b:h+/k+-transporting atpase chain b:potassium-transporting atpase chain b (cl:h+/k+-transporting atpase chain b:atpase nucleotide-binding domain homology) (ec:3.6.1.36) (db:pir1.dat) (mp:16 min) PWECEBK H64804 Escherichia coli 562 -11533861 7500877312 kdpb atpase of high-affinity potassium transport (fn:enzyme; transport of small molecules: cations) (db:genpept-bct2) (ec:3.6.1.36) (de:escherichia coli k-12 mg1655 section 63 of 400 of the completegenome.) (nt:f682; 99 pct identical to atkb\_ecoli sw: p03960) (le:4260) (re:6308) (di:complement) AE000173 AE000173 g1786914 Escherichia coli 562 -11533861 5000691206 (de:(ecoli\_671) (pn:high-affinity potassium transport system) (gn:kdpb) (gtcfc:12.5) (ec:3.6.1.36) (atkb\_ecoli) (keggfc:11.1) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_671 ECOLI\_671 Escherichia coli 562 10122960

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837166	9191	31347	369	122

Description

GTC ORF with score 127 to: (db:genpept-pln2) (de:emerella nidulans alternatively spliced cyclin-dependent proteinkinase phoa(m1) and phoa(m47) isoforms (phoa) gene, complete cds.) (nt:contains pstaire motif; non-essential) (le:843:1088:1194) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837167	9192	31348	378	126

Description

GTC ORF with score 515 to: (db:genpept-pln2) (de:emerella nidulans alternatively spliced cyclin-dependent proteinkinase phoa(m1) and phoa(m47) isoforms (phoa) gene, complete cds.) (nt:contains pstaire motif; non-essential) (le:843:1088:1194) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837179	9193	31349	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837206	9194	31350	1320	439

Description

6500730004 kdpa:b0698 potassium-transporting atpase:a chain:atp phosphohydrolase (gtcfc:12.5:12.13) (ec:3.6.1.36) (keggfc:12.1) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_):cell processes-metabolic regulators signal transduction--two component system sensory second messenger) b0698 b0698 Escherichia coli 562 -11533862 60545 kdpa (ec:3.6.1.36) (de:phosphohydrolase (potassium-transporting) a chain)) (db:swissprot) ATKA\_ECOLI P03959 ESCHERICHIA COLI 562 -11533862 125245 kdpa h+/k+-exchanging atpase:chain a:atp phosphohydrolase potassium-transporting chain a:h+/k+-transporting atpase chain a:potassium-transporting atpase chain a (cl:h+/k+-transporting atpase chain a) (ec:3.6.1.36) (db:pir1.dat) (mp:16 min) PWECAK A01071 Escherichia coli 562 -11533862 223161 kdpa potassium-transporting atpase:a chain (sr:escherichia coli(strain:k12) dna, clone:kohara clone #174) (db:genpept-bct1) (de:escherichia coli genomic dna. (15.6 - 15.9 min).) (le:245) (re:1918) (di:complement) D90709 D90709 g1651307 Escherichia coli 562 -11533862 7500877303 kdpa (db:genpept-bct1) (de:escherichia coli kdpabc operon coding for kdp-atpase proteinskdpa,-b,-c.) (le:136) (re:1809) (di:direct) ECOKDPABC K02670 g146547 Escherichia coli 562 -11533862 234924 kdpa atpase of high-affinity potassium transport (fn:enzyme; transport of small molecules: cations) (db:genpept-bct2) (ec:3.6.1.36) (de:escherichia coli k-12 mg1655 section 63 of 400 of the completegenome.) (nt:f557; 100 pct identical to atka\_ecoli sw: p03959) (le:6331) (re:8004) (di:complement) AE000173 AE000173 g1786915 Escherichia coli 562 -11533862 5000691207 kdpa potassium-transporting atpase ec 3.6.1.36:a (sr:escherichia coli(strain:k12) dna, clone:kohara clone #174) (db:genpept) (de:escherichia coli genomic dna. (15.7 - 16.0 min).) (nt:orf\_id:o174#1; similar to swissprot accession) (le:245) (re:1918) (di:complement) D90709 D90709 g1651307 Escherichia coli 562 -11533862

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837207	9195	31351	195	64

Description

6500730005 tors:b0993 sensor protein tors:histidine protein kinase:sensor protein tors (gtcfc:12.13) (ec:2.7.3.-) (keggfc:12.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0993 b0993 Escherichia coli 562 -11533863 101831 tors (ec:2.7.3.-) (de:sensor protein tors,) (db:swissprot) TORS\_ECOLI P39453 ESCHERICHIA COLI 562 -11533863 7000686817 tors histidine protein kinase::sensor protein tors (ec:2.7.3.-) (db:pir2.dat) G64840 G64840 Escherichia coli 562 -11533863 7500893275 tors sensor protein tors regulator torr (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (ec:2.7.3.-) (de:escherichia coli k-12 mgl655 section 91 of 400 of the completegenome.) (nt:f904; 99 pct identical to tors\_ecoli sw: p39453) (le:2207) (re:4921) (di:complement) AE000201 AE000201 g1787227 Escherichia coli 562 -11533863 5000691927 tors sensor protein tors ec 2.7.3.-. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept) (de:escherichia coli genomic dna. (22.6 - 23.0 min).) (nt:orf\_id:o226#12; similar to swissprot accession) (le:7929) (re:10643) (di:complement) D90736 D90736 g4062710 Escherichia coli 562 -11533863

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837208	9196	31352	225	74

Description

6500730006 tord:b0998 tord protein (gtcfc:12.13:14.2:14.3) (keggfc:12.1) (rileyfc:5.8.0:5.9.0) (db:gtc-escherichia coli) b0998 b0998 Escherichia coli 562 -11533864 101829 tord (de:tord protein) (db:swissprot) TORD\_ECOLI P36662 ESCHERICHIA COLI 562 -11533864 7000686815 tord tord protein (db:pir2.dat) D64841 D64841 Escherichia coli 562 -11533864 223320 tord tord protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept-bct1) (de:escherichia coli genomic dna. (22.5 - 22.9 min).) (le:16294) (re:16893) (di:direct) D90736 D90736 gl651490 Escherichia coli 562 -11533864 223325 tord tord protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #227) (db:genpept-bct1) (de:escherichia coli genomic dna. (22.7 - 23.0 min).) (le:7296) (re:7895) (di:direct) D90737 D90737 gl651496 Escherichia coli 562 -11533864 7500893273 tord part of trimethylamine-n-oxide oxidoreductase (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 91 of 400 of the completegenome.) (nt:o199; 99 pct identical to tord\_ecoli sw: p36662) (le:10572) (re:11171) (di:direct) AE000201 AE000201 gl787232 Escherichia coli 562 -11533864 5000691929 tord tord protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #227) (db:genpept) (de:escherichia coli genomic dna. (22.8 - 23.1 min).) (nt:orf\_id:o227#5; similar to pir accession number) (le:7296) (re:7895) (di:direct) D90737 D90737 gl651496 Escherichia coli 562 -11533864 7502851977 tord tord protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept) (de:escherichia coli genomic dna. (22.6 - 23.0 min).) (nt:orf\_id:o227#5; similar to pir accession number) (le:16294) (re:16893) (di:direct) D90736 D90736 gl651490 Escherichia coli 562 -11533864

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837230	9197	31353	654	217

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837244	9198	31354	1269	422
<u>Description</u>				
6500730007 rsta:urpt:b1608 rsta:transcriptional regulatory protein rsta (gtcfc:10.2) (keggfc:12.1) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1608 b1608 Escherichia coli 562 -11533865 97498 rsta:urpt (de:transcriptional regulatory protein rsta) (db:swissprot) RSTA_ECOLI P52108 ESCHERICHIA COLI 562 -11533865 7000686525 rsta transcription regulator rsta:rsta protein (cl:ompr protein:response regulator homology) (db:pir2.dat) B64917 B64917 Escherichia coli 562 -11533865 224024 rsta:urpt transcriptional regulatory protein rsta. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #312(36.0-36.3 min.)) (nt:orf_id:o312#8; similar to (swissprot accession) (le:9856) (re:10584) (di:direct) D90803 D90803 g1742647 Escherichia coli 562 -11533865 224034 rsta:urpt transcriptional regulatory protein rsta. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #313(36.1-36.4 min.)) (nt:orf_id:o312#8; similar to (swissprot accession) (le:5970) (re:6698) (di:direct) D90804 D90804 g1742658 Escherichia coli 562 -11533865 300729 rsta rsta (sr:escherichia coli strain=k-12) (db:genpept-bct1) (de:escherichia coli response regulator homolog (rsta) gene, and sensor kinase homolog (rstb) gene, complete cds, dna replication terminus binding protein tus (tus) gene, partial cds.) (nt:synonym = urp... ECU41101 U41101 g1079807 Escherichia coli 562 -11533865 239581 rsta response transcriptional regulatory protein (fn:regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 146 of 400 of the completgenome.) (nt:o242; 100 pct identical to gb: ecu41101_1) (le:4092) (re:4820) (di:direct) AE000256 AE000256 g1787893 Escherichia coli 562 -11533865 5000692373 (de:(ecoli_1567) (pn:transcriptional regulatory protein rsta) (gn:rsta) (gtcfc:13.7:14.1) (ec:) (rsta_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1567 ECOLI_1567 Escherichia coli 562 10039388				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501837269	9199	31355	564	187

#### Description

6500730008 rstb:uspt:b1609 unknown sensor protein in terminator region:sensor protein rstb (gtcfc:12.13:14.3) (ec:2.7.3.-) (keggfc:12.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1609 b1609 Escherichia coli 562 -11533866 97500 rstb:uspt (ec:2.7.3.-) (de:sensor protein rstb,) (db:swissprot) RSTB\_ECOLI P18392 ESCHERICHIA COLI 562 -11533866 7000686526 rstb terminator region sensor protein:rstb (cl:envz protein:sensor histidine kinase homology) (ec:2.7.3.-) (db:pir2.dat) (mp:36 min) C64917 C64917 Escherichia coli 562 -11533866 224025 rstb:uspt sensor protein rstb ec 2.7.3.-. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #312(36.0-36.3 min.)) (nt:orf\_id:o312#9; similar to (swissprot accession) (le:10588) (re:11889) (di:direct) D90803 D90803 g1742648 Escherichia coli 562 -11533866 224035 rstb:uspt sensor protein rstb ec 2.7.3.-. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #313(36.1-36.4 min.)) (nt:orf\_id:o312#9; similar to (swissprot accession) (le:6702) (re:8003) (di:direct) D90804 D90804 g1742659 Escherichia coli 562 -11533866 300730 rstb rstb (sr:escherichia coli strain=k-12) (db:genpept-bct1) (de:escherichia coli response regulator homolog (rsta) gene, and sensorkinase homolog (rstb) gene, complete cds, dna replication terminusbinding protein tus (tus) gene, partial cds.) (nt:synonym = usp... ECU41101 U41101 g1079808 Escherichia coli 562 -11533866 239582 rstb sensor histidine protein kinase rsta (fn:regulator; global regulatory functions) (db:genpept-bct2) (ec:2.7.3.-) (de:escherichia coli k-12 mg1655 section 146 of 400 of the completegenome.) (nt:o433; 100 pct identical to fragment uspt\_ecoli) (le:4824) (re:6125) (di:direct) AE000256 AE000256 g1787894 Escherichia coli 562 -11533866 5000692374 (de:(ecoli\_1568) (pn:sensor protein rstb) (gn:rstb) (gtcfc:13.7:14.1) (ec:2.7.3.-) (rstb\_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_1568 ECOLI\_1568 Escherichia coli 562 10039390

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837278	9200	31356	1491	496

Description

6500730009 atos:b2219 sensor protein atos (gtcfc:12.13:14.3) (ec:2.7.3.-)  
(keggfc:12.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2219 b2219  
Escherichia coli 562 -11533867 60606 atos (ec:2.7.3.-) (de:sensor protein  
atos,) (db:swissprot) ATOS\_ECOLI Q06067 ESCHERICHIA COLI 562 -11533867  
7000684662 atos sensor protein atos (ec:2.7.3.-) (db:pir2.dat) A64992  
A64992 Escherichia coli 562 -11533867 224699 atos sensor protein atos ec  
2.7.3.-. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda  
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#374(49.8-50.1 min.)) (nt:orf\_id:o374#2; similar to (swissprot accession)  
(le:5951) (re:7777) (di:direct) D90851 D90851 g1736874 Escherichia coli 562  
-11533867 301339 (fn:similarity with sensor kinases) (sr:escherichia coli  
(strain k-12) (library: lamda phage library of y) (db:genpept-bct1)  
(de:escherichia coli ornithine and arginine decarboxylases antizymegene,  
complete cds.) (nt:orf-1) (le:755) (re:2581) (di:direct) ECOANTZYM L13078  
g290419 Escherichia coli 562 -11533867 233804 atos sensor protein atos for  
response regulator atoc (fn:regulator; not classified) (db:genpept-bct2)  
(ec:2.7.3.-) (de:escherichia coli k-12 mg1655 section 201 of 400 of the  
completegenome.) (nt:o608; 100 pct identical to atos\_ecoli sw: q06067)  
(le:3146) (re:4972) (di:direct) AE000311 AE000311 g1788549 Escherichia coli  
562 -11533867 5000692784 (de:(ecoli\_2168) (pn:sensor protein atos)  
(gn:atos) (gtcfc:13.7:14.1) (ec:2.7.3.-) (atos\_ecoli) (keggfc:11.1)  
(rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2168 ECOLI\_2168 Escherichia  
coli 562 10003332

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837283	9201	31357	399	132

#### Description

6500730010 ygix:b3025 hypothetical protein:probable transcriptional regulatory protein ygix (gtcfc:10.2) (keggfc:12.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3025 b3025 Escherichia coli 562 -11533868 112405 ygix (de:probable transcriptional regulatory protein ygix) (db:swissprot) YGIX\_ECOLI P52076 ESCHERICHIA COLI 562 -11533868 7000687864 hypothetical protein b3025 (cl:ompr protein:response regulator homology) (db:pir2.dat) G65089 G65089 Escherichia coli 562 -11533868 7500924275 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf\_o219) (le:124215) (re:124874) (di:direct) ECU28377 U28377 g882555 Escherichia coli 562 -11533868 239239 ygix putative 2-component transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 274 of 400 of the completegenome.) (nt:o219; this 219 aa orf is 60 pct identical (0 gaps)) (le:8657) (re:9316) (di:direct) AE000384 AE000384 g1789402 Escherichia coli 562 -11533868 5000693320 (de:(ecoli\_2948) (pn:probable transcriptional regulatory protein ygix) (gtcfc:13.7:14.1) (ec:) (ygix\_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2948 ECOLI\_2948 Escherichia coli 562 10054133

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837289	9202	31358	186	62

#### Description

6500730011 ygiy:b3026 hypothetical protein:probable sensor protein ygiy (gtcfc:12.13:14.1) (ec:2.7.3.-) (keggfc:12.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3026 b3026 Escherichia coli 562 -11533869 112407 ygiy (ec:2.7.3.-) (de:probable sensor protein ygiy,) (db:swissprot) YGIY\_ECOLI P40719 ESCHERICHIA COLI 562 -11533869 7000687865 hypothetical protein b3026 (cl:hypothetical protein hi1707:sensor histidine kinase homology) (db:pir2.dat) H65089 H65089 Escherichia coli 562 -11533869 7500924277 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf\_o449) (le:124871) (re:126220) (di:direct) ECU28377 U28377 g882556 Escherichia coli 562 -11533869 239240 ygiy putative 2-component sensor protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 274 of 400 of the completegenome.) (nt:o449; this 449 aa orf is 44 pct identical (3 gaps)) (le:9313) (re:10662) (di:direct) AE000384 AE000384 g1789403 Escherichia coli 562 -11533869 5000693321 (de:(ecoli\_2949) (pn:probable sensor protein ygiy) (gtcfc:13.7:14.1) (ec:2.7.3.-) (ygiy\_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2949 ECOLI\_2949 Escherichia coli 562 10054135



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837312	9203	31359	384	127

Description

6500730012 uhpt:b3666 hexosephosphate transport protein:hexose phosphate transport protein (gtcfc:12.4) (keggfc:12.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of anions (cl\_so4\_po4\_etc\_)) b3666 b3666 Escherichia coli 562 -11533870 103369 uhpt (de:hexose phosphate transport protein) (db:swissprot) UHPT\_ECOLI P13408 ESCHERICHIA COLI 562 -11533870 130794 uhpt hexose phosphate transport protein uhpt (cl:hexose phosphate transport protein uhpt) (db:pir1.dat) (mp:82 min) MMECHP A30395 Escherichia coli 562 -11533870 236258 (sr:e.coli dna, clone prjk10) (db:genpept-bct1) (de:e.coli uhp operon encoding uhpa, uhpb, uhpc, and uhpt protein, (encoding hexose phosphate transport protein), complete cds, and anilvbn operon encoded protein, 3' end.) (nt:hexose phosphate transport p... ECOUHP M17102 g148115 Escherichia coli 562 -11533870 7500893774 uhpt hexosephosphate transport protein (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli uhpabct operon encoding hexosephosphateutilization protein (uhpa) gene, complete cds, and hexosephosphatetransport protein (uhpb, uhpc, uhpt) genes, complete cds.) (le:3722) (re:5113) (di... ECOUHPABCT M89479 g148120 Escherichia coli 562 -11533870 236254 uhpt hexose phosphate transport protein (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 334 of 400 of the completegenome.) (nt:f463; 99 pct identical amino acid sequence and) (le:5590) (re:6981) (di:complement) AE000444 AE000444 g2367259 Escherichia coli 562 -11533870

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837318	9204	31360	270	89

Description

6500730013 uhpc:b3667 regulatory protein uhpc (gtcfc:12.13:12.2) (keggfc:12.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3667 b3667 Escherichia coli 562 -11533871 7000688973 uhpc regulatory protein uhpc (cl:hexose phosphate transport protein uhpt) (db:pir1.dat) (mp:82 min) RGECUC D65168 Escherichia coli 562 -11533871 7500953614 (sr:e.coli dna, clone prjk10) (db:genpept-bct1) (de:e.coli uhp operon encoding uhpa, uhpb, uhpc, and uhpt protein, (encoding hexose phosphate transport protein), complete cds, and anilvbn operon encoded protein, 3' end.) (nt:uhpc protein) (le:2262) (re:... ECOUHP M17102 g148114 Escherichia coli 562 -11533871 236253 uhpc regulator of uhpt (fn:regulator; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 334 of 400 of the completegenome.) (nt:f440; 99 pct identical amino acid sequence and) (le:7119) (re:8441) (di:complement) AE000444 AE000444 g2367260 Escherichia coli 562 -11533871

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837320	9205	31361	288	95

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837321	9206	31362	636	211

Description

6500730014 uhp:b3668 sensor protein uhp (gtcfc:12.13:12.2) (ec:2.7.3.-) (keggfc:12.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3668 b3668 Escherichia coli 562 -11533872 7000688987 uhp sensor protein uhp (cl:regulatory protein uhp) (ec:2.7.3.-) (db:pir1.dat) (mp:82) RGEUCB E65168 Escherichia coli 562 -11533872 7500953661 uhp::cg site no. 1... hexosephosphate transport protein (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:38028) (re:39533) (di:complement) ECOUW82 L10328 g290517 Escherichia coli 562 -11533872 236905 uhp sensor histidine protein kinase phosphorylates (fn:enzyme; transport of small molecules:) (db:genpept-bct2) (ec:2.7.3.-) (de:escherichia coli k-12 mg1655 section 334 of 400 of the completegenome.) (nt:f501; 100 pct identical amino acid sequence and) (le:8448) (re:9953) (di:complement) AE000444 AE000444 g1790101 Escherichia coli 562 -11533872 5000691150 (de:(ecoli\_3587) (pn:regulator of uhpt, sensor histidine protein kinase) (gn:uhpb) (gtcfc:12.2) (ec:2.7.3.-) (uhpb\_ecoli) (keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_3587 ECOLI\_3587 Escherichia coli 562 10124063

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837325	9207	31363	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837343	9208	31364	573	190

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837344	9209	31365	903	300

Description

6500730015 uhpab3669 transcriptional regulatory protein uhpab  
(gtcfc:10.2:12.13:12.2) (keggfc:12.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3669 b3669 Escherichia coli 562 -11533873 103363 uhpab  
(de:transcriptional regulatory protein uhpab) (db:swissprot) UHPAB\_ECOLI  
P10940 ESCHERICHIA COLI 562 -11533873 130887 uhpab transcription regulator  
uhpab (cl:regulatory protein comA:response regulator homology) (db:pir1.dat)  
(mp:82) BVECAU A26925 Escherichia coli 562 -11533873 236255 (sr:e.coli dna, clone prjk10) (db:genpept-bct1) (de:e.coli uhp operon encoding uhpab, uhpbc, uhpcc, and uhpct protein, (encoding hexose phosphate transport protein), complete cds, and anilvbn operon encoded protein, 3' end.) (nt:uhpab protein) (le:163) (re:7... ECUHP M17102 g148112 Escherichia coli 562 -11533873 236906 uhpab hexosephosphate utilization protein (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli uhpabct operon encoding hexosephosphateutilization protein (uhpab) gene, complete cds, and hexosephosphatetransport protein (uhpbc, uhpcc, uhpct) genes, complete cds.) (le:163) (re:753) (di:d... ECUHPABCT M89479 g148117 Escherichia coli 562 -11533873 7500893771 uhpab::cg site no. 1... hexosephosphate utilization protein (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:39530) (re:40120) (di:complement) ECUW82 L10328 g290518 Escherichia coli 562 -11533873 236251 uhpab response regulator:positive activator of uhpct (fn:regulator; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 334 of 400 of the completegenome.) (nt:f196; 100 pct identical amino acid sequence and) (le:9950) (re:10540) (di:complement) AE000444 AE000444 g1790102 Escherichia coli 562 -11533873 5000691151 (de:(ecoli\_3588) (pn:response regulator, positive activator of uhpct transcription,:sensor, uhpbc) (gn:uhpab) (gtcfc:12.2) (ec:) (uhpab\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_3588 ECOLI\_3588 Escherichia coli 562 10045133

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837350	9210	31366	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837355	9211	31367	228	75

Description

6500730016 cpxr:b3912 transcriptional regulatory protein:transcriptional regulatory protein cpxr (gtcfc:10.2:12.13) (keggfc:12.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3912 b3912 Escherichia coli 562 -11533874 66237 cpxr (de:transcriptional regulatory protein cpxr) (db:swissprot) CPXR\_ECOLI P16244 ESCHERICHIA COLI 562 -11533874 7000684903 cpxr transcription regulator cpxr:transcription factor cpxa 5 region (cl:ompr protein:response regulator homology) (db:pir2.dat) C65197 C65197 Escherichia coli 562 -11533874 7500879351 cpxr transcriptional regulator in 2-component system (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 356 of 400 of the completegenome.) (nt:f232; 99 pct identical amino acid sequence and) (le:2249) (re:2947) (di:complement) AE000466 AE000466 g2367329 Escherichia coli 562 -11533874 236135 cpxr transcription factor (sr:escherichia coli (strain 1547) dna) (db:genpept-bct2) (de:escherichia coli transcription factor (cpxr) gene, complete cds.) (nt:the sequence analysis indicates that cpxr is) (le:1246) (re:1944) (di:direct) ECOTRANS L14579 g410157 Escherichia coli 562 -11533874 164730 cpxr transcriptional regulatory protein cpxr:transcription factor cpxa 5 region (cl:ompr protein:response regulator homology) (db:pir) C65197 C65197 Escherichia coli 562 -11533874

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501837356	9212	31368	189	62

# Description

6500730017 lacy:b0343 lactose permease:lactose-proton symport (gtcfc:12.2) (keggfc:14.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b0343 b0343  
Escherichia coli 562 -11533875 239960 lacy (de:lactose permease (lactose-proton symport)) (db:swissprot) LACY\_ECOLI P02920 ESCHERICHIA COLI 562 -11533875 130798 lacy lactose permease:lactose transport protein:lactose-proton symport protein (cl:lactose permease) (db:pir1.dat) (mp:8 min) GREC A03418 Escherichia coli 562 -11533875 234948 (db:genpept-bct1) (de:e. coli lacy gene (codes for lactose permease).) (nt:reading frame (lacy)) (le:106) (re:1359) (di:direct) ECLACY V00295 g41899 Escherichia coli 562 -11533875 237822 lacy (sr:escherichia coli dna; mrna; clone lambda-h80dlac dna; clone puk217) (db:genpept-bct1) (de:e.coli lactose operon with laci, lacz, lacy and laca genes.) (nt:lactose permease) (le:4410) (re:5663) (di:direct) ECOLAC J01636 g146578 Escherichia coli 562 -11533875 5000691121 lacy lactose permease (db:genpept-bct1) (de:e.coli plasmid dna of lac promoter-operator, lacy and amp genes for lactose permease and beta-lactamase.) (le:298) (re:1551) (di:direct) ECPLAS X56095 g42418 Escherichia coli 562 -11533875 407338 lacy lactose permease (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (le:69721) (re:70974) (di:complement) ECU73857 U73857 g1657539 Escherichia coli 562 -11533875 233306 lacy galactoside permease m protein (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 31 of 400 of the complete genome.) (nt:f417; 100 pct identical to lacy\_ecoli sw: p02920) (le:4334) (re:5587) (di:complement) AE000141 AE000141 g1786538 Escherichia coli 562 -11533875 407343 lacy lactose permease (db:genpept-syn) (de:cloning vector lambda txf97, lacz transcriptional fusion vector, complete sequence.) (le:19507) (re:20760) (di:complement) CVU37692 U37692 g1051182 Cloning vector lambda TXF97 43300 -11533875 407346 lacy lactose permease (db:genpept-syn) (de:cloning vector tlf97-1, lambda phage lacz translational fusionvector, complete sequence.) (le:19507) (re:20760) (di:complement) CVU39284 U39284 g1066305 Cloning vector TLF97-1 43840 -11533875 407349 lacy lactose permease (db:genpept-syn) (de:cloning vector tlf97-2, phage lambda lacz translational fusionvector, complete sequence.) (le:19507) (re:20760) (di:complement) CVU39285 U39285 g1066309 Cloning vector TLF97-2 43841 -11533875 1500685309 lacy lactose permease (db:genpept-syn) (de:cloning vector tlf97-3, phage lambda lacz translational fusionvector, complete sequence.) (le:19507) (re:20760) (di:complement) CVU39286 U39286 g1066313 Cloning vector TLF97-3 43842 -11533875 7500884791 lacy lactose permease (db:genpept-syn) (de:synthetic transposon tn5lac, complete sequence.) (le:4127) (re:5380) (di:direct) XXU90436 U90436 g2055399 synthetic construct 32630 -11533875 81448 lacy (de:lactose permease (lactose-proton symport)) (db:swissprot) LACY\_ECOLI P02920 ESCHERICHIA COLI 562 -11533875

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501837373	9213	31369	1635	545

# Description

6500730018 many:ptsp:pel:bl1818 pts system:mannose-specific iic component:eiic-man:mannose-permease iic component:phosphotransferase enzyme ii:c component:eii-p-man (gtcfc:12.2) (keggfc:14.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) bl1818 bl1818 Escherichia coli 562 -11533876 92251 many:ptsp:pel (de:(eii-p-man)) (db:swissprot) PTNC\_ECOLI P08187 ESCHERICHIA COLI 562 -11533876 123808 many:ptsp:pel phosphotransferase system enzyme ii::mannose-specific:factor ii-p:mannose permease:factor ii-p:phosphotransferase system enzyme ii-b:mannose-specific:phosphotransferase system enzyme ii-p:mannose-specific:protein-npi-phosphohistidine--mannose phosphotransferase:factor ii-p:protein-npi-phosphohistidine--sugar phosphotransferase:mannose-specific enzyme ii-p (cl:phosphotransferase system mannose-specific enzyme ii, factor ii-p) (ec:2.7.1.69) (db:pir1.dat) (mp:40 min) WQECMP A30285 Escherichia coli 562 -11533876 224307 many:ptsp:pel phosphotransferase system enzyme ii ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #334(40.6-41.0 min.)) (nt:orf\_id:o334#11; similar to (pir accession number) (le:15788) (re:16588) (di:direct) D90825 D90825 g1736456 Escherichia coli 562 -11533876 300953 many:ptsp:pel phosphotransferase system enzyme ii ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #335(40.9-41.3 min.)) (nt:orf\_id:o334#11; similar to (pir accession number) (le:4246) (re:5046) (di:direct) D90826 D90826 g1736463 Escherichia coli 562 -11533876 300948 ptsp mannose permease subunit ii-p-man (sr:e.coli dna, clone rp7029) (db:genpept-bct1) (de:e.coli pts1, ptsp and ptsm genes encoding mannose permease subunitsiii-man, ii-p-man and ii-m-man, complete cds.) (le:1410) (re:2210) (di:direct) ECOPTSLPM J02699 g147403 Escherichia coli 562 -11533876 235597 many pts enzyme iic:mannose-specific (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 166 of 400 of the completegenome.) (nt:o266; 100 pct identical to ptnc\_ecoli sw: p08187;) (le:4766) (re:5566) (di:direct) AE000276 AE000276 g1788121 Escherichia coli 562 -11533876 224313 many:ptsp:pel phosphotransferase system enzyme ii ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #335(40.9-41.3 min.)) (nt:orf\_id:o334#11; similar to (pir accession number) (le:4246) (re:5046) (di:direct) D90826 D90826 g1736463 Escherichia coli 562 -11533876 5000691122 (de:(ecoli\_1775) (pn:pts system, mannose-specific iic component:eiic-man:mannose- permease iic component:phosphotransferase enzyme ii, c component:eii-p-man) (gn:many) (gtcfc:12.2) (ec:) (ptnc\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) ECOLI\_1775 ECOLI\_1775 Escherichia coli 562 10034284

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837380	9214	31370	279	92

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837384	9215	31371	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837393	9216	31372	732	244

Description

6500730019 manz:ptsm:gptb:b1819 pts system:mannose-specific iid component:eiid-man:mannose-permease iid component:phosphotransferase enzyme ii:d component:eii-m-man (gtcfc:12.2) (keggfc:14.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b1819 b1819 Escherichia coli 562 -11533877 92254 manz:ptsm:gptb (de:(eii-m-man)) (db:swissprot) PTND\_ECOLI P08188 ESCHERICHIA COLI 562 -11533877 123807 manz:ptsm phosphotransferase system enzyme ii::mannose-specific:factor ii-m:mannose permease:factor ii-m:protein-npi-phosphohistidine--mannose phosphotransferase:factor ii-m:protein-npi-phosphohistidine--sugar phosphotransferase:mannose-specific:enzyme ii-m (cl:phosphotransferase system mannose-specific enzyme ii, factor ii-m) (ec:2.7.1.69) (db:pir1.dat) (mp:40 min) WQECMM A30288 Escherichia coli 562 -11533877 224314 manz:ptsm:gptb pts system:mannose-specific iid component (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #335(40.9-41.3 min.)) (nt:orf\_id:o335#1; similar to (swissprot accession) (le:5050) (re:5910) (di:direct) D90826 D90826 g1736464 Escherichia coli 562 -11533877 300954 ptsm mannose permease subunit ii-m-man (sr:e.coli dna, clone rp7029) (db:genpept-bct1) (de:e.coli pts1, ptsp and ptsm genes encoding mannose permease subunitsiii-man, ii-p-man and ii-m-man, complete cds.) (le:2214) (re:3074) (di:direct) ECOPTSLPM J02699 g147404 Escherichia coli 562 -11533877 235598 manz pts enzyme iid:mannose-specific (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 166 of 400 of the completegenome.) (nt:o286; 100 pct identical to ptnd\_ecoli sw: p08188;) (le:5570) (re:6430) (di:direct) AE000276 AE000276 g1788122 Escherichia coli 562 -11533877 5000691123 (de:(ecoli\_1776) (pn:pts system, mannose-specific iid component:eiid-man:mannose- permease iid component:phosphotransferase enzyme ii, d component:eii-m-man) (gn:manz) (gtcfc:12.2) (ec:) (ptnd\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) ECOLI\_1776 ECOLI\_1776 Escherichia coli 562 10034287

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837401	9217	31373	432	144

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837424	9218	31374	840	279

Description

GTC ORF with score 242 to: (sr:baker's yeast) (db:genpept-pln2)  
(de:saccharomyces cerevisiae putative transmembrane protein hum1p(hum1)  
gene, complete cds.) (nt:novel protein; putative transmembrane protein;)  
(le:1) (re:1236) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837427	9219	31375	312	103

Description

6500730020 arah:b1898 l-arabinose transport system permease protein arah  
(gtcfc:12.2) (keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b1898  
b1898 Escherichia coli 562 -11533878 7500974861 arah\_2 high-affinity  
l-arabinose transport system (fn:transport; transport of small molecules:)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 173 of 400 of the  
completegenome.) (nt:f86; frameshift in arah relative to arah\_ecoli sw:)  
(le:5382) (re:5642) (di:complement) AE000283 AE000283 g1788208 Escherichia  
coli 562 -11533878 5000691124 (de:(ecoli\_1855) (pn:high-affinity  
l-arabinose transport system; membrane protein) (gn:arah) (gtcfc:12.2) (ec:)  
(arah\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli))  
ECOLI\_1855 ECOLI\_1855 Escherichia coli 562 -11533878 7000691855 b64953  
(de:(pn:l-arabinose transport system permease protein arah) (gn:arah)  
(db:pir)) B64953 B64953 Escherichia coli 562 10123502

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837434	9220	31376	303	100

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837440	9221	31377	564	187

Description

6500730021 arag:b1900 l-arabinose transport atp-binding protein arag (gtcfc:12.2) (keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b1900 b1900 Escherichia coli 562 -11533879 301043 arag (de:l-arabinose transport atp-binding protein arag) (db:swissprot) ARAG\_ECOLI P08531 ESCHERICHIA COLI 562 -11533879 162744 arag l-arabinose transport atp-binding protein arag (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) S01074 S01074 Escherichia coli 562 -11533879 224403 arag arag protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #339(42.4-42.8 min.)) (nt:orf\_id:o339#14; similar to (pir accession number) (le:15295) (re:16809) (di:complement) D90831 D90831 g1736558 Escherichia coli 562 -11533879 301047 arag arag protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #341(42.7-43.1 min.)) (nt:orf\_id:o339#14; similar to (pir accession number) (le:85) (re:1599) (di:complement) D90832 D90832 g1736563 Escherichia coli 562 -11533879 5000691125 (db:genpept-bct1) (de:e. coli l-arabinose transport operon with genes araf, arag andarah.) (nt:arag gene product (aa 1 - 504)) (le:1571) (re:3085) (di:direct) ECARAFGH X06091 g40946 Escherichia coli 562 -11533879 232376 arag atp-binding component of high-affinity (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 173 of 400 of the completegenome.) (nt:f504; 100 pct identical to arag\_ecoli sw: p08531;) (le:6382) (re:7896) (di:complement) AE000283 AE000283 g1788210 Escherichia coli 562 -11533879 59969 arag (de:l-arabinose transport atp-binding protein arag) (db:swissprot) ARAG\_ECOLI P08531 ESCHERICHIA COLI 562 -11533879 224407 arag arag protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #341(42.7-43.1 min.)) (nt:orf\_id:o339#14; similar to (pir accession number) (le:85) (re:1599) (di:complement) D90832 D90832 g1736563 Escherichia coli 562 -11533879

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837441	9222	31378	1098	365

Description

GTC ORF with score 362 to: (fn:conversion of o-methylsterigmatocystin to) (db:genpept-pln2) (de:aspergillus flavus omst-oxidoreductase (ord1) mrna, complete cds.) (nt:cytochrome p450 monooxygenase (cyp64)) (le:235) (re:1821) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837452	9223	31379	237	78
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837484	9224	31380	1005	334
<u>Description</u>				

6500730022 araf:b1901 l-arabinose-binding periplasmic protein precursor:abp (gtcfc:12.2:11.1) (keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b1901 b1901 Escherichia coli 562 -11533880 59968 araf (de:l-arabinose-binding periplasmic protein precursor (abp)) (db:swissprot) ARAF\_ECOLI P02924 ESCHERICHIA COLI 562 -11533880 7000684603 araf l-arabinose-binding protein precursor (cl:l-arabinose-binding protein) (db:pir1.dat) (mp:45 min) JGECA E64953 Escherichia coli 562 -11533880 224404 araf l-arabinose-binding protein precursor (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #339(42.4-42.8 min.)) (nt:orf\_id:o339#15; similar to (pir accession number) (le:16879) (re:17868) (di:complement) D90831 D90831 g1736559 Escherichia coli 562 -11533880 301048 araf l-arabinose-binding protein precursor (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #341(42.7-43.1 min.)) (nt:orf\_id:o339#15; similar to (pir accession number) (le:1669) (re:2658) (di:complement) D90832 D90832 g1736564 Escherichia coli 562 -11533880 301044 araf l-arabinose-binding periplasmic protein (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 173 of 400 of the completegenome.) (nt:f329; 99 pct identical to araf\_ecoli sw: p02924; cg) (le:7966) (re:8955) (di:complement) AE000283 AE000283 g1788211 Escherichia coli 562 -11533880 224408 araf l-arabinose-binding protein precursor (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #341(42.7-43.1 min.)) (nt:orf\_id:o339#15; similar to (pir accession number) (le:1669) (re:2658) (di:complement) D90832 D90832 g1736564 Escherichia coli 562 -11533880 5000691126 (de:(ecoli\_1858) (pn:l-arabinose-binding protein) (gn:araf) (gtcfc:12.2) (ec:) (araf\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_1858 ECOLI\_1858 Escherichia coli 562 10119900

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837487	9225	31381	678	225

#### Description

6500730023 gatc:b2092 pts system:galactitol-specific iic component:eiic-gat:galacticol-permease iic component:phosphotransferase enzyme ii:c component (gtcfc:12.2) (keggfc:14.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b2092 b2092 Escherichia coli 562 -11533881 92210 gatc (de:permease iic component) (phosphotransferase enzyme ii, c component)) (db:swissprot) PTKC\_ECOLI P37189 ESCHERICHIA COLI 562 -11533881 7000686222 gatc gatc protein (cl:phosphotransferase enzyme ii galactitol-specific) (db:pir2.dat) C64976 C64976 Escherichia coli 562 -11533881 224638 gatc pts system:galactitol-specific iic component (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #358(46.6-46.9 min.)) (nt:orf\_id:o358#2; similar to (swissprot accession) (le:10318) (re:11673) (di:complement) D90847 D90847 g1736809 Escherichia coli 562 -11533881 301278 gatc pts system galactitol-specific enzyme iic (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 188 of 400 of the completegenome.) (nt:f451; residues 1-415 are 93 pct identical to) (le:7877) (re:9232) (di:complement) AE000298 AE000298 g1788408 Escherichia coli 562 -11533881 5000691127 (de:(ecoli\_2040) (pn:galactitol-specific enzyme iicof phosphotransferase system) (gn:gatc) (gtcfc:12.2) (ec:) (ptkc\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_2040 ECOLI\_2040 Escherichia coli 562 10120002

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837489	9226	31382	192	63

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837490	9227	31383	453	150

Description

6500730024 mglc:b2148 galactoside transport system permease protein mglc (gtcfc:12.2) (keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b2148 b2148 Escherichia coli 562 -11533882 83641 mglc (de:galactoside transport system permease protein mglc) (db:swissprot) MGLC\_ECOLI P23200 ESCHERICHIA COLI 562 -11533882 164742 mglc transmembrane pore-generating protein mglc (db:pir2.dat) C37277 C37277 Escherichia coli 562 -11533882 7500885593 mglc (sr:e.coli (strain k-12), dna) (db:genpept-bct1) (de:escherichia coli mglb, mglc, and mglc genes, complete cds.) (le:2958) (re:3968) (di:direct) ECOMGLABCO M59444 g146855 Escherichia coli 562 -11533882 235139 mglc methyl-galactoside transport and galactose (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 194 of 400 of the completegenome.) (nt:f336; 100 pct identical to mglc\_ecoli sw: p23200) (le:152) (re:1162) (di:complement) AE000304 AE000304 g1788471 Escherichia coli 562 -11533882 5000691128 (de:(ecoli\_2097) (pn:methyl-galactoside transport and galactose taxis) (gn:mglc) (gtcfc:12.2) (ec:) (mglc\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_2097 ECOLI\_2097 Escherichia coli 562 10025855

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837497	9228	31384	927	308

Description

6500730025 mglc:b2149 galactoside transport atp-binding protein mglc (gtcfc:12.2) (keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b2149 b2149 Escherichia coli 562 -11533883 7000690885 mglc galactoside transport atp-binding protein mglc (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) D64983 D64983 Escherichia coli 562 -11533883 7500955270 mglc atp-binding component of methyl-galactoside (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 194 of 400 of the completegenome.) (nt:f506; 99 pct identical to mglc\_ecoli sw: p23199) (le:1178) (re:2698) (di:complement) AE000304 AE000304 g1788472 Escherichia coli 562 -11533883 5000691129 (de:(ecoli\_2098) (pn:methyl-galactoside transport and galactose taxis, cytoplasmic membrane protein) (gn:mglc) (gtcfc:12.2) (ec:) (mglc\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_2098 ECOLI\_2098 Escherichia coli 562 10123584

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837499	9229	31385	618	205

#### Description

6500730026 mglb:b2150 d-galactose-binding periplasmic protein precursor:gbp:d-galactose/ d-glucose binding protein:ggbp (gtcfc:12.2:11.1:12.9) (keggfc:11.1:12.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b2150 b2150 Escherichia coli 562 -11533884 234757 mglb (de:d-glucose binding protein) (ggbp)) (db:swissprot) DGAL\_ECOLI P02927 ESCHERICHIA COLI 562 -11533884 130816 mglb:mglm d-galactose-binding periplasmic protein precursor:mglb protein (cl:d-galactose-binding protein) (db:pir1.dat) (mp:46 min) JGECG A37277 Escherichia coli 562 -11533884 5000691130 gbp mglb (db:genpept-bct1) (de:e.coli k12 mglb gene for galactose-binding protein (gbp).) (le:107) (re:1105) (di:direct) ECMGLB1 X05646 g762931 Escherichia coli 562 -11533884 235137 d-galactose periplasmic binding protein (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (le:47095) (re:48093) (di:complement) ECOHU47 U00007 g405891 Escherichia coli 562 -11533884 304587 mglb galactoside binding protein (sr:e.coli (strain k-12), dna) (db:genpept-bct1) (de:escherichia coli mglb, mglA, and mglC genes, complete cds.) (le:363) (re:1361) (di:direct) ECOMGLABCO M59444 g146853 Escherichia coli 562 -11533884 233381 mglb galactose-binding transport protein:receptor (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 194 of 400 of the completgenome.) (nt:f332; 100 pct identical to dgal\_ecoli sw: p02927) (le:2759) (re:3757) (di:complement) AE000304 AE000304 g1788473 Escherichia coli 562 -11533884 68327 mglb (de:d-glucose binding protein) (ggbp)) (db:swissprot) DGAL\_ECOLI P02927 ESCHERICHIA COLI 562 -11533884

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837503	9230	31386	186	61

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837517	9231	31387	258	85

Description

6500730027 glpt:b2240 glycerol-3-phosphatase  
transporter:glycerol-3-phosphate transporter:g-3-p transporter:g-3-p  
permease (gtcfc:12.2:11.1) (keggfc:14.2) (rileyfc:4.1.3) (db:gtc-escherichia  
coli) b2240 b2240 Escherichia coli 562 -11533885 7500882522 glpt  
(de:permease)) (db:swissprot) GLPT\_ECOLI P08194 ESCHERICHIA COLI 562  
-11533885 130797 glpt glycerol-3-phosphate transport  
protein:glycerol-3-phosphate permease (cl:hexose phosphate transport protein  
uhpt) (db:pir1.dat) (mp:49 min) JNECGT S00868 Escherichia coli 562 -11533885  
224746 glpt glycerol-3-phosphate transport protein (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #377(50.5-50.9 min.)) (nt:similar to  
(pir accession number s00868)) (le:11300) (re:12658) (di:complement) D90855  
D90855 g1799587 Escherichia coli 562 -11533885 5000691131 (db:genpept-bct1)  
(de:e. coli genes glpt and glpq (partial).) (nt:glycerol-3-phosphatase  
transporter (aa 1 - 452,) (le:170) (re:1528) (di:direct) ECGLPT Y00536  
g41587 Escherichia coli 562 -11533885 233012 glpt sn-glycerol-3-phosphate  
permease (fn:transport; transport of small molecules:) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 204 of 400 of the completegenome.)  
(nt:f452; 100 pct identical to glpt\_ecoli sw: p08194) (le:1467) (re:2825)  
(di:complement) AE000314 AE000314 g1788573 Escherichia coli 562 -11533885  
74055 glpt (de:permease)) (db:swissprot) GLPT\_ECOLI P08194 ESCHERICHIA COLI  
562 -11533885

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837520	9232	31388	201	66

Description

6500730028 fadl:ttr:b2344 long-chain fatty acid transport protein precursor:outer membrane fadl protein:outer membrane flp protein (gtcfc:12.2) (ec:3.1.1.35) (keggfc:14.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b2344 b2344 Escherichia coli 562 -11533886 7000689381 fadl long-chain fatty acid transport protein fadl precursor:flp protein (cl:long-chain fatty acid transport protein fadl) (db:pir2.dat) F65007 F65007 Escherichia coli 562 -11533886 224892 fadl long-chain fatty acid transport protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #410(53.0-53.4 min.)) (nt:similar to (swissprot accession number p10384)) (le:5800) (re:7146) (di:direct) D90865 D90865 g1799743 Escherichia coli 562 -11533886 7500955305 fadl transport of long-chain fatty acids:sensitivity (fn:enzyme; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 213 of 400 of the completegenome.) (nt:o448; 99 pct identical to fadl\_ecoli sw: p10384) (le:771) (re:2117) (di:direct) AE000323 AE000323 g1788686 Escherichia coli 562 -11533886 5000691132 (de:(ecoli\_2293) (pn:transport of long-chain fatty acids; sensitivity to phage t2) (gn:fadl) (gtcfc:12.2) (ec:3.1.1.35) (fadl\_ecoli) (keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_2293 ECOLI\_2293 Escherichia coli 562 10120135

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837523	9233	31389	1779	593

# Description

6500730029 ptsi:b2416 phosphoenolpyruvate-protein  
phosphotransferase:phosphotransferase system:enzyme i (gtcfc:12.2)  
(ec:2.7.3.9) (keggfc:14.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b2416  
b2416 Escherichia coli 562 -11533887 92087 ptsi (ec:2.7.3.9)  
(de:(phosphotransferase system, enzyme i)) (db:swissprot) PT1\_ECOLI P08839  
ESCHERICHIA COLI 562 -11533887 123881 ptsi phosphotransferase system enzyme  
i (cl:phosphotransferase system enzyme i:phosphotransferase system enzyme i  
homology) (ec:2.7.3.9) (db:pir1.dat) (mp:52 min) WQECPI B29785 Escherichia  
coli 562 -11533887 224978 ptsi phosphoenolpyruvate-protein  
phosphotransferase (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara  
lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#418(54.6-54.9 min.)) (nt:similar to (swissprot accession number p08839))  
(le:2434) (re:4161) (di:direct) D90871 D90871 g1799835 Escherichia coli 562  
-11533887 235594 (sr:e.coli (strain tp2110) dna, clone pdia3206)  
(db:genpept-bct1) (de:e.coli cysk gene, 3' end, ptsh, ptsi, and crr  
phototransferasesystem genes, complete cds.) (nt:enzyme i) (le:719)  
(re:2446) (di:direct) ECOPHOSYS M21994 g147264 Escherichia coli 562  
-11533887 7500888903 ptsi (sr:e.coli dna, clone pds20) (db:genpept-bct1)  
(de:e.coli ptsh, ptsi and crr genes encoding cytoplasmic proteins ofthe  
phosphoenolpyruvate:glycose phosphotransferase system (hpr,enzymes i and  
glc-iii), complete cds.) (nt:enzyme i) (le:516) (re:2243) (d... ECOPTSHI  
J02796 g147399 Escherichia coli 562 -11533887 235488 ptsi pep-protein  
phosphotransferase system enzyme i (fn:enzyme; transport of small  
molecules:) (db:genpept-bct2) (ec:2.7.3.9) (de:escherichia coli k-12 mg1655  
section 219 of 400 of the completegenome.) (nt:o575; 100 pct identical to  
pt1\_ecoli sw: p08839) (le:3885) (re:5612) (di:direct) AE000329 AE000329  
g1788756 Escherichia coli 562 -11533887 5000691133 (de:(ecoli\_2357)  
(pn:phosphoenolpyruvate-protein phosphotransferase:phosphotransferase  
system, enzyme i) (gn:ptsi) (gtcfc:12.2) (ec:2.7.3.9) (pt1\_ecoli)  
(keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_2357  
ECOLI\_2357 Escherichia coli 562 10034121



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837533	9234	31390	618	205

Description

6500730030 kgtp:wita:b2587 alpha-ketoglutarate permease (gtcfc:12.2) (keggfc:14.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b2587 b2587 Escherichia coli 562 -11533888 7500884601 kgtp:wita (de:alpha-ketoglutarate permease) (db:swissprot) KGTP\_ECOLI P17448 ESCHERICHIA COLI 562 -11533888 162713 kgtp:wita alpha-ketoglutarate permease (cl:citrate utilization determinant) (db:pir2.dat) (mp:56.5 min) JN0080 JN0080 Escherichia coli 562 -11533888 225162 kgtp alpha-ketoglutarate permease. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #436(58.4-58.8 min.)) (nt:similar to (swissprot accession number p17448)) (le:9751) (re:11049) (di:complement) D90886 D90886 g1799990 Escherichia coli 562 -11533888 225165 kgtp alpha-ketoglutarate permease. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #437(58.6-59.0 min.)) (nt:similar to (swissprot accession number p17448)) (le:2598) (re:3896) (di:complement) D90887 D90887 g1799994 Escherichia coli 562 -11533888 5000691134 kgtp::gene alpha-ketoglutarate transporter (db:genpept-bct1) (de:e.coli kgtp gene.) (le:152) (re:1450) (di:direct) ECWITAG X53027 g43305 Escherichia coli 562 -11533888 240378 kgtp alpha-ketoglutarate permease (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 235 of 400 of the completegenome.) (nt:f432; 100 pct identical to kgtp\_ecoli sw: p17448) (le:1810) (re:3108) (di:complement) AE000345 AE000345 g1788942 Escherichia coli 562 -11533888 80653 kgtp:wita (de:alpha-ketoglutarate permease) (db:swissprot) KGTP\_ECOLI P17448 ESCHERICHIA COLI 562 -11533888

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837535	9235	31391	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837538	9236	31392	474	157

Description

6500730031 gabp:b2663 gaba permease:4-amino butyrate transport carrier:gama-aminobutyrate permease (gtcfc:12.2) (keggfc:14.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b2663 b2663 Escherichia coli 562 -11533889 72878 gabp (de:permease)) (db:swissprot) GABP\_ECOLI P25527 ESCHERICHIA COLI 562 -11533889 7000685344 gabp gamma-aminobutyrate permease:gaba permease 4-amino butyrate transport carrier (cl:arginine permease) (db:pir2.dat) H65045 H65045 Escherichia coli 562 -11533889 225217 gabp gaba permease 4-amino butyrate transport (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #443(59.8-60.2 min.)) (nt:similar to (swissprot accession number p25527)) (le:14422) (re:15822) (di:direct) D90890 D90890 g1800049 Escherichia coli 562 -11533889 236056 gabp transport permease protein of (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 241 of 400 of the completengenome.) (nt:o466; 100 pct identical to gabp\_ecoli sw: p25527) (le:5976) (re:7376) (di:direct) AE000351 AE000351 g1789017 Escherichia coli 562 -11533889 7500882058 gabp gaba permease (sr:escherichia coli (strain k-12) dna) (db:genpept-bct2) (de:e.coli succinic semialdehyde dehydrogenase (gabd) gene, completecds; gaba transaminase (gabt) gene, complete cds; gaba permease(gabp) gene, complete cds.) (le:3616) (re:5016) (di:direct) ECOSUSEDEH M88334 g147903 Escherichia coli 562 -11533889 5000691135 (de:(ecoli\_2596) (pn:transport of gamma-aminobutyrate) (gn:gabp) (gtcfc:12.2) (ec:) (gabp\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_2596 ECOLI\_2596 Escherichia coli 562 10015424

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837541	9237	31393	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837542	9238	31394	453	150

Description

6500730032 fucp:b2801 l-fucose permease (gtcfc:12.2) (keggfc:14.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b2801 b2801 Escherichia coli 562 -11533890 239375 fucp (de:l-fucose permease) (db:swissprot) FUCP\_ECOLI P11551 ESCHERICHIA COLI 562 -11533890 130801 fucp l-fucose permease (cl:fucose permease) (db:pir1.dat) (mp:60 min) WQECFP JS0184 Escherichia coli 562 -11533890 5000691136 (db:genpept-bct1) (de:escherichia coli fucose operon.) (nt:fucp orf (aa 1-438)) (le:2608) (re:3924) (di:direct) ECFUCOSE X15025 g41504 Escherichia coli 562 -11533890 7500881906 fucp l-fucose permease (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:cg site no. 10875; orf\_o438) (le:15790) (re:17106) (di:direct) ECU29581 U29581 g882696 Escherichia coli 562 -11533890 232931 fucp fucose permease (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 254 of 400 of the completegenome.) (nt:o438; 100 pct identical to fucp\_ecoli sw: p11551;) (le:304) (re:1620) (di:direct) AE000364 AE000364 g1789166 Escherichia coli 562 -11533890 72509 fucp (de:l-fucose permease) (db:swissprot) FUCP\_ECOLI P11551 ESCHERICHIA COLI 562 -11533890

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837554	9239	31395	624	207

Description

6500730033 galp:b2943 galactose-proton symport:galactose transporter (gtcfc:12.2) (keggfc:14.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b2943 b2943 Escherichia coli 562 -11533891 73087 galp (de:galactose-proton symport (galactose transporter)) (db:swissprot) GALP\_ECOLI P37021 ESCHERICHIA COLI 562 -11533891 7000685364 galp galactose-proton symport galactose transporter (cl:glucose transport protein) (db:pir2.dat) F65079 F65079 Escherichia coli 562 -11533891 7500882092 galp (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf\_o464) (le:42678) (re:44072) (di:direct) ECU28377 U28377 g882472 Escherichia coli 562 -11533891 239156 galp galactose-proton symport of transport system (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 267 of 400 of the completegenome.) (nt:o464; 100 pct identical to galp\_ecoli sw: p37021) (le:6602) (re:7996) (di:direct) AE000377 AE000377 g1789312 Escherichia coli 562 -11533891 5000691137 (de:(ecoli\_2865) (pn:galactose permease) (gn:galp) (gtcfc:12.2) (ec:) (galp\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_2865 ECOLI\_2865 Escherichia coli 562 10015634

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837563	9240	31396	231	76

Description

6500730034 exut:b3093 hexuronate transporter (gtcfc:12.2) (keggfc:14.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3093 b3093 Escherichia coli 562 -11533892 7500881255 exut (de:hexuronate transporter) (db:swissprot) EXUT\_ECOLI P42609 ESCHERICHIA COLI 562 -11533892 7000690903 exut hexuronate transporter (cl:hexuronate transporter) (db:pir2.dat) B65098 B65098 Escherichia coli 562 -11533892 237616 exut aldohexuronate transport system (sr:escherichia coli (strain:k12) cell\_line:w3110 dna) (db:genpept-bct1) (de:escherichia coli uxaa, uxac, exut and exur genes for altronatedehydratase, uronate isomerase, aldohexuronate transport system andexu regulon repressor, complete cds.) (le:4362... D13328 D13328 g1160319 Escherichia coli 562 -11533892 7500881257 exut transport of hexuronates (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 281 of 400 of the completegenome.) (nt:o472; 99 pct identical to exut\_ecoli sw: p42609) (le:6694) (re:8112) (di:direct) AE000391 AE000391 g2367193 Escherichia coli 562 -11533892 303403 exut aldohexuronate transport system (sr:escherichia coli (strain:k12) cell\_line:w3110 dna) (db:genpept-bct1) (de:escherichia coli uxaa, uxac, exut and exur genes for altronatedehydratase, uronate isomerase, aldohexuronate transport system andexu regulon repressor, complete cds.) (le:4362... D13328 D13328 g1160319 Escherichia coli 562 -11533892

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837574	9241	31397	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837575	9242	31398	534	177

#### Description

6500730035 gntt:usga:gntm:b3415 high-affinity gluconate transporter:gluconate permease:gnt-i system (gtcfc:12.2) (keggfc:14.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3415 b3415 Escherichia coli 562 -11533893 74257 gntt:usga:gntm (de:system)) (db:swissprot) GNTT\_ECOLI P39835 ESCHERICHIA COLI 562 -11533893 1500685250 gntt high-affinity gluconate transporter:gluconate permease component t (cl:d-serine permease) (db:pir2.dat) JC4988 JC4988 Escherichia coli 562 -11533893 7500882621 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf\_o437) (le:327302) (re:328615) (di:direct) ECOUW67 U18997 g606350 Escherichia coli 562 -11533893 236649 gntt high-affinity transport of gluconate / gluconate (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 307 of 400 of the completegenome.) (nt:o437; 100 pct identical amino acid sequence and) (le:3524) (re:4837) (di:direct) AE000417 AE000417 g1789820 Escherichia coli 562 -11533893 5000691139 (de:(ecoli\_3333) (pn:high-affinity gluconate transporter:gluconate permease) (gn:gntt) (gtcfc:12.2) (ec:) (gntt\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_3333 ECOLI\_3333 Escherichia coli 562 10016779

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837595	9243	31399	216	71

#### Description

6500730036 ugpc:b3450 sn-glycerol-3-phosphate transport atp-binding protein (gtcfc:12.2) (keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3450 b3450 Escherichia coli 562 -11533894 130729 ugpc sn-glycerol-3-phosphate transport atp-binding protein (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir1.dat) (mp:76 min) QRECUC S47669 Escherichia coli 562 -11533894 7500953605 ugpc (fn:sn-glycerol-3-phosphate transport system) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 17794) (le:2372) (re:3481) (di:complement) ECOUW76 U00039 g912455 Escherichia coli 562 -11533894 236685 ugpc atp-binding component of sn-glycerol 3-phosphate (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 311 of 400 of the completegenome.) (nt:f369; 100 pct identical to ugpc\_ecoli sw: p10907;) (le:3663) (re:4772) (di:complement) AE000421 AE000421 g1789859 Escherichia coli 562 -11533894 5000691140 (de:(ecoli\_3368) (pn:sn-glycerol 3-phosphate transport system, permease) (gn:ugpc) (gtcfc:12.2) (ec:) (ugpc\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_3368 ECOLI\_3368 Escherichia coli 562 10067954

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837599	9244	31400	513	170

Description

6500730037 ugpe:b3451 sn-glycerol-3-phosphate transport system permease protein:sn-glycerol-3-phosphate transport system permease protein ugpe (gtcfc:12.2:11.1) (keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3451 b3451 Escherichia coli 562 -11533895 7500893761 ugpe (de:sn-glycerol-3-phosphate transport system permease protein ugpe) (db:swissprot) UGPE\_ECOLI P10906 ESCHERICHIA COLI 562 -11533895 130792 ugpe sn-glycerol-3-phosphate transport system permease protein (cl:maltose transport protein malg) (db:pir1.dat) (mp:76 min) MMECUE S03782 Escherichia coli 562 -11533895 240331 ugpe (fn:sn-glycerol-3-phosphate transport system) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 17791; membrane protein) (le:3444) (re:42... ECOUW76 U00039 g466587 Escherichia coli 562 -11533895 5000691141 (db:genpept-bct1) (de:e. coli ugp locus dna with genes ugpbace.) (nt:ugpe protein (aa 1-281)) (le:2653) (re:3498) (di:direct) ECUGP X13141 g43248 Escherichia coli 562 -11533895 236686 ugpe sn-glycerol 3-phosphate transport system (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 311 of 400 of the completengenome.) (nt:f281; 100 pct identical to ugpe\_ecoli sw: p10906;) (le:4735) (re:5580) (di:complement) AE000421 AE000421 g1789860 Escherichia coli 562 -11533895 103345 ugpe (de:sn-glycerol-3-phosphate transport system permease protein ugpe) (db:swissprot) UGPE\_ECOLI P10906 ESCHERICHIA COLI 562 -11533895

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837603	9245	31401	231	76

Description

6500730038 ugpa:b3452 sn-glycerol-3-phosphate transport system permease protein:sn-glycerol-3-phosphate transport system permease protein ugpa (gtcfc:12.2:11.1) (keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3452 b3452 Escherichia coli 562 -11533896 7500893759 ugpa (de:sn-glycerol-3-phosphate transport system permease protein ugpa) (db:swissprot) UGPA\_ECOLI P10905 ESCHERICHIA COLI 562 -11533896 130772 ugpa sn-glycerol-3-phosphate transport system permease protein (cl:inner membrane protein ugpa) (db:pir1.dat) (mp:76 min) MMECUA S03781 Escherichia coli 562 -11533896 240330 ugpa (fn:sn-glycerol-3-phosphate transport system) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 40) (le:4286) (re:5173) (di:complement) ECOUW76 U00039 g466588 Escherichia coli 562 -11533896 5000691142 (db:genpept-bct1) (de:e. coli ugp locus dna with genes ugpbase.) (nt:ugpa protein (aa 1-295)) (le:1769) (re:2656) (di:direct) ECUGP X13141 g43247 Escherichia coli 562 -11533896 236687 ugpa sn-glycerol 3-phosphate transport system (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 311 of 400 of the completegenome.) (nt:f295; 100 pct identical to ugpa\_ecoli sw: p10905;) (le:5577) (re:6464) (di:complement) AE000421 AE000421 g1789861 Escherichia coli 562 -11533896 103342 ugpa (de:sn-glycerol-3-phosphate transport system permease protein ugpa) (db:swissprot) UGPA\_ECOLI P10905 ESCHERICHIA COLI 562 -11533896

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837610	9246	31402	414	137

Description

6500730039 ugpb:b3453 glycerol-3-phosphate-binding periplasmic protein precursor (gtcfc:12.2:11.1) (keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3453 b3453 Escherichia coli 562 -11533897 153226 ugpb glycerol-3-phosphate-binding protein precursor:ugpb protein (cl:glycerol-3-phosphate-binding protein) (db:pir1.dat) (mp:76 min) JGECGP S47672 Escherichia coli 562 -11533897 7500953617 ugpb (fn:sn-glycerol-3-phosphate transport system) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 39; periplasmic binding protein) (le:5271... ECOUW76 U00039 g466589 Escherichia coli 562 -11533897 236688 ugpb sn-glycerol 3-phosphate transport system (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 311 of 400 of the completegenome.) (nt:f438; 99 pct identical amino acid sequence and) (le:6562) (re:7878) (di:complement) AE000421 AE000421 g1789862 Escherichia coli 562 -11533897 5000691143 (de:(ecoli\_3371) (pn:sn-glycerol 3-phosphate transport system; periplasmic binding protein) (gn:ugpb) (gtcfc:12.2) (ec:) (ugpb\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_3371 ECOLI\_3371 Escherichia coli 562 10080848

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837615	9247	31403	216	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837619	9248	31404	249	82

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837622	9249	31405	498	165

#### Description

6500730040 dcta:b3528 c4-dicarboxylate transport protein (gtcfc:12.2) (keggfc:14.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3528 b3528 Escherichia coli 562 -11533898 68120 dcta (de:c4-dicarboxylate transport protein) (db:swissprot) DCTA\_ECOLI P37312 ESCHERICHIA COLI 562 -11533898 162910 dcta c4-dicarboxylate transport protein dcta (cl:c4-dicarboxylate carrier protein) (db:pir2.dat) S47749 S47749 Escherichia coli 562 -11533898 7500880091 dcta (fn:uptake of c4-dicarboxylic acids) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 872) (le:96417) (re:97703) (di:complement) ECOUW76 U00039 g466666 Escherichia coli 562 -11533898 236765 dcta uptake of c4-dicarboxylic acids (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 319 of 400 of the completegenome.) (nt:f428; cg site no. 872) (le:7647) (re:8933) (di:complement) AE000429 AE000429 g1789947 Escherichia coli 562 -11533898 5000691144 (de:(ecoli\_3448) (pn:uptake of c4-dicarboxylic acids) (gn:dcta) (gtcfc:12.2) (ec:) (dcta\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_3448 ECOLI\_3448 Escherichia coli 562 10010713

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837623	9250	31406	456	151

#### Description

6500730041 xylf:xylt:b3566 xylf:d-xylose-binding periplasmic protein precursor (gtcfc:12.2:11.1) (keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3566 b3566 Escherichia coli 562 -11533899 108224 xylf:xylt (de:d-xylose-binding periplasmic protein precursor) (db:swissprot) XYL\_F\_ECOLI P37387 ESCHERICHIA COLI 562 -11533899 164836 xylf xylf protein (db:pir2.dat) S47787 S47787 Escherichia coli 562 -11533899 7500894489 xylf (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:145382) (re:146374) (di:direct) ECOUW76 U00039 g466704 Escherichia coli 562 -11533899 236803 xylf xylose binding protein transport system (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 324 of 400 of the completegenome.) (nt:o330) (le:274) (re:1266) (di:direct) AE000434 AE000434 g1789990 Escherichia coli 562 -11533899 5000691145 (de:(ecoli\_3486) (pn:xylose binding protein transport system) (gn:xylf) (gtcfc:12.2) (ec:) (xylf\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_3486 ECOLI\_3486 Escherichia coli 562 10049956

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837636	9251	31407	432	143

Description

6500730042 xylg:b3567 d-xylose transport atp-binding protein xylg (gtcfc:12.2) (keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3567 b3567 Escherichia coli 562 -11533900 108227 xylg (de:d-xylose transport atp-binding protein xylg) (db:swissprot) XYLG\_ECOLI P37388 ESCHERICHIA COLI 562 -11533900 164837 xylg d-xylose transport atp-binding protein xylg (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) S47788 S47788 Escherichia coli 562 -11533900 7500894491 xylg (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:146452) (re:147993) (di:direct) ECOUW76 U00039 g466705 Escherichia coli 562 -11533900 236804 xylg putative atp-binding protein of xylose transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 324 of 400 of the completegenome.) (nt:o513; 100 pct identical amino acid sequence and) (le:1344) (re:2885) (di:direct) AE000434 AE000434 g1789991 Escherichia coli 562 -11533900 5000691146 (de:(ecoli\_3487) (pn:putative xylose transport, atp-binding protein) (gn:xylg) (gtcfc:12.2) (ec:) (xylg\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_3487 ECOLI\_3487 Escherichia coli 562 10049959

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837644	9252	31408	282	93

Description

6500730043 xylh:b3568 xylose transport permease protein xylh (gtcfc:12.2:11.1) (keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3568 b3568 Escherichia coli 562 -11533901 108230 xylh (de:xylose transport permease protein xylh) (db:swissprot) XYLH\_ECOLI P37389 ESCHERICHIA COLI 562 -11533901 164838 xylh xylose transport permease protein xylh (cl:l-arabinose transport system permease arah) (db:pir2.dat) S47789 S47789 Escherichia coli 562 -11533901 7500894493 xylh (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:147971) (re:149152) (di:direct) ECOUW76 U00039 g466706 Escherichia coli 562 -11533901 236805 xylh putative xylose transport:membrane component (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 324 of 400 of the completegenome.) (nt:o393; 100 pct identical amino acid sequence and) (le:2863) (re:4044) (di:direct) AE000434 AE000434 g1789992 Escherichia coli 562 -11533901 5000691147 (de:(ecoli\_3488) (pn:putative xylose transport, membrane component) (gn:xylh) (gtcfc:12.2) (ec:) (xylh\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_3488 ECOLI\_3488 Escherichia coli 562 10049962

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837645	9253	31409	1080	359

Description

6500730044 glvg:b3681 probable 6-phospho-beta-glucosidase (gtcfc:12.2) (ec:3.2.1.86) (keggfc:14.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3681 b3681 Escherichia coli 562 -11533902 74188 glvg (ec:3.2.1.86) (de:probable 6-phospho-beta-glucosidase,) (db:swissprot) GLVG\_ECOLI P31450 ESCHERICHIA COLI 562 -11533902 7000685431 glvg probable 6-phospho-beta-glucosidase (ec:3.2.1.86) (db:pir2.dat) B65170 B65170 Escherichia coli 562 -11533902 7500882586 f212 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:similar to e. coli cele protein) (le:50743) (re:51381) (di:complement) ECOUW82 L10328 g290530 Escherichia coli 562 -11533902 236918 glvg probable 6-phospho-beta-glucosidase (fn:putative enzyme; transport of small molecules:) (db:genpept-bct2) (ec:3.2.1.86) (de:escherichia coli k-12 mg1655 section 335 of 400 of the completegenome.) (nt:f212; 100 pct identical to glvg\_ecoli sw: p31450) (le:8524) (re:9162) (di:complement) AE000445 AE000445 g1790115 Escherichia coli 562 -11533902 5000691152 (de:(ecoli\_3600) (pn:probable 6-phospho-beta-glucosidase) (gn:glvg) (gtcfc:12.2) (ec:3.2.1.86) (glvg\_ecoli) (keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_3600 ECOLI\_3600 Escherichia coli 562 10016710

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837651	9254	31410	582	193

Description

6500730045 glvc:b3683 pts system arbutin-like iic component (gtcfc:12.2) (keggfc:14.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3683 b3683 Escherichia coli 562 -11533903 7000691901 glvc pts system arbutin-like iic component (db:pir2.dat) D65170 D65170 Escherichia coli 562 -11533903 7500960439 f455 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:similar to phosphotransferase system ii permeases) (le:51891) (re:53258) (di:complement) ECOUW82 L10328 g290532 Escherichia coli 562 -11533903 236920 glvc pts system:arbutin-like iic component (fn:enzyme; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 335 of 400 of the completegenome.) (nt:f455; 100 pct identical to ptic\_ecoli sw: p31452) (le:9672) (re:11039) (di:complement) AE000445 AE000445 g1790117 Escherichia coli 562 -11533903 5000691153 (de:(ecoli\_3602) (pn:pts system, arbutin-like iic component:phosphotransferase enzyme ii, c component) (gn:glvc) (gtcfc:12.2) (ec:) (ptic\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_3602 ECOLI\_3602 Escherichia coli 562 10124066

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837654	9255	31411	840	279

Description

GTC ORF with score 150 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k07c11.) (nt:coded for by c. elegans cdna cml2g2; coded for by) (le:11088:11496:12194) (re:11399:11750:12401) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837656	9256	31412	273	90

Description

6500730046 rbsd:b3748 high affinity ribose transport protein rbsd (gtcfc:12.2) (keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3748 b3748 Escherichia coli 562 -11533904 93576 rbsd (de:high affinity ribose transport protein rbsd) (db:swissprot) RBSD\_ECOLI P04982 ESCHERICHIA COLI 562 -11533904 7000686283 rbsd high affinity ribose transport protein rbsd (cl:fucoase operon u protein) (db:pir2.dat) (mp:84) E65178 Escherichia coli 562 -11533904 7500889475 rbsd::cg site no. 314 (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:alternate gene name rbsp) (le:122703) (re:123158) (di:direct) ECOUW82 L10328 g290598 Escherichia coli 562 -11533904 236986 rbsd d-ribose high-affinity transport system (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 342 of 400 of the completegenome.) (nt:o151; 100 pct identical to rbsd\_ecoli sw: p04982;) (le:320) (re:775) (di:direct) AE000452 AE000452 g1790189 Escherichia coli 562 -11533904 5000691154 (de:(ecoli\_3667) (pn:d-ribose high-affinity transport system; membrane-associated protein) (gn:rbsd) (gtcfc:12.2) (ec:) (rbsd\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_3667 ECOLI\_3667 Escherichia coli 562 10035569

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837678	9257	31413	939	312

Description

6500730047 rbsa:b3749 high affinity ribose transport protein:ribose transport atp-binding protein rbsa (gtcfc:12.2) (keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3749 b3749 Escherichia coli 562 -11533905 93562 rbsa (de:ribose transport atp-binding protein rbsa) (db:swissprot) RBSA\_ECOLI P04983 ESCHERICHIA COLI 562 -11533905 164549 rbsa ribose transport protein rbsa (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) (mp:84) B26304 B26304 Escherichia coli 562 -11533905 7500889467 rbsa high affinity ribose transport protein (sr:e.coli k12 dna) (db:genpept-bct1) (de:e.coli k12 rbsd, rbsa, rbsc, rbsb, rbsk, and rbsr genes encoding the high affinity ribose transport system, complete cds.) (le:612) (re:2117) (di:direct) ECORBS M13169 g147513 Escherichia coli 562 -11533905 235694 rbsa atp-binding component of d-ribose high-affinity (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 342 of 400 of the complete genome.) (nt:o501; 99 pct identical amino acid sequence and) (le:783) (re:2288) (di:direct) AE000452 AE000452 g1790190 Escherichia coli 562 -11533905 5000691155 (de:(ecoli\_3668) (pn:d-ribose high-affinity transport system; membrane-associated protein) (gn:rbsa) (gtcfc:12.2) (ec:) (rbsa\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_3668 ECOLI\_3668 Escherichia coli 562 10035555

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837701	9258	31414	381	126

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837703	9259	31415	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837710	9260	31416	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837713	9261	31417	1011	336

Description

6500730048 rbsc:b3750 high affinity ribose transport protein:ribose transport system permease protein rbsc (gtcfc:12.2:11.1) (keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3750 b3750 Escherichia coli 562 -11533906 93572 rbsc (de:ribose transport system permease protein rbsc) (db:swissprot) RBSC\_ECOLI P04984 ESCHERICHIA COLI 562 -11533906 7000686281 rbsc high affinity ribose transport protein rbsc (cl:l-arabinose transport system permease arah) (db:pir2.dat) (mp:84 min) G65178 G65178 Escherichia coli 562 -11533906 7500889472 rbsc high affinity ribose transport protein (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:alternate gene names rbsp, rbst) (le:124676) (re:125641) (di:direct) ECOUW82 L10328 g290600 Escherichia coli 562 -11533906 236988 rbsc d-ribose high-affinity transport system (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 342 of 400 of the completengenome.) (nt:o321; 100 pct identical to rbsc\_ecoli sw: p04984;) (le:2293) (re:3258) (di:direct) AE000452 AE000452 g1790191 Escherichia coli 562 -11533906 5000691156 (de:(ecoli\_3669) (pn:d-ribose high-affinity transport system; membrane-associated protein) (gn:rbsc) (gtcfc:12.2) (ec:) (rbsc\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_3669 ECOLI\_3669 Escherichia coli 562 10035565

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501837714	9262	31418	564	188

# Description

6500730049 rbsb:rbsp:prlb:b3751 periplasmic ribose-binding protein precursor:d-ribose-binding periplasmic protein precursor (gtcfc:12.2:11.1:12.9) (keggfc:11.1:12.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3751 b3751 Escherichia coli 562 -11533907 93566 rbsb:rbsp:prlb (de:d-ribose-binding periplasmic protein precursor) (db:swissprot) RBSB\_ECOLI P02925 ESCHERICHIA COLI 562 -11533907 130811 rbsb periplasmic ribose-binding protein precursor (cl:lac repressor) (db:pir1.dat) JGECR A03425 Escherichia coli 562 -11533907 235699 rbsb periplasmic ribose-binding protein (sr:e.coli k12 dna) (db:genpept-bct1) (de:e.coli k12 rbsd, rbsa, rbsc, rbsb, rbsk, and rbsr genes encodingthe high affinity ribose transport system, complete cds.) (le:3112) (re:4002) (di:direct) ECORBS M13169 g147515 Escherichia coli 562 -11533907 236989 rbsp pre-d-ribose-binding protein (sr:escherichia coli k12 dna) (db:genpept-bct1) (de:e.coli d-ribose-binding protein (rbsp) gene, complete cds.) (le:1) (re:891) (di:direct) ECORBSP K00511 g147519 Escherichia coli 562 -11533907 7500889470 rbsb::cg site no. 1... periplasmic ribose-binding protein precursor (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:alternate gene name rbsp) (le:125666) (re:126556) (di:direct) ECOUW82 L10328 g290601 Escherichia coli 562 -11533907 235696 rbsb d-ribose periplasmic binding protein (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 342 of 400 of the completegenome.) (nt:o296; 100 pct identical to rbsb\_ecoli sw: p02925;) (le:3283) (re:4173) (di:direct) AE000452 AE000452 g1790192 Escherichia coli 562 -11533907 5000691157 (de:(ecoli\_3670) (pn:d-ribose periplasmic binding protein) (gn:rbsb) (gtcfc:12.2) (ec:) (rbsb\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_3670 ECOLI\_3670 Escherichia coli 562 10035559

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837719	9263	31419	639	212

Description

6500730050 frvr:b3897 putative frv operon regulatory protein (gtcfc:12.2) (keggfc:14.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3897 b3897  
Escherichia coli 562 -11533908 72376 frvr (de:putative frv operon regulatory protein) (db:swissprot) FRVR\_ECOLI P32152 ESCHERICHIA COLI 562 -11533908 163679 frvr probable frv operon regulatory protein:hypothetical protein f582 (db:pir2.dat) S40841 S40841 Escherichia coli 562 -11533908 7500881764 (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:49747) (re:51495) (di:complement) ECOUW87 L19201 g305001 Escherichia coli 562 -11533908 237115 frvr putative frv operon regulatory protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 355 of 400 of the completegenome.) (nt:f582; 100 pct identical amino acid sequence and) (le:2285) (re:4033) (di:complement) AE000465 AE000465 g1790331 Escherichia coli 562 -11533908 5000691158 (de:(ecoli\_3796) (pn:putative frv operon regulatory protein) (gn:frvr) (gtcfc:12.2) (ec:) (frvr\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_3796 ECOLI\_3796 Escherichia coli 562 10014927

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837737	9264	31420	228	75

Description

6500730051 rhat:b3907 rhamnose permease:l-rhamnose-proton  
symport:l-rhamnose-h+ transport protein (gtcfc:12.2:11.1) (keggfc:14.2)  
(rileyfc:4.1.3) (db:gtc-escherichia coli) b3907 b3907 Escherichia coli 562  
-11533909 304624 rhat (de:l-rhamnose-proton symport (l-rhamnose-h+  
transport protein)) (db:swissprot) RHAT\_ECOLI P27125 ESCHERICHIA COLI 562  
-11533909 163986 rhat l-rhamnose-h+ transport protein:rhamnose permease  
(db:pir2.dat) B42436 B42436 Escherichia coli 562 -11533909 237125 rhat  
l-rhamnose-h+ transport protein (sr:escherichia coli (strain k-12) (library:  
lambda from kohara et al.) (db:genpept-bct1) (de:escherichia coli  
l-rhamnose-h+ transport protein (rhat) gene,complete cds.) (le:474)  
(re:1508) (di:direct) ECRHAT M85158 g147595 Escherichia coli 562 -11533909  
238070 rhat rhamnose permease (sr:escherichia coli (sub\_strain mg1655,  
strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal  
region from 87.2 to 89.2 minutes.) (le:61124) (re:62158) (di:complement)  
ECOUW87 L19201 g305011 Escherichia coli 562 -11533909 5000691159 rhat  
l-rhamnose permease (db:genpept-bct1) (de:e. coli rhat gene for l-rhamnose  
permease, rhac (3' end) and soda(5' end) genes.) (le:573) (re:1607)  
(di:direct) ECRHAT X60699 g42728 Escherichia coli 562 -11533909 235785 rhat  
rhamnose transport (fn:transport; transport of small molecules:)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 355 of 400 of the  
completegenome.) (nt:f344; 100 pct identical amino acid sequence and)  
(le:13669) (re:14703) (di:complement) AE000465 AE000465 g1790341 Escherichia  
coli 562 -11533909 94266 rhat (de:l-rhamnose-proton symport (l-rhamnose-h+  
transport protein)) (db:swissprot) RHAT\_ECOLI P27125 ESCHERICHIA COLI 562  
-11533909

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837738	9265	31421	1134	377

Description

6500730052 kdgt:b3909 2-keto-3-deoxygluconate permease:kdg permease  
 (gtcfc:12.2) (keggfc:14.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3909  
 b3909 Escherichia coli 562 -11533910 164368 kdgt probable  
 2-keto-3-deoxygluconate transport protein:kdgt protein (db:pir2.dat) S40853  
 S40853 Escherichia coli 562 -11533910 237127 kdgt  
 (fn:2-keto-3-deoxygluconate transport) (sr:escherichia coli (sub\_strain  
 mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli  
 chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 589; similar  
 to erwinia chrysanthemi) (le:63314)... ECOUW87 L19201 g305013 Escherichia  
 coli 562 -11533910 7500960422 kdgt 2-keto-3-deoxy-d-gluconate transport  
 system (fn:transport; transport of small molecules:) (db:genpept-bct2)  
 (de:escherichia coli k-12 mg1655 section 355 of 400 of the completegenome.)  
 (nt:o330; 100 pct identical to kdgt\_ecoli sw: p32172;) (le:15859) (re:16851)  
 (di:direct) AE000465 AE000465 g1790343 Escherichia coli 562 -11533910 80590  
 kdgt\_ecoli (de:2-keto-3-deoxygluconate permease (kdg permease).) P32172  
 P32172 Escherichia coli 562 -11533910 5000691160 (de:(ecoli\_3808)  
 (pn:2-keto-3-deoxy-d-gluconate transport system) (gn:kdgt) (gtcfc:12.2)  
 (ec:) (kdgt\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli))  
 ECOLI\_3808 ECOLI\_3808 Escherichia coli 562 10022832

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837739	9266	31422	279	92

Description

6500730053 glpf:b3927 glycerol uptake facilitator protein (gtcfc:12.2) (keggfc:14.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b3927 b3927 Escherichia coli 562 -11533911 74028 glpf (de:glycerol uptake facilitator protein) (db:swissprot) GLPF\_ECOLI P11244 ESCHERICHIA COLI 562 -11533911 154808 glpf glycerol facilitator protein:glpf protein:glycerol diffusion facilitator (cl:glycerol facilitator protein) (db:pir1.dat) (mp:88 min) XMECGF A42157 Escherichia coli 562 -11533911 237144 glpf glycerol diffusion facilitator (sr:e.coli (k-12) dna) (db:genpept-bct1) (de:e.coli glycerol diffusion facilitator (glpf) and glycerol kinase(glpk) genes, complete cds.) (le:201) (re:1046) (di:direct) ECOGLPFK M55990 g146188 Escherichia coli 562 -11533911 7500882497 glpf (fn:facilitates glycerol diffusion) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 692) (le:78878) (re:79723) (di:complement) ECOUW87 L19201 g305030 Escherichia coli 562 -11533911 234522 glpf facilitated diffusion of glycerol (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 357 of 400 of the completegenome.) (nt:f281; 100 pct identical to glpf\_ecoli sw: p11244;) (le:4371) (re:5216) (di:complement) AE000467 AE000467 g1790362 Escherichia coli 562 -11533911 5000691161 (de:(ecoli\_3825) (pn:facilitated diffusion of glycerol) (gn:glpf) (gtcfc:12.2) (ec:) (glpf\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_3825 ECOLI\_3825 Escherichia coli 562 10016558

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837747	9267	31423	405	134

Description

6500730054 xyle:b4031 xylose-proton symport:xylose transporter (gtcfc:12.2) (keggfc:14.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b4031 b4031  
 Escherichia coli 562 -11533912 108222 xyle (de:d-xylose-proton symport (d-xylose transporter)) (db:swissprot) XYLE\_ECOLI P09098 ESCHERICHIA COLI 562 -11533912 164839 xyle xylose transport protein:xylose-proton symport protein (cl:glucose transport protein) (db:pir2.dat) (mp:91.4) A26430 A26430  
 Escherichia coli 562 -11533912 237650 xyle xylose-proton symport (sr:escherichia coli (strain k-12) (clone: pej3.) dna) (db:genpept-bct1) (de:escherichia coli xylose-proton symport (xyle) gene, complete cds and maltose transport (malg) gene, 3' end.) (le:404) (re:1879) (di:direct) ECOXYLE J02812 g148284 Escherichia coli 562 -11533912 237237 xyle xylose-proton symport (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 366 of 400 of the complete genome.) (nt:f491; 100 pct identical to xyle\_ecoli sw: p09098;) (le:7490) (re:8965) (di:complement) AE000476 AE000476 g1790463 Escherichia coli 562 -11533912 7500894488 xyle xylose-proton symport (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 17776) (le:106021) (re:107496) (di:complement) ECOUW89 U00006 g396366 Escherichia coli 562 -11533912 5000691162 (de:(ecoli\_3917) (pn:xylose-proton symport) (gn:xyle) (gtcfc:12.2) (ec:) (xyle\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_3917 ECOLI\_3917 Escherichia coli 562 10049954

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837751	9268	31424	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837762	9269	31425	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837783	9270	31426	459	153

Description

6500730055 malg:b4032 maltose transport inner membrane protein:maltose transport system permease protein malg (gtcfc:12.2:11.1) (keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b4032 b4032 Escherichia coli 562 -11533913 237238 malg (de:maltose transport system permease protein malg) (db:swissprot) MALG\_ECOLI P07622 ESCHERICHIA COLI 562 -11533913 130788 malg maltose transport inner membrane protein malg (cl:maltose transport protein malg) (db:pir1.dat) (mp:92 min) MMECMG A24361 Escherichia coli 562 -11533913 5000691163 (db:genpept-bct1) (de:e. coli gene malg for maltose transport.) (nt:put. mal g protein (aa 1-296)) (le:156) (re:1046) (di:direct) ECMALG X02871 g41951 Escherichia coli 562 -11533913 233340 malg part of maltose permease:inner membrane (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 366 of 400 of the completegenome.) (nt:f296; 100 pct identical to malg\_ecoli sw: p07622;) (le:9337) (re:10227) (di:complement) AE000476 AE000476 g1790464 Escherichia coli 562 -11533913 7500885270 malg maltose transport inner membrane protein (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 530) (le:107868) (re:108758) (di:complement) ECOUW89 U00006 g396367 Escherichia coli 562 -11533913 82898 malg (de:maltose transport system permease protein malg) (db:swissprot) MALG\_ECOLI P07622 ESCHERICHIA COLI 562 -11533913

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837787	9271	31427	318	105

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837815	9272	31428	456	151

Description

6500730056 malf:b4033 maltose transport inner membrane protein:maltose transport system permease protein malf (gtcfc:12.2:11.1) (keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b4033 b4033 Escherichia coli 562 -11533914 82895 malf (de:maltose transport system permease protein malf) (db:swissprot) MALF\_ECOLI P02916 ESCHERICHIA COLI 562 -11533914 130771 malf maltose transport inner membrane protein malf (cl:inner membrane protein malf) (db:pir1.dat) (mp:92 min) MMECMF A03414 Escherichia coli 562 -11533914 237239 malf (sr:e.coli k12: clone phc1; strains se2078; mc4100, clones plg1 an) (db:genpept-bct1) (de:e.coli malb region promoter, malk-lamb and malefg operons:including male, malf, malg, malk, lamb, and mola genes coding formaltose binding and maltose uptake prot... ECOMALB J01648 g455175 Escherichia coli 562 -11533914 235040 malf part of maltose permease:periplasmic (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 366 of 400 of the completegenome.) (nt:f514; 100 pct identical to malf\_ecoli sw: p02916;) (le:10242) (re:11786) (di:complement) AE000476 AE000476 g1790465 Escherichia coli 562 -11533914 7500885269 malf maltose transport inner membrane protein (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 531) (le:108773) (re:110317) (di:complement) ECOUW89 U00006 g396368 Escherichia coli 562 -11533914 5000691164 (de:(ecoli\_3919) (pn:part of maltose permease, periplasmic) (gn:malf) (gtcfc:12.2) (ec:) (malf\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_3919 ECOLI\_3919 Escherichia coli 562 10025115

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837819	9273	31429	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837822	9274	31430	396	131

Description

6500730057 male:b4034 periplasmic maltose-binding protein:maltose-binding periplasmic protein precursor:maltodextrin-binding protein:mmbp (gtcfc:12.2:11.1:12.9) (keggfc:11.1:12.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b4034 b4034 Escherichia coli 562 -11533915 82890 male (de:protein) (mmbp)) (db:swissprot) MALE\_ECOLI P02928 ESCHERICHIA COLI 562 -11533915 130817 male periplasmic maltose-binding protein precursor:maltose binding protein 16-1 (cl:maltose-binding protein) (db:pir1.dat) (mp:92 min) JGECM A03428 Escherichia coli 562 -11533915 237240 male periplasmic maltose-binding protein (sr:e.coli k12: clone phc1; strains se2078; mc4100, clones plg1 an) (db:genpept-bct1) (de:e.coli malb region promoter, malk-lamb and malefg operons:including male, malf, malg, malk, lamb, and mola genes coding formaltose binding and maltose uptake prot... ECOMALB J01648 g457109 Escherichia coli 562 -11533915 235041 male periplasmic maltose-binding protein:substrate (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 366 of 400 of the completgenome.) (nt:f396; cg site no. 532) (le:11940) (re:13130) (di:complement) AE000476 AE000476 g1790466 Escherichia coli 562 -11533915 7500885268 male periplasmic maltose-binding protein (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 532) (le:110471) (re:111661) (di:complement) ECOUW89 U00006 g396369 Escherichia coli 562 -11533915 5000691165 (de:(ecoli\_3920) (pn:periplasmic maltose-binding protein; substrate recognition for transport and chemotaxis) (gn:male) (gtcfc:12.2) (ec:) (male\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_3920 ECOLI\_3920 Escherichia coli 562 10025110

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837825	9275	31431	270	89

#### Description

6500730058 malk:b4035 cytoplasmic membrane protein for maltose uptake:maltose/maltodextrin transport atp-binding protein malk (gtcfc:12.2) (keggfc:11.1) (rileyfc:4.1.3) (db:gtc-escherichia coli) b4035 b4035 Escherichia coli 562 -11533916 7000688965 malk inner membrane protein malk (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir1.dat) (mp:92 min) MMECMK B65211 Escherichia coli 562 -11533916 237241 malk atp-binding component of transport system for (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 366 of 400 of the completegenome.) (nt:o371; 99 pct identical amino acid sequence and) (le:13495) (re:14610) (di:direct) AE000476 AE000476 g1790467 Escherichia coli 562 -11533916 7500953603 malk cytoplasmic membrane protein for maltose uptake (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 529) (le:112026) (re:113141) (di:direct) ECOUW89 U00006 g409797 Escherichia coli 562 -11533916 5000691166 (de:(ecoli\_3921) (pn:abc transporter for maltose) (gn:malk) (gtcfc:12.2) (ec:) (malk\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_3921 ECOLI\_3921 Escherichia coli 562 10124136

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837832	9276	31432	600	199

Description

6500730059 lamb:malb:b4036 phage lambda receptor protein:maltoporin precursor:lambda receptor protein (gtcfc:12.2) (keggfc:14.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b4036 b4036 Escherichia coli 562 -11533917 234955 lamb:malb (de:protein)) (db:swissprot) LAMB\_ECOLI P02943 ESCHERICHIA COLI 562 -11533917 130906 lamb lambda receptor protein precursor:lamb protein precursor:maltoporin precursor (cl:lambda receptor protein) (db:pir1.dat) (mp:92 min) QRECL A03443 Escherichia coli 562 -11533917 235043 (db:genpept-bct1) (de:e. coli genes lamb (encoding lambda receptor protein) and mola.mola is an unidentified gene, probably for an exported protein.) (nt:lamb (precursor)) (le:100) (re:1440) (di:direct) ECLAMBA V00298 g41908 Escherichia coli 562 -11533917 5000691167 (sr:e.coli (strain k12) dna) (db:genpept-bct1) (de:e.coli lambda receptor (lamb) gene, complete cds.) (nt:lambda receptor) (le:100) (re:1440) (di:direct) ECOLAMBBB M26131 g146594 Escherichia coli 562 -11533917 7500884804 lamb lambda receptor protein (sr:e.coli k12: clone phc1; strains se2078; mc4100, clones plg1 an) (db:genpept-bct1) (de:e.coli malb region promoter, malk-lamb and malefg operons:including male, malf, malg, malk, lamb, and mola genes coding formaltose binding and maltose uptake prot... ECOMALB J01648 g146702 Escherichia coli 562 -11533917 233311 lamb phage lambda receptor protein:maltose (fn:is, phage, tn; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 367 of 400 of the completegenome.) (nt:o446; 99 pct identical amino acid sequence and) (le:66) (re:1406) (di:direct) AE000477 AE000477 g1790469 Escherichia coli 562 -11533917 81487 lamb:malb (de:maltoporin precursor (lambda receptor protein)) (db:swissprot) LAMB\_ECOLI P02943 ESCHERICHIA COLI 562 -11533917

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837838	9277	31433	1206	401

Description

GTC ORF with score 731 to: (fn:convert udp-glucose to udp-glucuronate) (sr:house mouse) (db:genpept-rod) (ec:1.1.1.22) (de:mus musculus udp-glucose dehydrogenase (ugdh) mrna, complete cds.) (nt:udpgdh; nad+-linked oxidoreductase) (le:111) (re:1592) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837840	9278	31434	411	136

Description

6500730060 melb:mel-4:b4120 melibiose carrier protein:thiomethylgalactoside permease ii:melibiose permease:na+:li+/melibiose symporter (gtcfc:12.2) (keggfc:14.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b4120 b4120 Escherichia coli 562 -11533918 83416 melb:mel-4 (de:transporter)) (db:swissprot) MELB\_ECOLI P02921 ESCHERICHIA COLI 562 -11533918 130785 melb melibiose carrier protein:thiomethylgalactoside permease ii (cl:melibiose carrier protein) (db:pir1.dat) (mp:93 min) BDEC A03421 Escherichia coli 562 -11533918 237329 melb (sr:e.coli genomic dna, library of clarke-carbon, clone psty81) (db:genpept-bct1) (de:e.coli melb gene coding for melibiose carrier.) (nt:melibiose carrier) (le:61) (re:1470) (di:direct) ECOMELB K01991 g146804 Escherichia coli 562 -11533918 7500885470 melb thiomethylgalactoside permease ii (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 521; alternate gene name mel-4) (le:34209) (re:35618) (di:direct) ECOUW93 U14003 g536965 Escherichia coli 562 -11533918 235100 melb melibiose permease ii (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 374 of 400 of the completegenome.) (nt:o469; 100 pct identical to melb\_ecoli sw: p02921;) (le:7754) (re:9163) (di:direct) AE000484 AE000484 g1790561 Escherichia coli 562 -11533918 5000691168 (de:(ecoli\_4007) (pn:melibiose permease ii) (gn:melb) (gtcfc:12.2) (ec:) (melb\_ecoli) (keggfc:11.2) (rileyfc:4.1.3) (db:gtc-escherichia coli)) ECOLI\_4007 ECOLI\_4007 Escherichia coli 562 10025630

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837845	9279	31435	936	311

Description

GTC ORF with score 1102 to: (fn:implicated in golgi-to-lysosome trafficking) (db:genpept-pln1) (de:aspergillus fumigatus putative vacuolar protein sorting homologgene, partial cds.) (nt:similar to yeast vacuolar protein sorting (vps)) (le:<458) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837846	9280	31436	480	159

Description

GTC ORF with score 366 to: (fn:implicated in golgi-to-lysosome trafficking) (db:genpept-pln1) (de:aspergillus fumigatus putative vacuolar protein sorting homologgene, partial cds.) (nt:similar to yeast vacuolar protein sorting (vps)) (le:<458) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837855	9281	31437	819	272

Description

6500730061 dcub:genf:b4123 anaerobic c4-dicarboxylate transporter dcub (gtcfc:12.2) (keggfc:14.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b4123 b4123 Escherichia coli 562 -11533919 237332 dcub:genf (de:anaerobic c4-dicarboxylate transporter dcub) (db:swissprot) DCUB\_ECOLI P14409 ESCHERICHIA COLI 562 -11533919 162918 dcub:genf dicarboxylate transport protein dcub (db:pir2.dat) S56352 S56352 Escherichia coli 562 -11533919 5000691169 dcub dicarboxylate membrane transporter protein (db:genpept-bct1) (de:e.coli dcub gene.) (le:170) (re:1510) (di:direct) ECDCUB X79886 g510886 Escherichia coli 562 -11533919 7500880094 genf (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:38232) (re:39572) (di:complement) ECOUW93 U14003 g536968 Escherichia coli 562 -11533919 232652 dcub anaerobic dicarboxylate transport (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 375 of 400 of the completegenome.) (nt:f446; 100 pct identical amino acid sequence and) (le:1815) (re:3155) (di:complement) AE000485 AE000485 g1790565 Escherichia coli 562 -11533919 68139 dcub:genf (de:anaerobic c4-dicarboxylate transporter dcub) (db:swissprot) DCUB\_ECOLI P14409 ESCHERICHIA COLI 562 -11533919

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837861	9282	31438	432	143

Description

GTC ORF with score 257 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 0438.) (nt:unnamed protein product) (le:141) (re:1340) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837870	9283	31439	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837874	9284	31440	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837877	9285	31441	291	96

Description

6500730062 dcua:gena:b4138 anaerobic c4-dicarboxylate transporter dcua (gtcfc:12.2) (keggfc:14.2) (rileyfc:4.1.3) (db:gtc-escherichia coli) b4138 b4138 Escherichia coli 562 -11533920 237346 dcua:gena (de:anaerobic c4-dicarboxylate transporter dcua) (db:swissprot) DCUA\_ECOLI P04539 ESCHERICHIA COLI 562 -11533920 157277 dcua:gena dicarboxylate membrane-transporter protein a:anaerobic c4-dicarboxylate transporter dcua:aspartase membrane transport protein gena (cl:dicarboxylate membrane-transporter protein a) (db:pir1.dat) (mp:94 min) QQEC94 S56366 Escherichia coli 562 -11533920 5000691170 dcub dicarboxylate membrane-transporter protein (db:genpept-bct1) (de:e.coli dcua gene.) (le:129) (re:1430) (di:direct) ECDUCA X79887 g510888 Escherichia coli 562 -11533920 7500880093 gena (fn:membrane transport of aspartase) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:56300) (re:57601) (di:complement) ECOUW93 U14003 g536982 Escherichia coli 562 -11533920 232713 dcua anaerobic dicarboxylate transport (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 376 of 400 of the completegenome.) (nt:f433; 100 pct identical amino acid sequence and) (le:6845) (re:8146) (di:complement) AE000486 AE000486 g1790580 Escherichia coli 562 -11533920 68137 dcua:gena (de:anaerobic c4-dicarboxylate transporter dcua) (db:swissprot) DCUA\_ECOLI P04539 ESCHERICHIA COLI 562 -11533920

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837878	9286	31442	1341	446

Description

6500730063 codb:b0336 cytosine permease (gtcfc:12.3) (keggfc:14.2) (rileyfc:4.1.4) (db:gtc-escherichia coli) b0336 b0336 Escherichia coli 562 -11533921 239953 codb (de:cytosine permease) (db:swissprot) CODB\_ECOLI P25525 ESCHERICHIA COLI 562 -11533921 162899 codb cytosine transport protein:cytosine permease (db:pir2.dat) S22661 S22661 Escherichia coli 562 -11533921 5000691171 codb cytosine permease (db:genpept-bct1) (de:e.coli codba operon encoding cytosine permease and cytosinedeaminase.) (le:393) (re:1652) (di:direct) ECCODAB X63656 g581051 Escherichia coli 562 -11533921 7500879046 codb cytosine permease (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (le:62717) (re:63976) (di:direct) ECU73857 U73857 g1657532 Escherichia coli 562 -11533921 232531 codb cytosine permease/transport (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 30 of 400 of the completegenome.) (nt:o419; 100 pct identical to codb\_ecoli sw: p25525) (le:9770) (re:11029) (di:direct) AE000140 AE000140 g1786530 Escherichia coli 562 -11533921 65299 codb (de:cytosine permease) (db:swissprot) CODB\_ECOLI P25525 ESCHERICHIA COLI 562 -11533921

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837905	9287	31443	225	74

Description

6500730064 tsx:nupa:b0411 nucleoside-specific channel-forming protein tsx precursor (gtcfc:12.3) (keggfc:14.2) (rileyfc:4.1.4) (db:gtc-escherichia coli) b0411 b0411 Escherichia coli 562 -11533922 102678 tsx:nupa (de:nucleoside-specific channel-forming protein tsx precursor) (db:swissprot) TSX\_ECOLI P22786 ESCHERICHIA COLI 562 -11533922 164220 tsx nucleoside-specific channel-forming protein tsx precursor:phage t6 receptor protein (db:pir2.dat) (mp:9.4 min) JQ0798 JQ0798 Escherichia coli 562 -11533922 240188 tsx outer membrane protein tsx (sr:e.coli dna) (db:genpept-bct1) (de:e.coli outer membrane protein tsx (tsx) gene, complete cds.) (le:456) (re:1340) (di:direct) ECOTSX M57685 g148079 Escherichia coli 562 -11533922 7500893564 tsx nucleoside-specific channel-forming protein tsx (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:10579) (re:11463) (di:complement) ECU82664 U82664 g1773095 Escherichia coli 562 -11533922 236228 tsx nucleoside channel:receptor of phage t6 and (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 37 of 400 of the completegenome.) (nt:f294; 100 pct identical to tsx\_ecoli sw: p22786) (le:8722) (re:9606) (di:complement) AE000147 AE000147 g1786612 Escherichia coli 562 -11533922 5000691172 (de:(ecoli\_395) (pn:nucleoside channel; receptor of phage t6 and colicin k) (gn:tsx) (gtcfc:12.3) (ec:) (tsx\_ecoli) (keggfc:11.2) (rileyfc:4.1.4) (db:gtc-escherichia coli)) ECOLI\_395 ECOLI\_395 Escherichia coli 562 10044496

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837915	9288	31444	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837917	9289	31445	321	106

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837929	9290	31446	708	235

Description

GTC ORF with score 338 to: (sr:mouse (strain balb/c) cell line 3t3 dna, clones ide and h1) (db:genpept-rod) (de:mouse surfeit locus surfeit 3 gene, exon 8, and surfeit 1 and 2genes, complete cds.) (nt:surfeit 1 protein) (le:285:426:790:1052) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837937	9291	31447	1473	490

Description

6500730065 pnuc:b0751 pnuc protein (gtcfc:12.3) (keggfc:14.2)  
(rileyfc:4.1.4) (db:gtc-escherichia coli) b0751 b0751 Escherichia coli 562  
-11533923 90187 pnuc (de:pnuc protein) (db:swissprot) PNUC\_ECOLI P31215  
ESCHERICHIA COLI 562 -11533923 7000686158 pnuc pnuc protein (db:pir2.dat)  
G64810 G64810 Escherichia coli 562 -11533923 223188 pnuc pnuc protein  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #179)  
(db:genpept-bct1) (de:escherichia coli genomic dna.(16.8 - 17.1 min).)  
(le:3230) (re:3949) (di:direct) D90714 D90714 g1651338 Escherichia coli 562  
-11533923 7500888239 pnuc required for nmh transport (fn:transport;  
transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12  
mg1655 section 67 of 400 of the completegenome.) (nt:o239; 96 pct identical  
66 aa fragment pnuc\_ecoli) (le:8951) (re:9670) (di:direct) AE000177 AE000177  
g1786965 Escherichia coli 562 -11533923 5000691173 pnuc pnuc protein .  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #179) (db:genpept)  
(de:escherichia coli genomic dna. (16.8 - 17.1 min).) (nt:orf\_id:o179#2;  
similar to swissprot accession) (le:3230) (re:3949) (di:direct) D90714  
D90714 g1651338 Escherichia coli 562 -11533923

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837951	9292	31448	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837952	9293	31449	423	140

Description

6500730066 nupc:cru:b2393 nucleoside permease nupc:nucleoside-transport system protein nupc (gtcfc:12.3:11.1) (keggfc:14.2) (rileyfc:4.1.4) (db:gtc-escherichia coli) b2393 b2393 Escherichia coli 562 -11533924 87216 nupc:cru (de:nucleoside permease nupc (nucleoside-transport system protein nupc)) (db:swissprot) NUPC\_ECOLI P33031 ESCHERICHIA COLI 562 -11533924 7000686017 nupc nucleoside transport protein nupc:nucleoside permease nupc (cl:pyrimidine nucleoside transport protein nupc) (db:pir2.dat) F65013 F65013 Escherichia coli 562 -11533924 224950 cru nucleoside permease nupc nucleoside-transport (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #416(54.1-54.5 min.)) (nt:similar to (swissprot accession number p33031)) (le:5886) (re:7088) (di:direct) D90869 D90869 g1799805 Escherichia coli 562 -11533924 7500887005 nupc permease of transport system for 3 nucleosides (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 217 of 400 of the completegenome.) (nt:o400; 99 pct identical (2 gaps) to nupc\_ecoli) (le:4721) (re:5923) (di:direct) AE000327 AE000327 g1788737 Escherichia coli 562 -11533924 5000691174 (de:(ecoli\_2340) (pn:transport of nucleosides, except guanosine) (gn:nupc) (gtcfc:12.3) (ec:) (nupc\_ecoli) (keggfc:11.2) (rileyfc:4.1.4) (db:gtc-escherichia coli)) ECOLI\_2340 ECOLI\_2340 Escherichia coli 562 10120172

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837962	9294	31450	567	188

Description

6500730067 uraa:b2497 uracil permease:uracil transporter (gtcfc:12.3) (keggfc:14.2) (rileyfc:4.1.4) (db:gtc-escherichia coli) b2497 b2497 Escherichia coli 562 -11533925 7500893837 uraa (de:uracil permease (uracil transporter)) (db:swissprot) URAA\_ECOLI P33780 ESCHERICHIA COLI 562 -11533925 164809 uraa uracil transport protein uraa:uracil permease (cl:uracil transport protein uraa) (db:pir2.dat) A56265 A56265 Escherichia coli 562 -11533925 225073 uraa uracil transport protein uraa (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #425(56.2-56.5 min.)) (nt:similar to (pir accession number a56265)) (le:6792) (re:8081) (di:complement) D90878 D90878 g1805557 Escherichia coli 562 -11533925 5000691175 uraa uracil permease (db:genpept-bct1) (de:e.coli uraa gene for uracil permease.) (le:49) (re:1338) (di:direct) ECURAA X73586 g313777 Escherichia coli 562 -11533925 240359 uraa uracil transport (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 226 of 400 of the completegenome.) (nt:f429; 100 pct identical to uraa\_ecoli sw: p33780) (le:2914) (re:4203) (di:complement) AE000336 AE000336 g1788843 Escherichia coli 562 -11533925 103804 uraa (de:uracil permease (uracil transporter)) (db:swissprot) URAA\_ECOLI P33780 ESCHERICHIA COLI 562 -11533925

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501837971	9295	31451	507	169

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837973	9296	31452	1014	337

Description

6500730068 nupg:b2964 nucleoside permease nupg (gtcfc:12.3) (keggfc:14.2) (rileyfc:4.1.4) (db:gtc-escherichia coli) b2964 b2964 Escherichia coli 562 -11533926 7000691874 nupg nucleoside-transporting protein nupg (db:pir2.dat) (mp:66 min) C65082 C65082 Escherichia coli 562 -11533926 7500960401 nupg (fn:transport of nucleosides) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:cg site no. 442; ecnupg sites 2nd start codon, no) (le:60060) (re:61364) (di:direct) ECU28377 U28377 g882494 Escherichia coli 562 -11533926 239178 nupg transport of nucleosides:permease protein (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 269 of 400 of the completegenome.) (nt:o434; 100 pct identical to nupg\_ecoli sw: p09452) (le:1297) (re:2601) (di:direct) AE000379 AE000379 g1789336 Escherichia coli 562 -11533926 5000691176 (de:(ecoli\_2887) (pn:transport of nucleosides) (gn:nupg) (gtcfc:12.3) (ec:) (nupg\_ecoli) (keggfc:11.2) (rileyfc:4.1.4) (db:gtc-escherichia coli)) ECOLI\_2887 ECOLI\_2887 Escherichia coli 562 10123918

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501837974	9297	31453	579	192

# Description

6500730069 moda:b0763 24 aa signal peptide:molybdate-binding periplasmic protein precursor (gtcfc:12.6:11.1) (keggfc:11.1) (rileyfc:4.1.5) (db:gtc-escherichia coli) b0763 b0763 Escherichia coli 562 -11533927 83979 moda (de:molybdate-binding periplasmic protein precursor) (db:swissprot) MODA\_ECOLI P37329 ESCHERICHIA COLI 562 -11533927 7000685861 moda molybdate-binding periplasmic protein precursor (cl:molybdate-binding periplasmic protein) (db:pir2.dat) C64812 C64812 Escherichia coli 562 -11533927 223197 moda molybdate-binding periplasmic protein moda (sr:escherichia coli(strain:k12) dna, clone:kohara clone #180) (db:genpept-bct1) (de:escherichia coli genomic dna.(17.0 - 17.3 min).) (le:1895) (re:2668) (di:direct) D90715 D90715 g1651348 Escherichia coli 562 -11533927 238537 moda periplasmic molybdate-binding protein precursor (db:genpept-bct1) (de:escherichia coli periplasmic molybdate-binding protein (moda),hydrophobic membrane-bound protein (modb) and hydrophilicmembrane-bound protein (modc) genes, complete cds and modd gene, 5'end.) (nt:putative) (le:641) (re:1414) (di:d... ECOMODA L34009 g504498 Escherichia coli 562 -11533927 239053 moda (fn:molybdenum transport) (db:genpept-bct1) (de:escherichia coli k12, substrain mc1000 molybdenum transport (modr), (moda), (modb), (modc), (modd), genes, complete cds.) (nt:part of a molybdenum periplasmic binding protein) (le:3128) (re:3901) (di:direct) ECU07867 U07867 g1147817 Escherichia coli 562 -11533927 7500885748 moda moda (fn:periplasmic molybdate-binding protein) (db:genpept-bct1) (de:escherichia coli molybdate transport operon (moda, modb, modc,modd), mode (mode) and modf (modf) genes, complete cds.) (le:2827) (re:3600) (di:direct) ECU27192 U27192 g973214 Escherichia coli 562 -11533927 235157 moda molybdate-binding periplasmic protein:permease (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 69 of 400 of the completegenome.) (nt:o257; 99 pct identical to moda\_ecoli sw: p37329) (le:114) (re:887) (di:direct) AE000179 AE000179 g1786979 Escherichia coli 562 -11533927 5000691177 moda molybdate-binding periplasmic protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #180) (db:genpept) (de:escherichia coli genomic dna. (17.1 - 17.4 min).) (nt:orf\_id:o180#3; similar to swissprot accession) (le:1895) (re:2668) (di:direct) D90715 D90715 g1651348 Escherichia coli 562 -11533927

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501837975	9298	31454	924	307

Description

6500730070 modb:chlj:b0764 molybdenum transport system permease protein modb (gtcfc:12.6) (keggfc:11.1) (rileyfc:4.1.5) (db:gtc-escherichia coli) b0764 b0764 Escherichia coli 562 -11533928 7000688972 modb:chlj molybdenum transport protein modb (cl:maltose transport protein malg) (db:pir1.dat) (mp:17 min) BVECHJ D64812 Escherichia coli 562 -11533928 223198 modb molybdenum transport system permease protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #180) (db:genpept-bct1) (de:escherichia coli genomic dna.(17.0 - 17.3 min).) (le:2668) (re:3357) (di:direct) D90715 D90715 g1651349 Escherichia coli 562 -11533928 7500953613 modb molybdate transport permease protein (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 69 of 400 of the completegenome.) (nt:o229; 99 pct identical to modb\_ecoli sw: p09834;) (le:887) (re:1576) (di:direct) AE000179 AE000179 g1786980 Escherichia coli 562 -11533928 5000691178 chl j molybdenum transport system permease protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #180) (db:genpept) (de:escherichia coli genomic dna. (17.1 - 17.4 min).) (nt:orf\_id:o180#4; similar to swissprot accession) (le:2668) (re:3357) (di:direct) D90715 D90715 g1651349 Escherichia coli 562 -11533928

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838005	9299	31455	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838012	9300	31456	1044	347

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501838034	9301	31457	597	198

Description

6500730071 modc:chld:nard:b0765 molybdenum transport atp-binding protein modc (gtcfc:12.6) (keggfc:11.1) (rileyfc:4.1.5) (db:gtc-escherichia coli) b0765 b0765 Escherichia coli 562 -11533929 7000688966 modc:chld molybdenum transport protein modc:molybdenum transport protein chld (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir1.dat) (mp:17 min) BVECHD E64812 Escherichia coli 562 -11533929 223199 modc molybdenum transport atp-binding protein modc (sr:escherichia coli(strain:k12) dna, clone:kohara clone #180) (db:genpept-bct1) (de:escherichia coli genomic dna.(17.0 - 17.3 min).) (le:3360) (re:4418) (di:direct) D90715 D90715 g1651350 Escherichia coli 562 -11533929 7500953604 modc modc (fn:molybdate transport-atpase) (db:genpept-bct1) (de:escherichia coli molybdate transport operon (moda, modb, modc,modd), mode (mode) and modf (modf) genes, complete cds.) (nt:hydrophilic membrane-bound protein) (le:4292) (re:5350) (di:direct) ECU27192 U27192 g973216 Escherichia coli 562 -11533929 239055 modc atp-binding component of molybdate transport (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 69 of 400 of the completegenome.) (nt:o352; 100 pct identical to modc\_ecoli sw: p09833;) (le:1579) (re:2637) (di:direct) AE000179 AE000179 g1786981 Escherichia coli 562 -11533929 5000691179 chld molybdenum transport atp-binding protein modc. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #180) (db:genpept) (de:escherichia coli genomic dna. (17.1 - 17.4 min).) (nt:orf\_id:o180#5; similar to swissprot accession) (le:3360) (re:4418) (di:direct) D90715 D90715 g1651350 Escherichia coli 562 -11533929

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838055	9302	31458	1362	453

# Description

6500730072 nark:b1223 nitrite extrusion protein:nitrite facilitator:nitrite extrusion protein 1:nitrite facilitator 1 (gtcfc:12.4) (keggfc:14.2) (rileyfc:4.1.5) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of anions (cl\_so4\_po4\_etc\_)) b1223 b1223 Escherichia coli 562 -11533930

7500886306 nark (de:nitrite extrusion protein 1 (nitrite facilitator 1)) (db:swissprot) NARK\_ECOLI P10903 ESCHERICHIA COLI 562 -11533930 130701 nark nitrite extrusion protein:nitrite facilitator (cl:nitrate transport protein nark) (db:pir1.dat) (mp:27 min) GRECNK S05239 Escherichia coli 562 -11533930

223428 nark nitrate transport protein nark (sr:escherichia coli(strain:k12) dna, clone:kohara clone #248) (db:genpept-bct1) (de:escherichia coli genomic dna (27.2-27.6 min).) (le:13081) (re:14472) (di:direct) D90757 D90757 g1651617 Escherichia coli 562 -11533930 5000691180 nark (db:genpept-bct1) (de:e.coli nark gene and partial sequence of narx and narc genes.) (le:505) (re:1896) (di:direct) ECNARK X15996 g42091 Escherichia coli 562 -11533930

233458 nark nitrite extrusion protein (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 110 of 400 of the completegenome.) (nt:o465; 100 pct identical to nark\_ecoli sw: p10903) (le:8103) (re:9494) (di:direct) AE000220 AE000220 g1787475 Escherichia coli 562 -11533930 7502851978 nark nitrate transport protein nark. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #248) (db:genpept) (de:escherichia coli genomic dna. (27.3 - 27.7 min).) (nt:orf\_id:o248#13; similar to pir accession number) (le:13081) (re:14472) (di:direct) D90757 D90757 g1651617 Escherichia coli 562 -11533930 85245 nark (de:nitrite extrusion protein 1 (nitrite facilitator 1)) (db:swissprot) NARK\_ECOLI P10903 ESCHERICHIA COLI 562 -11533930

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838064	9303	31459	462	153

Description

6500730073 cysz:b2413 putative sulfate transport protein cysz:cysz protein (gtcfc:12.4) (keggfc:14.2) (rileyfc:4.1.5) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of anions (cl\_so4\_po4\_etc\_)) b2413 b2413 Escherichia coli 562 -11533931 67719 cysz (de:cysz protein) (db:swissprot) CYSZ\_ECOLI P12610 ESCHERICHIA COLI 562 -11533931 7000684971 cysz probable sulfate transport protein cysz (cl:cysz protein) (db:pir1.dat) (mp:52 min) BVECCZ D65015 Escherichia coli 562 -11533931 7500879931 cysz required for sulfate transport (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 219 of 400 of the completegenome.) (nt:o253; 100 pct identical to 196 aa) (le:1282) (re:2043) (di:direct) AE000329 AE000329 g1788753 Escherichia coli 562 -11533931 5000691181 (de:(ecoli\_2354) (pn:required for sulfate transport) (gn:cysz) (gtcfc:12.4) (ec:) (cysz\_ecoli) (keggfc:11.2) (rileyfc:4.1.5) (db:gtc-escherichia coli)) ECOLI\_2354 ECOLI\_2354 Escherichia coli 562 10123674

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838070	9304	31460	273	90

Description

GTC ORF with score 211 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac f1216 genomic sequence,complete sequence.) (nt:unknown protein) (le:40434:40859:41173) (re:40781:41092:41253) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838074	9305	31461	456	151

Description

6500730074 cysa:b2422 sulfate transport atp-binding protein cysa (gtcfc:12.4) (keggfc:11.1) (rileyfc:4.1.5) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of anions (cl\_so4\_po4\_etc\_)) b2422 b2422 Escherichia coli 562 -11533932 67634 cysa (de:sulfate transport atp-binding protein cysa) (db:swissprot) CYSA\_ECOLI P16676 ESCHERICHIA COLI 562 -11533932 7000684966 cysa sulfate transport atp-binding protein cysa:nucleotide-binding protein cysa (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir1.dat) (mp:52 min) QRECSA E65016 Escherichia coli 562 -11533932 224984 cysa sulfate/thiosulfate transport protein cysa (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #418(54.6-54.9 min.)) (nt:similar to (pir accession number c35402)) (le:8085) (re:9182) (di:complement) D90871 D90871 g1799841 Escherichia coli 562 -11533932 224993 cysa sulfate/thiosulfate transport protein cysa (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #419(54.7-55.1 min.)) (nt:similar to (pir accession number c35402)) (le:2846) (re:3943) (di:complement) D90872 D90872 g1799851 Escherichia coli 562 -11533932 7500879898 cysa atp-binding component of sulfate permease a (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 219 of 400 of the completegenome.) (nt:f365; 99 pct identical to cysa\_ecoli sw: p16676) (le:9536) (re:10633) (di:complement) AE000329 AE000329 g1788761 Escherichia coli 562 -11533932 5000691182 (de:(ecoli\_2362) (pn:sulfate permease a protein; chromate resistance) (gn:cysa) (gtcfc:12.4) (ec:) (cysa\_ecoli) (keggfc:11.2) (rileyfc:4.1.5) (db:gtc-escherichia coli)) ECOLI\_2362 ECOLI\_2362 Escherichia coli 562 10120192

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838086	9306	31462	438	146

Description

6500730075 cysw:b2423 sulfate transport system permease protein cysw (gtcfc:12.4) (keggfc:11.1) (rileyfc:4.1.5) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of anions (cl\_so4\_po4\_etc\_)) b2423 b2423 Escherichia coli 562 -11533933 7000688971 cysw sulfate/thiosulfate transport protein cysw (cl:maltose transport protein malg) (db:pir1.dat) (mp:52 min) QRECSW F65016 Escherichia coli 562 -11533933 7500953612 cysw sulfate transport system permease w protein (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 219 of 400 of the completegenome.) (nt:f149; this 149 aa orf is 100 pct identical to) (le:10623) (re:11072) (di:complement) AE000329 AE000329 g1788762 Escherichia coli 562 -11533933 5000691183 (de:(ecoli\_2363) (pn:sulfate permease w protein) (gn:cysw) (gtcfc:12.4) (ec:) (cysw\_ecoli) (keggfc:11.2) (rileyfc:4.1.5) (db:gtc-escherichia coli)) ECOLI\_2363 ECOLI\_2363 Escherichia coli 562 10123676

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501838102	9307	31463	828	275

#### Description

6500730076 cysp:b2425 thiosulfate-binding protein precursor (gtcfc:12.4) (keggfc:11.1) (rileyfc:4.1.5) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of anions (cl\_so4\_po4\_etc\_)) b2425 b2425 Escherichia coli 562 -11533934 67684 cysp (de:thiosulfate-binding protein precursor) (db:swissprot) CYSP\_ECOLI P16700 ESCHERICHIA COLI 562 -11533934 130681 cysp thiosulfate-binding protein cysp precursor (cl:sulfate-binding protein) (db:pir1.dat) (mp:52 min) JGECT A35403 Escherichia coli 562 -11533934 224987 cysp thiosulfate-binding protein cysp precursor (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #418(54.6-54.9 min.)) (nt:similar to (pir accession number a35403)) (le:10880) (re:11896) (di:complement) D90871 D90871 g1799844 Escherichia coli 562 -11533934 224996 cysp thiosulfate-binding protein cysp precursor (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #419(54.7-55.1 min.)) (nt:similar to (pir accession number a35403)) (le:5641) (re:6657) (di:complement) D90872 D90872 g1799854 Escherichia coli 562 -11533934 7500879920 cysp thiosulfate binding protein (sr:e.coli k12 dna) (db:genpept-bct1) (de:e.coli thiosulfate binding protein (cysp), sulfate permease (cyst,cysw, cysa) and o-acetylserine (thiol)-lyase-b (cysm) genes,complete cds.) (le:559) (re:1575) (di:direct) ECOCYS M32101 g145658 Escherichia coli 562 -11533934 234092 cysp thiosulfate binding protein (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 220 of 400 of the completegenome.) (nt:f338; 100 pct identical to cysp\_ecoli sw: p16700) (le:1076) (re:2092) (di:complement) AE000330 AE000330 g1788765 Escherichia coli 562 -11533934 5000691184 (de:(ecoli\_2365) (pn:thiosulfate binding protein) (gn:cysp) (gtcfc:12.4) (ec:) (cysp\_ecoli) (keggfc:11.2) (rileyfc:4.1.5) (db:gtc-escherichia coli)) ECOLI\_2365 ECOLI\_2365 Escherichia coli 562 10010282

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838105	9308	31464	630	209

#### Description

6500730077 pitb:b2987 probable low-affinity inorganic phosphate transporter 2 (gtcfc:12.4) (keggfc:14.2) (rileyfc:4.1.5) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of anions (cl\_so4\_po4\_etc\_)) b2987 b2987 Escherichia coli 562 -11533935 89837 pitb (de:probable low-affinity inorganic phosphate transporter 2) (db:swissprot) PITB\_ECOLI P43676 ESCHERICHIA COLI 562 -11533935 7000686145 pitb probable low-affinity inorganic phosphate transporter 2 (db:pir2.dat) A65085 A65085 Escherichia coli 562 -11533935 7500888111 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf\_f499) (le:89263) (re:90762) (di:complement) ECU28377 U28377 g882516 Escherichia coli 562 -11533935 239200 pitb low-affinity phosphate transport (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 271 of 400 of the completegenome.) (nt:f499; 100 pct identical to pitb\_ecoli sw: p43676) (le:6756) (re:8255) (di:complement) AE000381 AE000381 g1789360 Escherichia coli 562 -11533935 5000691185 (de:(ecoli\_2909) (pn:low-affinity phosphate transport) (gn:pitb) (gtcfc:12.4) (ec:) (pitb\_ecoli) (keggfc:11.2) (rileyfc:4.1.5) (db:gtc-escherichia coli)) ECOLI\_2909 ECOLI\_2909 Escherichia coli 562 10031957

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838122	9309	31465	1398	465

#### Description

6500730078 pita:pit:b3493 pita:low-affinity inorganic phosphate transporter 1 (gtcfc:12.4) (keggfc:14.2) (rileyfc:4.1.5) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of anions (cl\_so4\_po4\_etc\_)) b3493 b3493 Escherichia coli 562 -11533936 89836 pita:pit (de:low-affinity inorganic phosphate transporter 1) (db:swissprot) PITA\_ECOLI P37308 ESCHERICHIA COLI 562 -11533936 163853 pita pita protein:hypothetical protein o499 (db:pir2.dat) S47713 S47713 Escherichia coli 562 -11533936 7500888110 pit (fn:low-affinity phosphate transport) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 385) (le:51901) (re:53400) (di:direct) ECOUW76 U00039 g466630 Escherichia coli 562 -11533936 236729 pita low-affinity phosphate transport (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 315 of 400 of the completegenome.) (nt:o499; 100 pct identical to pita\_ecoli sw: p37308;) (le:6903) (re:8402) (di:direct) AE000425 AE000425 g1789907 Escherichia coli 562 -11533936 5000691186 (de:(ecoli\_3412) (pn:low-affinity phosphate transport) (gn:pita) (gtcfc:12.4) (ec:) (pita\_ecoli) (keggfc:11.2) (rileyfc:4.1.5) (db:gtc-escherichia coli)) ECOLI\_3412 ECOLI\_3412 Escherichia coli 562 10031956

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838140	9310	31466	285	94

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838159	9311	31467	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838172	9312	31468	1284	427

Description

6500730079 pstb:phot:b3725 phosphate transport atp-binding protein pstb (gtcfc:12.4) (keggfc:11.1) (rileyfc:4.1.5) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of anions (cl\_so4\_po4\_etc\_)) b3725 b3725 Escherichia coli 562 -11533937 7500888881 pstb:phot (de:phosphate transport atp-binding protein pstb) (db:swissprot) PSTB\_ECOLI P07655 ESCHERICHIA COLI 562 -11533937 130719 pstb phosphate transport atp-binding protein pstb (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir1.dat) (mp:84 min) BVECZB A30382 Escherichia coli 562 -11533937 236961 pstb peripheral membrane protein b (sr:e.coli strain k-12 dna, clones pan92 (1), psn518 (2), and pan12) (db:genpept-bct1) (de:e.coli phosphate-repressible periplasmic phosphate-binding protein(phos), peripheral membrane proteins (pstc, pstb and phou) andintegral membrane protein (psta) ... ECOPHOS K01992 g147259 Escherichia coli 562 -11533937 237809 pstb::cg site no. 1... peripheral membrane protein b (fn:phosphate-specific transport system) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:alternate gene name phot) (le:96984) (re:97757) (di:complement) ECOUW82 L10328 g290573 Escherichia coli 562 -11533937 5000691187 (db:genpept-bct1) (de:e. coli dna for psta-phou region involved in phosphate transportand regulation of the phosphate regulon.) (nt:pstb gene product (aa 1-257)) (le:2057) (re:2830) (di:direct) ECPHOWTU X02723 g42398 Escherichia coli 562 -11533937 235484 pstb atp-binding component of high-affinity (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 339 of 400 of the completegenome.) (nt:f257; 100 pct identical amino acid sequence and) (le:8977) (re:9750) (di:complement) AE000449 AE000449 g1790162 Escherichia coli 562 -11533937 92040 pstb:phot (de:phosphate transport atp-binding protein pstb) (db:swissprot) PSTB\_ECOLI P07655 ESCHERICHIA COLI 562 -11533937

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838179	9313	31469	369	122

Description

6500730080 psta:phot:b3726 phosphate transport system permease protein psta (gtcfc:12.4) (keggfc:11.1) (rileyfc:4.1.5) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of anions (cl\_so4\_po4\_etc\_)) b3726 b3726 Escherichia coli 562 -11533938 7500888874 psta:phot (de:phosphate transport system permease protein psta) (db:swissprot) PSTA\_ECOLI P07654 ESCHERICHIA COLI 562 -11533938 131353 psta:phot phosphate transport system permease protein psta (cl:phot protein) (db:pirl.dat) (mp:84 min) BVECPT B23311 Escherichia coli 562 -11533938 236962 psta integral membrane protein (sr:e.coli strain k-12 dna, clones pan92 (1), psn518 (2), and pan12) (db:genpept-bct1) (de:e.coli phosphate-repressible periplasmic phosphate-binding protein(phos), peripheral membrane proteins (pstc, pstb and phou) and integral membrane protein (psta) ... ECOPHOS K01992 g147258 Escherichia coli 562 -11533938 237808 psta::cg site no. 1... integral membrane protein (fn:phosphate-specific transport system) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e.coli; the region from 81.5 to 84.5 minutes.) (nt:alternate gene name phot) (le:97940) (re:98830) (di:complement) ECOUW82 L10328 g290574 Escherichia coli 562 -11533938 5000691188 (db:genpept-bct1) (de:e. coli dna for psta-phou region involved in phosphate transport and regulation of the phosphate regulon.) (nt:phot (psta) gene product (aa 1-296)) (le:984) (re:1874) (di:direct) ECPHOWTU X02723 g42397 Escherichia coli 562 -11533938 235483 psta high-affinity phosphate-specific transport (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 339 of 400 of the complete genome.) (nt:f296; 100 pct identical to psta\_ecoli sw: p07654;) (le:9933) (re:10823) (di:complement) AE000449 AE000449 g1790163 Escherichia coli 562 -11533938 92037 psta:phot (de:phosphate transport system permease protein psta) (db:swissprot) PSTA\_ECOLI P07654 ESCHERICHIA COLI 562 -11533938

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838190	9314	31470	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838191	9315	31471	738	245

Description

6500730081 pstc:phow:b3727 phosphate transport system permease protein pstc (gtcfc:12.4) (keggfc:11.1) (rileyfc:4.1.5) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of anions (cl\_so4\_po4\_etc\_)) b3727 b3727 Escherichia coli 562 -11533939 7500888887 pstc:phow (de:phosphate transport system permease protein pstc) (db:swissprot) PSTC\_ECOLI P07653 ESCHERICHIA COLI 562 -11533939 7000686203 pstc:phow phosphate transport system permease protein pstc:phow protein (cl:phow protein) (db:pir1.dat) (mp:84 min) BVECPW H65175 Escherichia coli 562 -11533939 236963 pstc peripheral membrane protein c (sr:e.coli strain k-12 dna, clones pan92 (1), psn518 (2), and pan12) (db:genpept-bct1) (de:e.coli phosphate-repressible periplasmic phosphate-binding protein(phos), peripheral membrane proteins (pstc, pstb and phou) and integral membrane protein (psta) ... ECOPHOS K01992 g147257 Escherichia coli 562 -11533939 237807 pstc::cg site no. 1... peripheral membrane protein c (fn:phosphate-specific transport system) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:alternate gene name phow) (le:98830) (re:99789) (di:complement) ECOUW82 L10328 g290575 Escherichia coli 562 -11533939 5000691189 (db:genpept-bct1) (de:e. coli dna for psta-phou region involved in phosphate transport and regulation of the phosphate regulon.) (nt:phow gene product (aa 1-319)) (le:25) (re:984) (di:direct) ECPHOWTU X02723 g42396 Escherichia coli 562 -11533939 235482 pstc high-affinity phosphate-specific transport (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 339 of 400 of the complete genome.) (nt:f319; 100 pct identical to pstc\_ecoli sw: p07653;) (le:10823) (re:11782) (di:complement) AE000449 AE000449 g1790164 Escherichia coli 562 -11533939 92042 pstc:phow (de:phosphate transport system permease protein pstc) (db:swissprot) PSTC\_ECOLI P07653 ESCHERICHIA COLI 562 -11533939

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838198	9316	31472	1137	378

Description

6500730082 psts:phos:b3728 periplasmic phosphate-binding protein:phosphate-binding periplasmic protein precursor:pbp (gtcfc:12.4:12.6) (keggfc:11.1) (rileyfc:4.1.5) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of anions (cl\_so4\_po4\_etc\_):cell processes-transporters of unknown specificity (abc\_atpases\_drug) or metals) b3728 b3728 Escherichia coli 562 -11533940 92044 psts:phos (de:phosphate-binding periplasmic protein precursor (pbp)) (db:swissprot) PSTS\_ECOLI P06128 ESCHERICHIA COLI 562 -11533940 130709 psts:phos phosphate-repressible phosphate-binding protein precursor (cl:phosphate-repressible phosphate-binding protein) (db:pir1.dat) (mp:84 min) BYECPR A30277 Escherichia coli 562 -11533940 7500888892 phos phosphate-binding protein (sr:e.coli strain k-12 dna, clones pan92 (1), psn518 (2), and pan12) (db:genpept-bct1) (de:e.coli phosphate-repressible periplasmic phosphate-binding protein(phos), peripheral membrane proteins (pstc, pstb and phou) and integral membrane protein (psta) ... ECOPHOS K01992 g147256 Escherichia coli 562 -11533940 235481 psts high-affinity phosphate-specific transport (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 339 of 400 of the complete genome.) (nt:f346; 99 pct identical amino acid sequence and) (le:11869) (re:12909) (di:complement) AE000449 AE000449 g2367271 Escherichia coli 562 -11533940

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838199	9317	31473	828	275

Description

GTC ORF with score 181 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 0555.) (nt:unnamed protein product) (le:<1) (re:851) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838227	9318	31474	354	117

#### Description

6500730083 sbp:b3917 periplasmic sulphate binding protein:sulfate-binding protein precursor:sulfate starvation-induced protein 2:ssi2 (gtcfc:12.4:12.6) (keggfc:11.1) (rileyfc:4.1.5) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of anions (cl\_so4\_po4\_etc\_):cell processes-transporters of unknown specificity (abc\_atpases\_drug) or metals) b3917 b3917 Escherichia coli 562 -11533941 152981 sbp sulphate binding protein precursor:periplasmic:sulfate starvation-induced protein ssi2 (cl:sulfate-binding protein) (db:pir1.dat) (mp:88 min) BYEC S40860 Escherichia coli 562 -11533941 7500953599 sbp periplasmic sulphate binding protein (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:cg site no. 17911) (le:70467) (re:71456) (di:direct) ECOUW87 L19201 g305020 Escherichia coli 562 -11533941 237134 sbp periplasmic sulfate-binding protein (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 356 of 400 of the completgenome.) (nt:o329; 99 pct identical amino acid sequence and) (le:6110) (re:7099) (di:direct) AE000466 AE000466 g1790351 Escherichia coli 562 -11533941 5000691191 (de:(ecoli\_3815) (pn:periplasmic sulfate-binding protein) (gn:sbp) (gtcfc:12.4) (ec:) (subi\_ecoli) (keggfc:11.2) (rileyfc:4.1.5) (db:gtc-escherichia coli)) ECOLI\_3815 ECOLI\_3815 Escherichia coli 562 10080726

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838228	9319	31475	711	237

#### Description

6500730084 nhaa:ant:b0019 na:/h:antiporter 1 (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_)) b0019 b0019 Escherichia coli 562 -11533942 85768 nhaa:ant (de:na(+)/h(+)) antiporter 1 (db:swissprot) NHAA\_ECOLI P13738 ESCHERICHIA COLI 562 -11533942 7000685962 nhaa:ant na+/h+-exchanging protein nhaa:na+/h+ antiporter (cl:na+/h+-exchanging protein nhaa) (db:pir2.dat) (mp:0 min) C64722 C64722 Escherichia coli 562 -11533942 7500886413 nhaa na+/h antiporter:ph dependent (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 2 of 400 of the completgenome.) (nt:o388; 100 pct identical to nhaa\_ecoli sw: p13738) (le:6951) (re:8117) (di:direct) AE000112 AE000112 g1786201 Escherichia coli 562 -11533942 5000691192 (de:(ecoli\_19) (pn:na) (gn:nhaa) (gtcfc:12.5) (ec:) (nhaa\_ecoli) (keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_19 ECOLI\_19 Escherichia coli 562 10027935

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838236	9320	31476	711	236

Description

GTC ORF with score 176 to: (gtcfc:9.10:9.1:9.11) (ec:2.7.6.2) (keggfc:9.1) (sgdfc:1.7.1) (db:gtc-saccharomyces cerevisiae) (gtcfc:metabolism of cofactors and vitamins-porphyrin and chlorophyll metabolism:metabolism of cofactors and vitamins-thiamine ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838237	9321	31477	456	151

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838244	9322	31478	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838247	9323	31479	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838248	9324	31480	432	143

Description

GTC ORF with score 170 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac f16m14 genomic sequence,complete sequence.) (nt:unknown protein) (le:64914:65305:65470:65697) (re:65024:65382:65610:65773) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838261	9325	31481	192	64

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838262	9326	31482	885	294

#### Description

6500730085 nhar:anto:b0020 transcriptional activator protein nhar (gtcfc:10.2:12.5) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:metabolism of macromolecules-transcription--mrna synthesis and modification (including transriptional regulators):cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_)) b0020 b0020 Escherichia coli 562 -11533943 7000688994 nhar transcription activator nhar (cl:regulatory protein nhar) (db:pir1.dat) (mp:0 min) QQEC3R D64722 Escherichia coli 562 -11533943 7500953698 nhar transcriptional activator of nhaa (fn:regulator; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 2 of 400 of the completegenome.) (nt:o301; 100 pct identical to nhar\_ecoli sw: p10087) (le:8177) (re:9082) (di:direct) AE000112 AE000112 g1786202 Escherichia coli 562 -11533943 5000691193 (de:(ecoli\_20) (pn:activator of nhaa) (gn:nhar) (gtcfc:12.5) (ec:) (nhar\_ecoli) (keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_20 ECOLI\_20 Escherichia coli 562 10122620

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838278	9327	31483	453	150

#### Description

6500730086 kefc:trkc:b0047 glutathione-regulated potassium-efflux system protein kefc:k:/h:antiporter (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_)) b0047 b0047 Escherichia coli 562 -11533944 233582 kefc:trkc (de:antiporter)) (db:swissprot) KEFC\_ECOLI P03819 ESCHERICHIA COLI 562 -11533944 135157 kefc glutathione-regulated potassium efflux system protein kefc (cl:glutathione-regulated potassium efflux system protein kefc) (db:pir1.dat) (mp:1 min) QQECDR S40568 Escherichia coli 562 -11533944 5000691194 kefc kefc potassium efflux system (db:genpept-bct1) (de:e. coli kefc gene for glutathione-regulated potassium-effluxsystem.) (le:241) (re:2103) (di:direct) ECKEFC X56742 g41875 Escherichia coli 562 -11533944 7500884587 kefc kefc potassium efflux system (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (le:47430) (re:49292) (di:direct) ECOL110K D10483 g216472 Escherichia coli 562 -11533944 233283 kefc k+ efflux antiporter:glutathione-regulated (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 5 of 400 of the completegenome.) (nt:o620; 100 pct identical to kefc\_ecoli sw: p03819) (le:607) (re:2469) (di:direct) AE000115 AE000115 g1786232 Escherichia coli 562 -11533944 80616 kefc:trkc (de:antiporter)) (db:swissprot) KEFC\_ECOLI P03819 ESCHERICHIA COLI 562 -11533944

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501838286	9328	31484	873	290

Description

6500730087 fhuc:b0151 ferrichrome transport atp-binding protein fhuc (gtcfc:12.6) (keggfc:11.1) (rileyfc:4.1.2) (db:gtc-escherichia coli) b0151 b0151 Escherichia coli 562 -11533945 71557 fhuc (de:ferrichrome transport atp-binding protein fhuc) (db:swissprot) FHUC\_ECOLI P07821 ESCHERICHIA COLI 562 -11533945 7000685239 fhuc ferrichrome transport atp-binding protein fhuc (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir1.dat) (mp:4 min) QRECFH G64738 Escherichia coli 562 -11533945 7500881442 fhuc ferrichrome-iron transport protein fhuc (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:853) (re:1650) (di:direct) ECU70214 U70214 g1552729 Escherichia coli 562 -11533945 239780 fhuc atp-binding component of hydroxymate-dependent (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 14 of 400 of the completegenome.) (nt:o265; 99 pct identical to gb:ecfhuacd\_2) (le:9115) (re:9912) (di:direct) AE000124 AE000124 g1786345 Escherichia coli 562 -11533945 5000691195 (de:(ecoli\_151) (pn:hydroxymate-dependent iron uptake, cytoplasmic membrane component) (gn:fhuc) (gtcfc:12.5) (ec:) (fhuc\_ecoli) (keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_151 ECOLI\_151 Escherichia coli 562 10122684

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501838304	9329	31485	3219	1073

Description

6500730088 fhud:b0152 ferrichrome-binding periplasmic protein precursor (gtcfc:12.6) (keggfc:11.1) (rileyfc:4.1.2) (db:gtc-escherichia coli) b0152 b0152 Escherichia coli 562 -11533946 71559 fhud (de:ferrichrome-binding periplasmic protein precursor) (db:swissprot) FHUD\_ECOLI P07822 ESCHERICHIA COLI 562 -11533946 7000685242 fhud ferrichrome-iron transport protein fhud precursor:ferrichrome-binding periplasmic protein (cl:ferrichrome-iron transport protein fhud) (db:pir1.dat) (mp:4 min) QRECFD H64738 Escherichia coli 562 -11533946 7500881444 fhud ferrichrome-iron transport protein fhud (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:1650) (re:2540) (di:direct) ECU70214 U70214 g1552730 Escherichia coli 562 -11533946 239781 fhud hydroxamate-dependent iron uptake:cytoplasmic (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 14 of 400 of the completegenome.) (nt:o296; 99 pct identical to fhud\_ecoli sw: p07822) (le:9912) (re:10802) (di:direct) AE000124 AE000124 g1786346 Escherichia coli 562 -11533946 5000691196 (de:(ecoli\_152) (pn:hydroxamate-dependent iron uptake, cytoplasmic membrane component) (gn:fhud) (gtcfc:12.5) (ec:) (fhud\_ecoli) (keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_152 ECOLI\_152 Escherichia coli 562 10122685

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838314	9330	31486	756	251
<u>Description</u>				
6500730089 fhub:b0153 ferrichrome transport protein fhub precursor (gtcfc:12.6) (keggfc:11.1) (rileyfc:4.1.2) (db:gtc-escherichia coli) b0153 b0153 Escherichia coli 562 -11533947 71555 fhub (de:ferrichrome transport protein fhub precursor) (db:swissprot) FHUB_ECOLI P06972 ESCHERICHIA COLI 562 -11533947 7000685236 fhub ferrichrome-iron transport protein fhub precursor (cl:vitamin b12 transport protein btuc) (db:pir2.dat) (mp:4 min) A64739 A64739 Escherichia coli 562 -11533947 7500881440 fhub ferrichrome-iron transport protein fhub (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:2537) (re:4519) (di:direct) ECU70214 U70214 g1552731 Escherichia coli 562 -11533947 239782 fhub hydroxamate-dependent iron uptake:cytoplasmic (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 14 of 400 of the completegenome.) (nt:o660; 99 pct identical (1 gap) to fhub_ecoli) (le:10799) (re:12781) (di:direct) AE000124 AE000124 g1786347 Escherichia coli 562 -11533947 5000691197 (de:(ecoli_153) (pn:hydroxamate-dependent iron uptake, cytoplasmic membrane component) (gn:fhub) (gtcfc:12.5) (ec:) (fhub_ecoli) (keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI_153 ECOLI_153 Escherichia coli 562 10122686				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838317	9331	31487	420	139
<u>Description</u>				
6500730090 fepa:fep:feub:b0584 ferrienterobactin receptor precursor:enterobactin outer-membrane receptor (gtcfc:12.6:11.3) (keggfc:11.1) (rileyfc:4.1.2) (db:gtc-escherichia coli) b0584 b0584 Escherichia coli 562 -11533948 71311 fepa:fep:feub (de:receptor) (db:swissprot) FEPA_ECOLI P05825 ESCHERICHIA COLI 562 -11533948 7000685226 fepa:fep ferrienterochelin receptor precursor (cl:ferrienterochelin receptor:tonb-dependent receptor amino-terminal homology:tonb-dependent receptor carboxyl-terminal homology) (db:pir1.dat) (mp:14 min) QRECFC F64791 Escherichia coli 562 -11533948 7500881401 fepa outer membrane receptor for ferric enterobactin (fn:membrane; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 53 of 400 of the completegenome.) (nt:f746; 99 pct identical (1 gap) to fepa_ecoli) (le:6909) (re:9149) (di:complement) AE000163 AE000163 g1786798 Escherichia coli 562 -11533948 5000691198 fep ferrienterochelin receptor precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #163) (db:genpept) (de:escherichia coli genomic dna. (12.8 - 13.2 min).) (nt:orf_id:o164#7; similar to pir accession number) (le:15592) (re:17832) (di:complement) D90700 D90700 g4062212 Escherichia coli 562 -11533948				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838321	9332	31488	279	92

#### Description

6500730091 fes:b0585 enterochelin esterase (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_)) b0585 b0585 Escherichia coli 562 -11533949 71467 fes (de:enterochelin esterase) (db:swissprot) FES\_ECOLI P13039 ESCHERICHIA COLI 562 -11533949 130821 fes enterochelin esterase (cl:fes protein) (ec:3.1.-.-) (db:pir1.dat) (mp:14 min) BVECES A31958 Escherichia coli 562 -11533949 7500881420 fes enterochelin esterase (sr:e.coli (strain k12, mc4100) dna, clone pits311) (db:genpept-bct1) (de:escherichia coli enterochelin esterase (fes) gene complete cds, andenterochelin synthetase component f (entf) andenterochelin-dependent iron transport protein (fepa) genes , 5'en... ECOFE6 J04216 g145918 Escherichia coli 562 -11533949 234314 fes enterochelin esterase (fn:enzyme; transport of small molecules: cations) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 53 of 400 of the completegenome.) (nt:o374; 100 pct identical to fes\_ecoli sw: p13039) (le:9470) (re:10594) (di:direct) AE000163 AE000163 g1786799 Escherichia coli 562 -11533949 5000691199 (de:(ecoli\_566) (pn:enterochelin esterase) (gn:fes) (gtcfc:12.5) (ec:) (fes\_ecoli) (keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_566 ECOLI\_566 Escherichia coli 562 10014039

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838322	9333	31489	345	114

#### Description

6500730092 fepe:b0587 ferric enterobactin transport protein fepe (gtcfc:12.6) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) b0587 b0587 Escherichia coli 562 -11533950 240099 fepe (de:ferric enterobactin transport protein fepe) (db:swissprot) FEPE\_ECOLI P26266 ESCHERICHIA COLI 562 -11533950 163028 fepe ferric enterobactin transport protein fepe (db:pir2.dat) S34703 S34703 Escherichia coli 562 -11533950 5000691200 fepe fepe (db:genpept-bct1) (de:e.coli fepe gene.) (le:310) (re:1443) (di:direct) ECFEPE X74129 g395270 Escherichia coli 562 -11533950 7500881405 fepe ferric enterobactin transport protein (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (le:58885) (re:60018) (di:direct) ECU82598 U82598 g1778503 Escherichia coli 562 -11533950 232855 fepe ferric enterobactin enterochelin transport (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 54 of 400 of the completegenome.) (nt:o377; 100 pct identical to fepe\_ecoli sw: p26266) (le:4236) (re:5369) (di:direct) AE000164 AE000164 g1786802 Escherichia coli 562 -11533950 71315 fepe (de:ferric enterobactin transport protein fepe) (db:swissprot) FEPE\_ECOLI P26266 ESCHERICHIA COLI 562 -11533950

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838345	9334	31490	186	61
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838351	9335	31491	642	213
<u>Description</u>				

6500730093 fepc:b0588 ferric enterobactin transport atp-binding protein fepc (gtcfc:12.6) (keggfc:11.1) (rileyfc:4.1.2) (db:gtc-escherichia coli) b0588 b0588 Escherichia coli 562 -11533951 71313 fepc (de:ferric enterobactin transport atp-binding protein fepc) (db:swissprot) FEPC\_ECOLI P23878 ESCHERICHIA COLI 562 -11533951 7000685227 fepc ferric enterobactin transport protein fepc (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) B64792 B64792 Escherichia coli 562 -11533951 7500881403 fepc atp-binding component of ferric enterobactin (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 54 of 400 of the completegenome.) (nt:f271; 99 pct identical to fepc\_ecoli sw: p23878) (le:5366) (re:6181) (di:complement) AE000164 AE000164 g1786803 Escherichia coli 562 -11533951 5000691201 (de:(ecoli\_569) (pn:ferric enterobactin:enterochelin uptake; cytoplasmic membrane component) (gn:fepc) (gtcfc:12.5) (ec:) (fepc\_ecoli) (keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_569 ECOLI\_569 Escherichia coli 562 10122914

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838373	9336	31492	1335	444
<u>Description</u>				

6500730094 fepg:b0589 ferric enterobactin transport protein fepg (gtcfc:12.6) (keggfc:11.1) (rileyfc:4.1.2) (db:gtc-escherichia coli) b0589 b0589 Escherichia coli 562 -11533952 71316 fepg (de:ferric enterobactin transport protein fepg) (db:swissprot) FEPG\_ECOLI P23877 ESCHERICHIA COLI 562 -11533952 7000685228 fepg ferric enterobactin transport protein fepg (db:pir2.dat) C64792 C64792 Escherichia coli 562 -11533952 7500881406 fepg ferric enterobactin transport protein (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (le:60827) (re:61819) (di:complement) ECU82598 U82598 g1778505 Escherichia coli 562 -11533952 240101 fepg ferric enterobactin transport protein (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 54 of 400 of the completegenome.) (nt:f330; 99 pct identical to fepg\_ecoli sw: p23877) (le:6178) (re:7170) (di:complement) AE000164 AE000164 g1786804 Escherichia coli 562 -11533952 5000691202 (de:(ecoli\_570) (pn:ferric enterobactin transport protein) (gn:fepg) (gtcfc:12.5) (ec:) (fepg\_ecoli) (keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_570 ECOLI\_570 Escherichia coli 562 10122915

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838388	9337	31493	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838406	9338	31494	873	290

Description

6500730095 fepd:b0590 ferric enterobactin transport protein fepd (gtcfc:12.6) (keggfc:11.1) (rileyfc:4.1.2) (db:gtc-escherichia coli) b0590 b0590 Escherichia coli 562 -11533953 7500881404 fepd (de:ferric enterobactin transport protein fepd) (db:swissprot) FEPD\_ECOLI P23876 ESCHERICHIA COLI 562 -11533953 163031 fepd ferric enterobactin transport protein fepd:ferrienterobactin permease fepd (db:pir2.dat) (mp:14 min) S16296 S16296 Escherichia coli 562 -11533953 5000691203 fepd (fn:ferric enterobactin transport protein) (db:genpept-bct1) (de:e.coli fepc, fepd and fepg genes for ferric enterobactin transportproteins.) (le:106) (re:1110) (di:direct) ECFEPCDG X57471 g41430 Escherichia coli 562 -11533953 232850 fepd ferric enterobactin enterochelin transport (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 54 of 400 of the completegenome.) (nt:f334; 100 pct identical to fepd\_ecoli sw: p23876) (le:7167) (re:8171) (di:complement) AE000164 AE000164 g1786805 Escherichia coli 562 -11533953 71314 fepd (de:ferric enterobactin transport protein fepd) (db:swissprot) FEPD\_ECOLI P23876 ESCHERICHIA COLI 562 -11533953

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838407	9339	31495	1626	541

#### Description

6500730096 fepb:b0592 ferrienterobactin-binding periplasmic protein precursor (gtcfc:12.5:12.6) (keggfc:11.1) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_):cell processes-transporters of unknown specificity (abc\_atpases\_drug) or metals) b0592 b0592 Escherichia coli 562 -11533954 71312 fepb (de:ferrienterobactin-binding periplasmic protein precursor) (db:swissprot) FEPB\_ECOLI P14609 ESCHERICHIA COLI 562 -11533954 163034 fepb ferrienterobactin-binding periplasmic protein precursor:ferrienterobactin transport protein (db:pir2.dat) (mp:14 min) JV0045 JV0045 Escherichia coli 562 -11533954 240104 fepb ferrienterobactin transport protein (sr:escherichia coli (strain k-12) (clone: pcp111.) dna) (db:genpept-bct1) (de:e.coli ferrienterobactin transport protein (fepb) gene, completecds.) (nt:precursor) (le:414) (re:1370) (di:direct) ECOFEPB M29730 g145944 Escherichia coli 562 -11533954 7500881402 fepb ferrienterobactin transport protein (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (le:64185) (re:65141) (di:complement) ECU82598 U82598 g1778508 Escherichia coli 562 -11533954 234334 fepb ferric enterobactin enterochelin binding (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 54 of 400 of the completegenome.) (nt:f318; 99 pct identical to fepb\_ecoli sw: p14609) (le:9536) (re:10492) (di:complement) AE000164 AE000164 g1786807 Escherichia coli 562 -11533954 5000691204 (de:(ecoli\_573) (pn:ferric enterobactin:enterochelin uptake; periplasmic component) (gn:fepb) (gtcfc:12.5) (ec:) (fepb\_ecoli) (keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_573 ECOLI\_573 Escherichia coli 562 10086732

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838418	9340	31496	1572	524

#### Description

GTC ORF with score 1226 to: (sr:humicola grisea var. thermoidea (sub\_species:ifo9854) dna) (db:genpept) (de:humicola grisea var. thermoidea bgl4 gene for beta-glucosidase,complete cds.) (le:289:437) (re:332:1823) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838420	9341	31497	432	143

Description

6500730097 putp:b1015 sodium/proline symporter:proline permease (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_)) b1015 b1015 Escherichia coli 562 -11533955 7500889107 putp (de:sodium/proline symporter (proline permease)) (db:swissprot) PUTP\_ECOLI P07117 ESCHERICHIA COLI 562 -11533955 130784 putp sodium/proline symporter:proline carrier protein:proline permease:proline transport protein (cl:proline carrier protein) (db:pir1.dat) (mp:23 min) JGECPP A30258 Escherichia coli 562 -11533955 223332 putp proline carrier protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #228) (db:genpept-bct1) (de:escherichia coli genomic dna. (22.9 - 23.3 min).) (le:13266) (re:14774) (di:direct) D90738 D90738 g1651504 Escherichia coli 562 -11533955 5000691208 (db:genpept-bct1) (de:e.coli putp gene for proline carrier and regulatory region putc.) (nt:putp proline carrier (aa 1-502)) (le:602) (re:2110) (di:direct) ECPUTP X05653 g42602 Escherichia coli 562 -11533955 237972 putp major sodium/proline symporter (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 93 of 400 of the completegenome.) (nt:o502; 99 pct identical to putp\_ecoli sw: p07117) (le:5209) (re:6717) (di:direct) AE000203 AE000203 g1787251 Escherichia coli 562 -11533955 7502851979 putp proline carrier protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #228) (db:genpept) (de:escherichia coli genomic dna. (23.0 - 23.4 min).) (nt:orf\_id:o228#14; similar to pir accession number) (le:13266) (re:14774) (di:direct) D90738 D90738 g1651504 Escherichia coli 562 -11533955 92495 putp (de:sodium/proline symporter (proline permease)) (db:swissprot) PUTP\_ECOLI P07117 ESCHERICHIA COLI 562 -11533955

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838436	9342	31498	1026	341

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838437	9343	31499	675	224

#### Description

6500730098 fhue:b1102 outer-membrane receptor for  
 fe:iii-coprogen:fe:iii-ferrioxamine b and fe:iii-rhodotruclic acid precursor  
 (gtcfc:12.5:11.3) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)  
 (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_):cell  
 envelope-surface proteins--glycoproteins--and structures) b1102 b1102  
 Escherichia coli 562 -11533956 71560 fhue (de:and fe(iii)-rhodotruclic acid  
 precursor) (db:swissprot) FHUE\_ECOLI P16869 ESCHERICHIA COLI 562 -11533956  
 7000685243 fhue ferric-coprogen receptor precursor:outer membrane protein  
 fhue (cl:tonb-dependent receptor amino-terminal homology:tonb-dependent  
 receptor carboxyl-terminal homology) (db:pir2.dat) (mp:16 min) C64854 C64854  
 Escherichia coli 562 -11533956 223363 fhue outer membrane protein fhue  
 precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #236)  
 (db:genpept-bct1) (de:escherichia coli genomic dna.(24.7 - 25.1 min).)  
 (le:10004) (re:12193) (di:complement) D90745 D90745 g1651542 Escherichia  
 coli 562 -11533956 223365 fhue outer membrane protein fhue precursor  
 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #237)  
 (db:genpept-bct1) (de:escherichia coli genomic dna.(24.9 - 25.3 min).)  
 (le:1303) (re:3492) (di:complement) D90746 D90746 g1651545 Escherichia coli  
 562 -11533956 7500881445 fhue outer membrane receptor for ferric iron  
 uptake (fn:transport; transport of small molecules:) (db:genpept-bct2)  
 (de:escherichia coli k-12 mg1655 section 100 of 400 of the completegenome.)  
 (nt:f729; 99 pct identical to fhue\_ecoli sw: p16869) (le:10667) (re:12856)  
 (di:complement) AE000210 AE000210 g1787344 Escherichia coli 562 -11533956  
 5000691209 fhue ferric-coprogen receptor protein precursor. (sr:escherichia  
 coli(strain:k12) dna, clone:kohara clone #236) (db:genpept) (de:escherichia  
 coli genomic dna. (24.8 - 25.2 min).) (nt:orf\_id:o237#1; similar to pir  
 accession number) (le:10004) (re:12193) (di:complement) D90745 D90745  
 g1651542 Escherichia coli 562 -11533956 7502851980 fhue ferric-coprogen  
 receptor protein precursor. (sr:escherichia coli(strain:k12) dna,  
 clone:kohara clone #237) (db:genpept) (de:escherichia coli genomic dna.  
 (25.0 - 25.4 min).) (nt:orf\_id:o237#1; similar to pir accession number)  
 (le:1303) (re:3492) (di:complement) D90746 D90746 g1651545 Escherichia coli  
 562 -11533956

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838440	9344	31500	711	236

#### Description

GTC ORF with score 115 to: (sr:caenorhabditis elegans strain=bristol n2)  
 (db:genpept-inv) (de:caenorhabditis elegans cosmid k07h8.) (nt:contains  
 similarity to rna recognition motifs) (le:27498:27637:28112)  
 (re:27575:28067:29075) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838476	9345	31501	213	70

# Description

6500730099 nhab:b1186 regulator of intracellular ph:na+/h+ antiporter (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_)) b1186 b1186 Escherichia coli 562 -11533957 85772 nhab (de:na(+)/h(+)) antiporter 2) (db:swissprot) NHAB\_ECOLI P27377 ESCHERICHIA COLI 562 -11533957 7000685963 nhab na+/h+-exchanging protein nhab:na+/h+ antiporter (db:pir2.dat) (mp:25.5 min) G64864 G64864 Escherichia coli 562 -11533957 223398 nhab na + /h + antiporter 2 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #243) (db:genpept-bct1) (de:escherichia coli genomic dna. (26.2 - 26.6 min).) (le:15067) (re:16608) (di:complement) D90752 D90752 g1651583 Escherichia coli 562 -11533957 223403 nhab na + /h + antiporter 2 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #244) (db:genpept-bct1) (de:escherichia coli genomic dna. (26.4 - 26.7 min).) (le:4922) (re:6463) (di:complement) D90753 D90753 g1651589 Escherichia coli 562 -11533957 7500886415 nhab na+/h+ antiporter:ph independent (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 107 of 400 of the completegenome.) (nt:f513; 100 pct identical to nhab\_ecoli sw: p27377) (le:103) (re:1644) (di:complement) AE000217 AE000217 g1787435 Escherichia coli 562 -11533957 5000691210 nhab na+/h+ antiporter protein nhab (sr:escherichia coli(strain:k12) dna, clone:kohara clone #243) (db:genpept) (de:escherichia coli genomic dna. (26.3 - 26.7 min).) (nt:orf\_id:o244#6; similar to pir accession number) (le:15067) (re:16608) (di:complement) D90752 D90752 g1651583 Escherichia coli 562 -11533957 7502851981 nhab na+/h+ antiporter protein nhab (sr:escherichia coli(strain:k12) dna, clone:kohara clone #244) (db:genpept) (de:escherichia coli genomic dna. (26.5 - 26.8 min).) (nt:orf\_id:o244#6; similar to pir accession number) (le:4922) (re:6463) (di:complement) D90753 D90753 g1651589 Escherichia coli 562 -11533957

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838481	9346	31502	612	203

Description

6500730100 chaa:b1216 putative calcium/proton antiporter:calcium/proton antiporter (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_)) b1216 b1216 Escherichia coli 562 -11533958 64201 chaa (de:calcium/proton antiporter) (db:swissprot) CHAA\_ECOLI P31801 ESCHERICHIA COLI 562 -11533958 164374 chaa ca2+/h+-exchanging protein chaa:ca2+/h+ antiporter (db:pir2.dat) A46716 A46716 Escherichia coli 562 -11533958 223416 chaa calcium/proton antiporter (sr:escherichia coli(strain:k12) dna, clone:kohara clone #247) (db:genpept-bct1) (de:escherichia coli genomic dna.(27.0 -27.4 min).) (le:15011) (re:16111) (di:complement) D90756 D90756 g1651604 Escherichia coli 562 -11533958 223423 chaa calcium/proton antiporter (sr:escherichia coli(strain:k12) dna, clone:kohara clone #248) (db:genpept-bct1) (de:escherichia coli genomic dna (27.2-27.6 min).) (le:5873) (re:6973) (di:complement) D90757 D90757 g1651612 Escherichia coli 562 -11533958 7500878626 chaa calcium/proton antiporter (sr:escherichia coli (strain nm8191) (library: delta-b) dna) (db:genpept-bct1) (de:escherichia coli (nm8191) calcium/proton antiporter protein (chaa,chac and chab) genes, complete cds.) (nt:putative) (le:2188) (re:3288) (di:direct) ECOCHAABC L28709 g501012 Escherichia coli 562 -11533958 233972 chaa sodium-calcium/proton antiporter (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 110 of 400 of the completegenome.) (nt:f366; 100 pct identical to chaa\_ecoli sw:) (le:895) (re:1995) (di:complement) AE000220 AE000220 g1787468 Escherichia coli 562 -11533958 5000691211 chaa probable ca2+/h+ antiporter chaa. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #247) (db:genpept) (de:escherichia coli genomic dna. (27.1 - 27.5 min).) (nt:orf\_id:o248#6; similar to pir accession number) (le:15011) (re:16111) (di:complement) D90756 D90756 g1651604 Escherichia coli 562 -11533958 7502851982 chaa probable ca2+/h+ antiporter chaa. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #248) (db:genpept) (de:escherichia coli genomic dna. (27.3 - 27.7 min).) (nt:orf\_id:o248#6; similar to pir accession number) (le:5873) (re:6973) (di:complement) D90757 D90757 g1651612 Escherichia coli 562 -11533958

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838500	9347	31503	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838501	9348	31504	303	100

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838502	9349	31505	573	190

Description

GTC ORF with score 130 to: (fn:has both arabinofuranosidase and exoxylanase) (db:genpept-bct1) (de:caldicellulosiruptor saccharolyticus putative transport protein(xyng), putative transport protein (xynh), xylanase (xynf),xylanase (xyme), xylanase ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838503	9350	31506	297	98

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838509	9351	31507	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838516	9352	31508	2010	669

Description

6500730101 kch:b1250 putative potassium channel protein (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_)) b1250 b1250 Escherichia coli 562 -11533959 80522 kch (de:putative potassium channel protein) (db:swissprot) KCH\_ECOLI P31069 ESCHERICHIA COLI 562 -11533959 164358 kch probable potassium channel protein (db:pir2.dat) A55252 A55252 Escherichia coli 562 -11533959 223456 kch putative potassium channel protein. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #252(28.1-28.4 min.)) (nt:orf\_id:o252#7; similar to (swissprot accession) (le:7337) (re:8590) (di:complement) D90763 D90763 g1742039 Escherichia coli 562 -11533959 238856 kch (fn:putative potassium channel) (sr:escherichia coli (sub\_strain w3110, strain k-12) dna) (db:genpept-bct1) (de:escherichia coli potassium channel homologue, complete cds.) (nt:possible transmembrane domains incorporate regions) (le:721) (re:1974) (di:... ECOKCH L12044 g146538 Escherichia coli 562 -11533959 238944 kch (db:genpept-bct1) (de:escherichia coli ecor 1 (ycid) gene, partial cds, and (ycic), (ycib), (ycia), membrane protein (tonb), (ycii), putative potassiumchannel (kch), and cardiolipin synthase (cls) genes, complete cds.) (nt:putative potassium channel) (l... ECU24195 U24195 g902385 Escherichia coli 562 -11533959 300259 kch (db:genpept-bct1) (de:escherichia coli k12 (ycid) gene, partial cds, and (ycic), (ycib), (ycia), membrane protein (tonb), (ycii), putative potassium channel(kch), and cardiolipin synthase (cls) genes, complete cds.) (nt:putative potassium channel) (le:4... ECU24206 U24206 g902484 Escherichia coli 562 -11533959 234915 kch putative potassium channel protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 113 of 400 of the completegenome.) (nt:f417; 99 pct identical to kch\_ecoli sw: p31069) (le:6190) (re:7443) (di:complement) AE000223 AE000223 g1787503 Escherichia coli 562 -11533959 5000691212 (de:(ecoli\_1210) (pn:putative potassium channel protein) (gn:kch) (gtcfc:12.5) (ec:) (kch\_ecoli) (keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_1210 ECOLI\_1210 Escherichia coli 562 10022764

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838532	9353	31509	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838545	9354	31510	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838550	9355	31511	729	242

Description

GTC ORF with score 224 to: (sr:thale cress) (db:genpept-pln1)  
(de:arabidopsis thaliana chromosome ii bac t9j22 genomic sequence, complete  
sequence.) (nt:hypothetical protein) (le:44981:45900:46046)  
(re:45748:45965:46155) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838570	9356	31512	2526	841

Description

6500730102 tonb:exba:b1252 tonb protein (gtcfc:12.5) (keggfc:14.2)  
(rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of  
cations (na\_k\_ca\_nh4\_etc\_)) b1252 b1252 Escherichia coli 562 -11533960  
101770 tonb:exba (de:tonb protein) (db:swissprot) TONB\_ECOLI P02929  
ESCHERICHIA COLI 562 -11533960 7000686808 tonb:exba tonb protein (cl:tonb  
protein) (db:pir1.dat) (mp:28 min) BVEC G64872 Escherichia coli 562  
-11533960 7500893254 tonb energy transducer:uptake of iron (fn:membrane;  
transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12  
mg1655 section 113 of 400 of the completegenome.) (nt:o239; 100 pct  
identical to tonb\_ecoli sw: p02929) (le:8263) (re:8982) (di:direct) AE000223  
AE000223 g1787505 Escherichia coli 562 -11533960 5000691213  
(de:(ecoli\_1212) (pn:energy transducer; uptake of iron, cyanocobalimin;  
sensitivity to phages, colicins) (gn:tonb) (gtcfc:12.5) (ec:) (tonb\_ecoli)  
(keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_1212  
ECOLI\_1212 Escherichia coli 562 10043599

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838581	9357	31513	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838599	9358	31514	372	123

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501838600	9359	31515	405	134

# Description

6500730103 trkg:b1363 trk system potassium uptake protein trkg (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_)) b1363 b1363 Escherichia coli 562 -11533961 300406 trkg (de:trk system potassium uptake protein trkg) (db:swissprot) TRKG\_ECOLI P23849 ESCHERICHIA COLI 562 -11533961

164359 trkg trk system potassium uptake protein trkg (cl:potassium uptake protein trkg) (db:pir2.dat) (mp:30.5 min) A39408 A39408 Escherichia coli 562 -11533961 223633 trkg potassium transport protein trkg (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #263(30.5-30.9 min..)) (nt:orf\_id:o263#14; similar to (pir accession number) (le:9694) (re:11151) (di:direct) D90774 D90774 g1742227 Escherichia coli 562 -11533961

5000691214 trkg trkg protein (db:genpept-bct1) (de:e.coli trkg gene for protein involved in potassium uptake via thetrk system.) (le:145) (re:1602) (di:direct) ECTRKG X56783 g43140 Escherichia coli 562 -11533961 238402 trkg trk system potassium uptake:part of rac (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 123 of 400 of the completegenome.) (nt:o485; 100 pct identical to trkg\_ecoli sw: p23849;) (le:6375) (re:7832) (di:direct) AE000233 AE000233 g1787626 Escherichia coli 562 -11533961 102254 trkg (de:trk system potassium uptake protein trkg) (db:swissprot) TRKG\_ECOLI P23849 ESCHERICHIA COLI 562 -11533961

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838605	9360	31516	408	135

Description

6500730104 ftn:rsga:gen-165:b1905 ferritin-like protein:ferritin (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_)) b1905 b1905 Escherichia coli 562 -11533962 301051 ftn:rsga:gen-165 (de:ferritin) (db:swissprot) FTN\_ECOLI P23887 ESCHERICHIA COLI 562 -11533962 163446 ftn ferritin-like protein:protein gen-165 (cl:ferritin) (db:pir2.dat) (mp:42 min) S14069 S14069 Escherichia coli 562 -11533962 224411 ftn:rsga:gen-165 ferritin. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #341(42.7-43.1 min.)) (nt:orf\_id:o341#5; similar to (swissprot accession) (le:5246) (re:5743) (di:direct) D90832 D90832 g1736567 Escherichia coli 562 -11533962 5000691215 rsga::gen-165 rsga product (db:genpept-bct1) (de:e.coli rsga (gen-165) gene for polypeptide with homology to humanferritin subunit.) (le:152) (re:649) (di:direct) ECRSGA X53513 g42898 Escherichia coli 562 -11533962 238193 ftn cytoplasmic ferritin an iron storage protein (fn:carrier; transport of small molecules: cations) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 174 of 400 of the completengenome.) (nt:o165; 100 pct identical to rsga\_ecoli sw: p23887;) (le:744) (re:1241) (di:direct) AE000284 AE000284 g1788216 Escherichia coli 562 -11533962 72430 ftn:rsga:gen-165 (de:ferritin) (db:swissprot) FTN\_ECOLI P23887 ESCHERICHIA COLI 562 -11533962

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838615	9361	31517	1203	400

Description

6500730105 molr\_1:b2115 molybdate metabolism regulator (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_)) b2115 b2115 Escherichia coli 562 -11533963 7000691865 molr\_1 molybdate metabolism regulator (db:pir2.dat) B64979 B64979 Escherichia coli 562 -11533963 7500960385 yehf (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (le:9242) (re:10066) (di:direct) ECOHU47 U00007 g405842 Escherichia coli 562 -11533963 234724 molr\_1 molybdate metabolism regulator:first fragment (fn:regulator; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 190 of 400 of the completengenome.) (nt:o274; residues 1-275 are 100 pct identical to) (le:9165) (re:9989) (di:direct) AE000300 AE000300 g1788433 Escherichia coli 562 -11533963 5000691216 (de:(ecoli\_2063) (pn:regulation of mod locus governing molybdate transport) (gn:molr) (gtcfc:12.5) (ec:) (molr\_ecoli) (keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_2063 ECOLI\_2063 Escherichia coli 562 10123569



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838617	9362	31518	1098	365

Description

5000691217 molr\_2 (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2)  
(db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations  
(na\_k\_ca\_nh4\_etc\_)) b2116 b2116 Escherichia coli 562 -11533964 7000691863  
molr\_2 molr\_2 protein (db:pir2.dat) C64979 C64979 Escherichia coli 562  
-11533964 7500960383 molr\_2 molybdate metabolism regulator:second fragment  
(fn:regulator; biosynthesis of cofactors, carriers:) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 190 of 400 of the completegenome.)  
(nt:o645; 99 pct identical to residues 314-949) (le:10101) (re:12038)  
(di:direct) AE000300 AE000300 g1788434 Escherichia coli 562 -11533964  
6500730106 molr\_2 (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2)  
(db:gtc-escherichia coli) b2116 b2116 Escherichia coli 562 -11533964

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838632	9363	31519	843	280

Description

5000691218 molr\_3 (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2)  
(db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations  
(na\_k\_ca\_nh4\_etc\_)) b2117 b2117 Escherichia coli 562 -11533965 7000691864  
molr\_3 molr\_3 protein (db:pir2.dat) D64979 D64979 Escherichia coli 562  
-11533965 7500960384 molr\_3 molybdate metabolism regulator:third fragment  
(fn:regulator; biosynthesis of cofactors, carriers:) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 190 of 400 of the completegenome.)  
(nt:o333; 100 pct identical to molr\_ecoli but) (le:11959) (re:12960)  
(di:direct) AE000300 AE000300 g1788435 Escherichia coli 562 -11533965  
6500730107 molr\_3 (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2)  
(db:gtc-escherichia coli) b2117 b2117 Escherichia coli 562 -11533965

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838638	9364	31520	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501838659	9365	31521	978	325

# Description

6500730108 cira:cir:feua:b2155 colicin i receptor precursor (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_)) b2155 b2155 Escherichia coli 562 -11533966 64649 cira:cir:feua (de:colicin i receptor precursor) (db:swissprot) CIRA\_ECOLI P17315 ESCHERICHIA COLI 562 -11533966 7000684819 cir:cira:feua colicin i receptor precursor (cl:ferrienterochelin receptor:tonb-dependent receptor amino-terminal homology:tonb-dependent receptor carboxyl-terminal homology) (db:pirl.dat) (mp:43 min) QREIC B64984 Escherichia coli 562 -11533966 7500878755 colicin i receptor (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (le:52523) (re:54514) (di:complement) ECOHU47 U00007 g405900 Escherichia coli 562 -11533966 234762 cira outer membrane receptor for iron-regulated (fn:membrane; outer membrane constituents) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 194 of 400 of the completegenome.) (nt:f663; 99 pct identical to cira\_ecoli sw: p17315) (le:8187) (re:10178) (di:complement) AE000304 AE000304 g1788478 Escherichia coli 562 -11533966 5000691219 (de:(ecoli\_2104) (pn:outer membrane receptor for iron-regulated colicin i receptor; porin; requires tonb gene product) (gn:cira) (gtcfc:12.5) (ec:) (cira\_ecoli) (keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_2104 ECOLI\_2104 Escherichia coli 562 10123587

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838660	9366	31522	336	111

#### Description

6500730109 exbd:b3005 biopolymer transport exbd protein (gtcfc:12.6) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) b3005 b3005 Escherichia coli 562 -11533967 70790 exbd (de:biopolymer transport exbd protein) (db:swissprot) EXBD\_ECOLI P18784 ESCHERICHIA COLI 562 -11533967 131575 exbd biopolymer transport exbd protein (cl:tolr protein) (db:pir1.dat) (mp:65 min) BVECED JV0030 Escherichia coli 562 -11533967 239218 (sr:e.coli dna) (db:genpept-bct1) (de:e.coli exbb and exbd genes encoding biopolymer transport proteins,complete cds.) (nt:exbd peptide) (le:1323) (re:1748) (di:direct) ECOEXBBD M28819 g145869 Escherichia coli 562 -11533967 7500881232 exbd (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (le:105206) (re:105631) (di:complement) ECU28377 U28377 g882534 Escherichia coli 562 -11533967 234267 exbd uptake of enterochelin:tonb-dependent uptake of (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 273 of 400 of the completegenome.) (nt:f141; 100 pct identical to exbd\_ecoli sw: p18784) (le:1282) (re:1707) (di:complement) AE000383 AE000383 g1789380 Escherichia coli 562 -11533967 5000691220 (de:(ecoli\_2927) (pn:uptake of enterochelin; tonb-dependent uptake of b colicins) (gn:exbd) (gtcfc:12.5) (ec:) (exbd\_ecoli) (keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_2927 ECOLI\_2927 Escherichia coli 562 10013365

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838661	9367	31523	489	162

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838669	9368	31524	528	176

#### Description

GTC ORF with score 154 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid b0238.) (nt:similar to acyltransferase; coded for by c. elegans) (le:6521:7012:7331) (re:6668:7283:7576) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838722	9369	31525	222	73

Description

GTC ORF with score 146 to: (sr:human) (db:genpept-pri2) (de:human ca2+ atpase of fast-twitch skeletal muscle sarcoplasmicreticulum adult and neonatal isoforms (atp2a1) gene, exons 16 to 23and complete cds.) (nt:sercalb) (le:u96773:1140:u96773:1565) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838723	9370	31526	504	167

Description

6500730110 exbb:b3006 biopolymer transport exbb protein (gtcfc:12.6) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) b3006 b3006 Escherichia coli 562 -11533968 70786 exbb (de:biopolymer transport exbb protein) (db:swissprot) EXBB\_ECOLI P18783 ESCHERICHIA COLI 562 -11533968 7000685206 exbb biopolymer transport exbb protein (cl:biopolymer transport protein) (db:pir1.dat) (mp:65 min) BVECXB D65087 Escherichia coli 562 -11533968 7500881230 exbb (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (le:105638) (re:106372) (di:complement) ECU28377 U28377 g882535 Escherichia coli 562 -11533968 239219 exbb uptake of enterochelin:tonb-dependent uptake of (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 273 of 400 of the completegenome.) (nt:f244; 99 pct identical to exbb\_ecoli sw: p18783) (le:1714) (re:2448) (di:complement) AE000383 AE000383 g1789381 Escherichia coli 562 -11533968 5000691221 (de:(ecoli\_2928) (pn:uptake of enterochelin; tonb-dependent uptake of b colicins) (gn:exbb) (gtcfc:12.5) (ec:) (exbb\_ecoli) (keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_2928 ECOLI\_2928 Escherichia coli 562 10013361

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838726	9371	31527	285	94

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838739	9372	31528	603	200

Description

6500730111 panf:b3258 sodium/pantothenate symporter:pantothenate permease (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_)) b3258 b3258 Escherichia coli 562 -11533969 7000691879 panf pantothenate permease:sodium/pantothenate symporter (cl:proline carrier protein) (db:pir2.dat) D65118 D65118 Escherichia coli 562 -11533969 7500960404 panf pantothenate permease (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 10818) (le:188346) (re:189803) (di:direct) ECOUW67 U18997 g606198 Escherichia coli 562 -11533969 236497 panf sodium/pantothenate symporter (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 294 of 400 of the completegenome.) (nt:o485; cg site no. 10818; 100 pct identical to) (le:11339) (re:12796) (di:direct) AE000404 AE000404 g1789656 Escherichia coli 562 -11533969 5000691222 (de:(ecoli\_3182) (pn:sodium) (gn:panf) (gtcfc:12.5) (ec:) (panf\_ecoli) (keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_3182 ECOLI\_3182 Escherichia coli 562 10124001

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838743	9373	31529	210	69

#### Description

6500730112 trka:b3290 trka protein of the constitutive k+ transport system trk:trk system potassium uptake protein trka (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_)) b3290 b3290 Escherichia coli 562 -11533970  
7500893395 trka (de:trk system potassium uptake protein trka) (db:swissprot) TRKA\_ECOLI P23868 ESCHERICHIA COLI 562 -11533970 164769 trka trka protein of the constitutive k+ transport system trk (cl:probable potassium transport system protein trka) (db:pir2.dat) S36252 S36252 Escherichia coli 562 -11533970 236523 trka (fn:k+ uptake protein component) (db:genpept-bct1) (de:e.coli fms, fmt, fmu, fmv, smf, smg and trka genes.) (le:4253) (re:5629) (di:direct) ECFMUV X77091 g443993 Escherichia coli 562 -11533970 238400 trka trka protein of the constitutive k+ transport (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 84) (le:217266) (re:218642) (di:direct) ECOUW67 U18997 g606224 Escherichia coli 562 -11533970 5000691223 trka trka protein of the constitutive k+ -transport (db:genpept-bct1) (de:e.coli trka gene for the trka protein of the constitutive k+-transport system trk.) (le:163) (re:1539) (di:direct) ECTRKAG X52114 g43137 Escherichia coli 562 -11533970 232905 trka transport of potassium (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 297 of 400 of the completegenome.) (nt:o458; cg site no. 84; 100 pct identical amino acid) (le:4588) (re:5964) (di:direct) AE000407 AE000407 g1789685 Escherichia coli 562 -11533970 102245 trka (de:trk system potassium uptake protein trka) (db:swissprot) TRKA\_ECOLI P23868 ESCHERICHIA COLI 562 -11533970

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838746	9374	31530	300	99

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838747	9375	31531	1212	403

#### Description

6500730113 kefb:trkb:b3350 glutathione-regulated potassium-efflux system protein:glutathione-regulated potassium-efflux system protein  
kefb:k:/h:antiporter:nem-activatable k+/h+ antiporter (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_)) b3350 b3350 Escherichia coli 562 -11533971 80615 kefb:trkb (de:antiporter) (nem-activatable k+/h+ antiporter)) (db:swissprot) KEFB\_ECOLI P45522 ESCHERICHIA COLI 562 -11533971 7000685680 kefb glutathione-regulated potassium-efflux system protein kefb (cl:glutathione-regulated potassium efflux system protein kefc) (db:pir2.dat) A65129 A65129 Escherichia coli 562 -11533971 7500884586 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf\_f601) (le:259550) (re:261355) (di:complement) ECOUW67 U18997 g606284 Escherichia coli 562 -11533971 236583 kefb k+ efflux:nem-activatable k+/h+ antiporter (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 301 of 400 of the completegenome.) (nt:f601; 100 pct identical amino acid sequence and) (le:1303) (re:3108) (di:complement) AE000411 AE000411 g1789749 Escherichia coli 562 -11533971 5000691224 (de:(ecoli\_3268) (pn:k) (gn:kefb) (gtcfc:12.5) (ec:) (kefb\_ecoli) (keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_3268 ECOLI\_3268 Escherichia coli 562 10022857

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838751	9376	31532	363	121

#### Description

6500730114 feoa:b3408 ferrous iron transport protein a (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_)) b3408 b3408 Escherichia coli 562 -11533972 236642 feoa (de:ferrous iron transport protein a) (db:swissprot) FEOA\_ECOLI P33649 ESCHERICHIA COLI 562 -11533972 163933 feoa iron ii transport system protein feoa (db:pir2.dat) B36932 B36932 Escherichia coli 562 -11533972 5000691225 feoa (db:genpept-bct1) (de:e.coli feoa and feob genes.) (le:334) (re:561) (di:direct) ECFEOAB X71063 g414746 Escherichia coli 562 -11533972 7500881398 feoa (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 28964) (le:320906) (re:321133) (di:direct) ECOUW67 U18997 g606343 Escherichia coli 562 -11533972 232848 feoa ferrous iron transport protein a (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 306 of 400 of the completegenome.) (nt:o75; cg site no. 28964; 100 pct identical amino) (le:7418) (re:7645) (di:direct) AE000416 AE000416 g1789812 Escherichia coli 562 -11533972 71309 feoa (de:ferrous iron transport protein a) (db:swissprot) FEOA\_ECOLI P33649 ESCHERICHIA COLI 562 -11533972

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838763	9377	31533	945	314

Description

6500730115 feob:b3409 ferrous iron transport protein b (gtcfc:12.6) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) b3409 b3409 Escherichia coli 562 -11533973 7500881399 feob (de:ferrous iron transport protein b) (db:swissprot) FEOB\_ECOLI P33650 ESCHERICHIA COLI 562 -11533973 163934 feob iron ii transport system protein feob (db:pir2.dat) A36932 A36932 Escherichia coli 562 -11533973 5000691226 feob ferrous iron transport protein b (db:genpept-bct1) (de:e.coli feoa and feob genes.) (le:578) (re:2899) (di:direct) ECFEOAB X71063 g1199515 Escherichia coli 562 -11533973 232849 feob ferrous iron transport protein b (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 306 of 400 of the completegenome.) (nt:o773; cg site no. 28967; 99 pct identical amino) (le:7662) (re:9983) (di:direct) AE000416 AE000416 g1789813 Escherichia coli 562 -11533973 71310 feob (de:ferrous iron transport protein b) (db:swissprot) FEOB\_ECOLI P33650 ESCHERICHIA COLI 562 -11533973

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838778	9378	31534	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838788	9379	31535	228	75

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838789	9380	31536	1809	602
<u>Description</u>				
6500730116 nika:b3476 nickel-binding periplasmic protein precursor (gtcfc:12.5:12.6) (keggfc:11.1) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_):cell processes-transporters of unknown specificity (abc_atpases_drug) or metals) b3476 b3476 Escherichia coli 562 -11533974 236711 nika (de:nickel-binding periplasmic protein precursor) (db:swissprot) NIKA_ECOLI P33590 ESCHERICHIA COLI 562 -11533974 164147 nika nickel-binding periplasmic protein precursor:nika protein (cl:dipeptide transport protein) (db:pir2.dat) S39594 S39594 Escherichia coli 562 -11533974 5000691227 nika nika (db:genpept-bct1) (de:e.coli dna sequence of nik locus.) (le:427) (re:2001) (di:direct) ECNIK X73143 g404845 Escherichia coli 562 -11533974 7500886457 nika (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:27929) (re:29503) (di:direct) ECOUW76 U00039 g466612 Escherichia coli 562 -11533974 233478 nika periplasmic binding protein for nickel (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 313 of 400 of the completegenome.) (nt:o524; 100 pct identical amino acid sequence and) (le:4981) (re:6555) (di:direct) AE000423 AE000423 g1789887 Escherichia coli 562 -11533974 86007 nika (de:nickel-binding periplasmic protein precursor) (db:swissprot) NIKA_ECOLI P33590 ESCHERICHIA COLI 562 -11533974				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838813	9381	31537	324	107
<u>Description</u>				
6500730117 nikb:b3477 nickel transport system permease protein:nickel transport system permease protein nikb (gtcfc:12.6) (keggfc:11.1) (rileyfc:4.1.2) (db:gtc-escherichia coli) b3477 b3477 Escherichia coli 562 -11533975 163804 nikb nickel transport system permease protein nikb:hypothetical protein o314 (cl:oligopeptide permease protein oppb) (db:pir2.dat) S47696 S47696 Escherichia coli 562 -11533975 7500960396 nikb (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:29503) (re:30447) (di:direct) ECOUW76 U00039 g466613 Escherichia coli 562 -11533975 236712 nikb transport of nickel:membrane protein (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 313 of 400 of the completegenome.) (nt:o314; 99 pct identical amino acid sequence and) (le:6555) (re:7499) (di:direct) AE000423 AE000423 g1789888 Escherichia coli 562 -11533975 5000691228 (de:(ecoli_3395) (pn:transport of nickel, membrane protein) (gn:nikb) (gtcfc:12.5) (ec:) (nikb_ecoli) (keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI_3395 ECOLI_3395 Escherichia coli 562 10087054				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838814	9382	31538	243	80

Description

6500730118 nikc:b3478 nickel transport system permease protein nikc (gtcfc:12.6) (keggfc:11.1) (rileyfc:4.1.2) (db:gtc-escherichia coli) b3478 b3478 Escherichia coli 562 -11533976 236713 nikc (de:nickel transport system permease protein nikc) (db:swissprot) NIKC\_ECOLI P33592 ESCHERICHIA COLI 562 -11533976 164151 nikc nikc protein (cl:oligopeptide permease protein oppb) (db:pir2.dat) S39596 S39596 Escherichia coli 562 -11533976 5000691229 nikc nikc (db:genpept-bct1) (de:e.coli dna sequence of nik locus.) (le:2942) (re:3775) (di:direct) ECNIK X73143 g581141 Escherichia coli 562 -11533976 7500886459 nikc (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:30444) (re:31277) (di:direct) ECOUW76 U00039 g912461 Escherichia coli 562 -11533976 233480 nikc transport of nickel:membrane protein (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 313 of 400 of the completegenome.) (nt:o277) (le:7496) (re:8329) (di:direct) AE000423 AE000423 g1789889 Escherichia coli 562 -11533976 86009 nikc (de:nickel transport system permease protein nikc) (db:swissprot) NIKC\_ECOLI P33592 ESCHERICHIA COLI 562 -11533976

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838815	9383	31539	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838819	9384	31540	720	239

Description

5000691230 nikd (gtcfc:12.5:12.6) (keggfc:11.1) (rileyfc:4.1.2)  
(db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations  
(na\_k\_ca\_nh4\_etc\_):cell processes-transporters of unknown specificity  
(abc\_atpases\_drug) or metals) b3479 b3479 Escherichia coli 562 -11533977  
164153 nikd nikd protein (cl:atp-binding cassette homology) (db:pir2.dat)  
S47698 S47698 Escherichia coli 562 -11533977 7500960398 nikd  
(sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda)  
(db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.)  
(le:31277) (re:32041) (di:direct) ECOUW76 U00039 g466615 Escherichia coli  
562 -11533977 236714 nikd atp-binding protein of nickel transport system  
(fn:transport; transport of small molecules:) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 313 of 400 of the completegenome.)  
(nt:o254) (le:8329) (re:9093) (di:direct) AE000423 AE000423 g1789890  
Escherichia coli 562 -11533977 6500730119 nikd (gtcfc:12.5:12.6)  
(keggfc:11.1) (rileyfc:4.1.2) (db:gtc-escherichia coli) b3479 b3479  
Escherichia coli 562 -11533977

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838839	9385	31541	1272	423

Description

6500730120 nike:b3480 nickel transport atp-binding protein nike (gtcfc:12.6)  
(keggfc:11.1) (rileyfc:4.1.2) (db:gtc-escherichia coli) b3480 b3480  
Escherichia coli 562 -11533978 7000689375 nike nike protein (cl:unassigned  
atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat)  
C65145 C65145 Escherichia coli 562 -11533978 7500955268 nike  
(sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda)  
(db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.)  
(le:32038) (re:32844) (di:direct) ECOUW76 U00039 g466616 Escherichia coli  
562 -11533978 236715 nike atp-binding protein of nickel transport system  
(fn:transport; transport of small molecules:) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 313 of 400 of the completegenome.)  
(nt:o268) (le:9090) (re:9896) (di:direct) AE000423 AE000423 g1789891  
Escherichia coli 562 -11533978 5000691231 (de:(ecoli\_3398) (pn:transport of  
nickel, atp-binding protein) (gn:nike) (gtcfc:12.5) (ec:) (nike\_ecoli)  
(keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_3398  
ECOLI\_3398 Escherichia coli 562 10124038

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838842	9386	31542	294	97

Description

5000691232 kup (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2)  
(db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations  
(na\_k\_ca\_nh4\_etc\_)) b3747 b3747 Escherichia coli 562 -11533979 7000691854  
kup kup protein (db:pir2.dat) D65178 D65178 Escherichia coli 562 -11533979  
7500960372 o519 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda  
clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5  
minutes.) (le:120705) (re:122264) (di:direct) ECOUW82 L10328 g290597  
Escherichia coli 562 -11533979 236985 kup low affinity potassium transport  
system (fn:transport; transport of small molecules:) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 341 of 400 of the completegenome.)  
(nt:o519; 100 pct identical (0 gaps) to 505 residues of) (le:8412) (re:9971)  
(di:direct) AE000451 AE000451 g1790187 Escherichia coli 562 -11533979  
6500730121 kup (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2)  
(db:gtc-escherichia coli) b3747 b3747 Escherichia coli 562 -11533979

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838847	9387	31543	297	98

Description

6500730122 cora:b3816 magnesium and cobalt transport protein cora  
(gtcfc:12.6) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) b3816  
b3816 Escherichia coli 562 -11533980 65477 cora (de:magnesium and cobalt  
transport protein cora) (db:swissprot) CORA\_ECOLI P27841 ESCHERICHIA COLI  
562 -11533980 164019 cora magnesium transport protein cora:magnesium  
transport system i (db:pir2.dat) B47157 B47157 Escherichia coli 562  
-11533980 7500879121 cora (fn:mg-transport system i) (sr:escherichia coli  
(individual\_isolate pbd434, strain k-12) dna) (db:genpept-bct1) (de:e. coli  
dna helicase ii (uvrd) gene, 3' end, mg-transport system i(cora) gene,  
complete cds, chloamphenicol sensitive (rard) gene, comple... ECOCORAX L02122  
g145577 Escherichia coli 562 -11533980 234034 cora mg2+ transport:system i  
(fn:transport; transport of small molecules:) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 347 of 400 of the completegenome.)  
(nt:o316; 99 pct identical amino acid sequence and) (le:7057) (re:8007)  
(di:direct) AE000457 AE000457 g2367297 Escherichia coli 562 -11533980

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838850	9388	31544	198	65

Description

6500730123 trkh (gtcfc:12.5) (keggfc:14.2) (rileyfc:4.1.2)  
(db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations  
(na\_k\_ca\_nh4\_etc\_)) b3849 b3849 Escherichia coli 562 -11533981 7000691926  
trkh trkh protein (cl:potassium uptake protein trkg) (db:pir2.dat) (mp:86  
min) B65190 B65190 Escherichia coli 562 -11533981 7500960474 trkh potassium  
uptake:requires trke (fn:transport; transport of small molecules:)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 350 of 400 of the  
completegenome.) (nt:o432; this 431 aa orf is 100 pct identical to)  
(le:5886) (re:7184) (di:direct) AE000460 AE000460 g2367317 Escherichia coli  
562 -11533981

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838878	9389	31545	336	111

Description

6500730124 fece:b4287 ironiii dicitrate transport atp-binding protein fece  
(gtcfc:12.6) (keggfc:11.1) (rileyfc:4.1.2) (db:gtc-escherichia coli) b4287  
b4287 Escherichia coli 562 -11533982 71279 fece (de:iron(iii) dicitrate  
transport atp-binding protein fece) (db:swissprot) FECE\_ECOLI P15031  
ESCHERICHIA COLI 562 -11533982 130715 fece membrane-bound iron iii  
dicitrate transport protein (cl:inner membrane protein malk:atp-binding  
cassette homology) (db:pir1.dat) (mp:7 min) QRECM3 JS0115 Escherichia coli  
562 -11533982 237492 fece (sr:escherichia coli (strain k-12) dna)  
(db:genpept-bct1) (de:k-12 feca gene, 3'end; fecb,c,d,and e genes, complete  
cds's.) (le:3032) (re:3799) (di:direct) ECOFECBCDE M26397 g145928  
Escherichia coli 562 -11533982 7500881390 fece (db:genpept-bct1)  
(de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.)  
(le:201524) (re:202291) (di:complement) ECOUW93 U14003 g537128 Escherichia  
coli 562 -11533982 234322 fece atp-binding component of citrate-dependent  
(fn:transport; transport of small molecules:) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 389 of 400 of the completegenome.)  
(nt:f255; 100 pct identical amino acid sequence and) (le:4186) (re:4953)  
(di:complement) AE000499 AE000499 g1790739 Escherichia coli 562 -11533982  
5000691235 (de:(ecoli\_4170) (pn:citrate-dependent iron:iii transport  
protein, membrane-bound) (gn:fece) (gtcfc:12.5) (ec:) (fece\_ecoli)  
(keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_4170  
ECOLI\_4170 Escherichia coli 562 10013852

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838881	9390	31546	495	164

Description

GTC ORF with score 98 to: (or:Anolis pulchellus) (fn:precursor of yolk proteins, serum transport) (db:genpept-vrt) (de:anolis pulchellus vitellogenin mrna, partial cds.) (nt:apvtg5; similar to chicken and xenopus phosvitin) (le:<1) (re:546) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838885	9391	31547	1209	402

Description

6500730125 fecd:b4288 ironiii dicitrate transport system permease protein fecd (gtcfc:12.6) (keggfc:11.1) (rileyfc:4.1.2) (db:gtc-escherichia coli) b4288 b4288 Escherichia coli 562 -11533983 71278 fecd (de:iron(iii) dicitrate transport system permease protein fecd) (db:swissprot) FECD\_ECOLI P15029 ESCHERICHIA COLI 562 -11533983 153018 fecd iron iii dicitrate transport protein 2:cytosolic:citrate-dependent iron transport protein fecd (cl:vitamin b12 transport protein btuc) (db:pirl.dat) (mp:7 min) QRECD2 S56513 Escherichia coli 562 -11533983 7500881389 fecd (fn:citrate-dependent iron transport; membrane) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 18394) (le:202292) (re:203248) (di:complement) ECOUW93 U14003 g537129 Escherichia coli 562 -11533983 237493 fecd citrate-dependent iron transport:membrane-bound (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 389 of 400 of the completegenome.) (nt:f318; 100 pct identical to fecd\_ecoli sw: p15029;) (le:4954) (re:5910) (di:complement) AE000499 AE000499 g1790740 Escherichia coli 562 -11533983 5000691236 (de:(ecoli\_4171) (pn:citrate-dependent iron transport, membrane-bound protein) (gn:fecd) (gtcfc:12.5) (ec:) (fecd\_ecoli) (keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_4171 ECOLI\_4171 Escherichia coli 562 10013851

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838886	9392	31548	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838910	9393	31549	558	185

Description

GTC ORF with score 112 to: (fn:fk506- and rapamycin-binding protein)  
(db:genpept-pln1) (de:saccharomyces cerevisiae (clone pbyng1) proline  
rotamase (fpr3)gene, complete cds.) (nt:localized to nucleolus) (le:279)  
(re:1520) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838914	9394	31550	762	253

Description

6500730126 fecc:b4289 ironiii dicitrate transport system permease protein  
fecc (gtcfc:12.6) (keggfc:11.1) (rileyfc:4.1.2) (db:gtc-escherichia coli)  
b4289 b4289 Escherichia coli 562 -11533984 71277 fecc (de:iron(iii)  
dicitrate transport system permease protein fecc) (db:swissprot) FECC\_ECOLI  
P15030 ESCHERICHIA COLI 562 -11533984 153019 fecc iron iii dicitrate  
transport protein 1:cytosolic (cl:vitamin b12 transport protein btuc)  
(db:pir1.dat) (mp:7 min) QRECD1 S56514 Escherichia coli 562 -11533984  
7500881388 fecc (db:genpept-bct1) (de:escherichia coli k-12 chromosomal  
region from 92.8 to 00.1 minutes.) (le:203245) (re:204243) (di:complement)  
ECOUW93 U14003 g537130 Escherichia coli 562 -11533984 237494 fecc  
citrate-dependent iron iii transport protein (fn:transport; transport of  
small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section  
389 of 400 of the completegenome.) (nt:f332; 100 pct identical amino acid  
sequence and) (le:5907) (re:6905) (di:complement) AE000499 AE000499 g1790741  
Escherichia coli 562 -11533984 5000691237 (de:(ecoli\_4172)  
(pn:citrate-dependent iron:iii transport protein, cytosolic) (gn:fecc)  
(gtcfc:12.5) (ec:) (fecc\_ecoli) (keggfc:11.2) (rileyfc:4.1.2)  
(db:gtc-escherichia coli)) ECOLI\_4172 ECOLI\_4172 Escherichia coli 562  
10013850

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838915	9395	31551	237	78

Description

6500730127 fecb:b4290 iron:iii dicitrate-binding periplasmic protein precursor (gtcfc:12.5:12.6) (keggfc:11.1) (rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na\_k\_ca\_nh4\_etc\_):cell processes-transporters of unknown specificity (abc\_atpases\_drug) or metals) b4290 b4290 Escherichia coli 562 -11533985 153016 fecb citrate-dependent iron transport protein fecb precursor (cl:ferrichrome-iron transport protein fecb) (db:pir1.dat) (mp:7 min) QRECD3 S56515 Escherichia coli 562 -11533985 7500953602 fecb (fn:citrate-dependent iron transport; periplasmic) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 782) (le:204240) (re:205148) (di:complement) ECOUW93 U14003 g537131 Escherichia coli 562 -11533985 237495 fecb citrate-dependent iron transport:periplasmic (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 389 of 400 of the completgenome.) (nt:f302; cg site no. 782) (le:6902) (re:7810) (di:complement) AE000499 AE000499 g1790742 Escherichia coli 562 -11533985 5000691238 (de:(ecoli\_4173) (pn:citrate-dependent iron transport, periplasmic protein) (gn:fech) (gtcfc:12.5) (ec:) (fech\_ecoli) (keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_4173 ECOLI\_4173 Escherichia coli 562 10080736

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838916	9396	31552	438	145

Description

6500730128 feca:b4291 ironiii dicitrate transport protein feca precursor (gtcfc:12.6) (keggfc:11.1) (rileyfc:4.1.2) (db:gtc-escherichia coli) b4291 b4291 Escherichia coli 562 -11533986 71275 feca (de:iron(iii) dicitrate transport protein feca precursor) (db:swissprot) FECA\_ECOLI P13036 ESCHERICHIA COLI 562 -11533986 7000685224 feca iron iii dicitrate transport system outer membrane receptor precursor:iron iii dicitrate transport protein feca (cl:vitamin b12 receptor:tonb-dependent receptor amino-terminal homology:tonb-dependent receptor carboxyl-terminal homology) (db:pir1.dat) (mp:7 min) QRECFA E65242 Escherichia coli 562 -11533986 7500881387 feca outer membrane receptor:citrate-dependent iron (fn:membrane; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 389 of 400 of the completgenome.) (nt:f774; 99 pct identical amino acid sequence and) (le:7849) (re:10173) (di:complement) AE000499 AE000499 g1790743 Escherichia coli 562 -11533986 5000691239 (de:(ecoli\_4174) (pn:outer membrane receptor; citrate-dependent iron transport, outer membrane receptor) (gn:feca) (gtcfc:12.5) (ec:) (feca\_ecoli) (keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_4174 ECOLI\_4174 Escherichia coli 562 10013848



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838920	9397	31553	282	93

Description

6500730129 fecr:b4292 fecr protein (gtcfc:12.5) (keggfc:14.2)  
(rileyfc:4.1.2) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of  
cations (na\_k\_ca\_nh4\_etc\_)) b4292 b4292 Escherichia coli 562 -11533987  
71282 fecr (de:fece protein) (db:swissprot) FECE\_ECOLI P23485 ESCHERICHIA  
COLI 562 -11533987 163024 fecr fecr protein (db:pir2.dat) (mp:93 min)  
B37804 B37804 Escherichia coli 562 -11533987 237497 fecr (sr:e.coli (k-12)  
dna) (db:genpept-bct1) (de:e.coli feci and fecr genes, complete cds, and  
feca gene, 5' end.) (le:1751) (re:2704) (di:direct) ECOFECIR M63115 g145931  
Escherichia coli 562 -11533987 7500881393 fecr (db:genpept-bct1)  
(de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.)  
(le:207598) (re:208551) (di:complement) ECOUW93 U14003 g537133 Escherichia  
coli 562 -11533987 234324 fecr regulator for fec operon:periplasmic  
(fn:regulator; transport of small molecules:) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 390 of 400 of the completegenome.)  
(nt:f317; 100 pct identical amino acid sequence and) (le:74) (re:1027)  
(di:complement) AE000500 AE000500 g1790745 Escherichia coli 562 -11533987  
5000691240 (de:(ecoli\_4175) (pn:regulator for fec operon, periplasmic)  
(gn:fece) (gtcfc:12.5) (ec:) (fece\_ecoli) (keggfc:11.2) (rileyfc:4.1.2)  
(db:gtc-escherichia coli)) ECOLI\_4175 ECOLI\_4175 Escherichia coli 562  
10013855

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838922	9398	31554	810	269

#### Description

6500730130 feci:b4293 probable rna polymerase sigma factor feci (gtcfc:10.2) (keggfc:14.2) (rileyfc:4.1.2) (db:gtc-escherichia coli) b4293 b4293  
 Escherichia coli 562 -11533988 71281 feci (de:probable rna polymerase sigma factor feci) (db:swissprot) FECI\_ECOLI P23484 ESCHERICHIA COLI 562 -11533988 164403 feci transcription activator feci (db:pir2.dat) (mp:93 min) JV0111 JV0111 Escherichia coli 562 -11533988 237498 feci (sr:e.coli (k-12) dna) (db:genpept-bct1) (de:e.coli feci and fecr genes, complete cds, and fecA gene, 5' end.) (le:1233) (re:1754) (di:direct) ECOFECIR M63115 g145930 Escherichia coli 562 -11533988 7500881392 feci (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:208548) (re:209069) (di:complement) ECOUW93 U14003 g537134 Escherichia coli 562 -11533988 234323 feci probable rna polymerase sigma factor (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 390 of 400 of the completegenome.) (nt:f173; 100 pct identical amino acid sequence and) (le:1024) (re:1545) (di:complement) AE000500 AE000500 g1790746 Escherichia coli 562 -11533988 5000691241 (de:(ecoli\_4176) (pn:regulator for fec operon, membrane location) (gn:feci) (gtcfc:12.5) (ec:) (feci\_ecoli) (keggfc:11.2) (rileyfc:4.1.2) (db:gtc-escherichia coli)) ECOLI\_4176 ECOLI\_4176 Escherichia coli 562 10013854

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838931	9399	31555	420	139

#### Description

6500730131 yabj:b0066 hypothetical abc transporter in arac-tbpa intergenic region:hypothetical abc transporter atp-binding protein in arac-tbpa intergenic region:orf100 (gtcfc:12.6) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0066 b0066 Escherichia coli 562 -11533989 109549 yabj (de:hypothetical abc transporter atp-binding protein yabj) (db:swissprot) YABJ\_ECOLI P31548 ESCHERICHIA COLI 562 -11533989 7000687134 yabj probable abc-type transport protein (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) B64728 B64728 Escherichia coli 562 -11533989 7500896004 yabj putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 7 of 400 of the completegenome.) (nt:f232; 99 pct identical to yabj\_ecoli sw: p31548) (le:2042) (re:2740) (di:complement) AE000117 AE000117 g1786253 Escherichia coli 562 -11533989 5000691363 (de:(ecoli\_66) (pn:hypothetical abc transporter atp-binding protein in arac-tbpa intergenic region:orf100) (gn:yabj) (gtcfc:13.7:14.1) (ec:) (yabj\_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_66 ECOLI\_66 Escherichia coli 562 10122640

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838947	9400	31556	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838949	9401	31557	591	196

Description

6500730132 yabk:b0067 hypothetical 59.6 kd protein in arac-tbpa intergenic region:orf101 (gtcfc:12.6:14.1) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0067 b0067 Escherichia coli 562 -11533990 109552 yabk (de:hypothetical 59.6 kd protein in arac-tbpa intergenic region (orf101)) (db:swissprot) YABK\_ECOLI P31549 ESCHERICHIA COLI 562 -11533990 7000687136 yabk probable membrane protein yabk (cl:sfub protein) (db:pir2.dat) C64728 C64728 Escherichia coli 562 -11533990 7500896006 yabk putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 7 of 400 of the completegenome.) (nt:f536; 99 pct identical to yabk\_ecoli sw: p31549) (le:2724) (re:4334) (di:complement) AE000117 AE000117 g1786254 Escherichia coli 562 -11533990 5000691364 (de:(ecoli\_67) (pn:hypothetical 59) (gn:yabk) (gtcfc:13.7:14.1) (ec:) (yabk\_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_67 ECOLI\_67 Escherichia coli 562 10122641

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838950	9402	31558	300	99

Description

6500730133 tbpa:b0068 thiamine-binding periplasmic protein precursor:thiamin-binding periplasmic protein precursor (gtcfc:12.6:14.3) (keggfc:11.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0068 b0068 Escherichia coli 562 -11533991 100799 tbpa (de:thiamin-binding periplasmic protein precursor) (db:swissprot) TBPA\_ECOLI P31550 ESCHERICHIA COLI 562 -11533991 7000686770 tbpa thiamine-binding periplasmic protein precursor (db:pir2.dat) D64728 D64728 Escherichia coli 562 -11533991 7500892805 tbpa thiamin-binding periplasmic protein (fn:putative transport; transport of small) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 7 of 400 of the completegenome.) (nt:f327; 100 pct identical to 315 residues) (le:4310) (re:5293) (di:complement) AE000117 AE000117 g1786255 Escherichia coli 562 -11533991 5000691365 (de:(ecoli\_68) (pn:thiamin-binding periplasmic protein precursor) (gn:tbpa) (gtcfc:13.7:14.1) (ec:) (tbpa\_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_68 ECOLI\_68 Escherichia coli 562 10122642

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501838973	9403	31559	738	245

Description

6500730134 glt1:b0652 glutamate/aspartate transport atp-binding protein glt1 (gtcfc:12.1:5.1) (keggfc:11.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0652 b0652 Escherichia coli 562 -11533992 74126 glt1 (de:glutamate/aspartate transport atp-binding protein glt1) (db:swissprot) GLTL\_ECOLI P41076 ESCHERICHIA COLI 562 -11533992 7000685427 glt1 glutamate/aspartate transport protein glt1 (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) B64800 B64800 Escherichia coli 562 -11533992 223129 glt1 glutamate/aspartate transport atp-binding (sr:escherichia coli(strain:k12) dna, clone:kohara clone #170) (db:genpept-bct1) (de:escherichia coli genomic dna. (14.6 - 14.9 min).) (le:7014) (re:7739) (di:complement) D90705 D90705 gl651271 Escherichia coli 562 -11533992 240166 glt1 glt1 (db:genpept-bct1) (de:escherichia coli k12-bk9mdg glutamate-aspartate bindingprotein-dependent transport system membrane bound components gltj(gltj), gltk (gltk), and glt1 (glt1) genes, complete cds.) (nt:membrane bound component of a glutamate-asparta... ECU10981 U10981 g624632 Escherichia coli 562 -11533992 7500882559 glt1 glutamate/aspartate transport atp-binding (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (le:125160) (re:125885) (di:complement) ECU82598 U82598 g1778570 Escherichia coli 562 -11533992 238596 glt1 atp-binding protein of glutamate/aspartate (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 59 of 400 of the completegenome.) (nt:f241; 100 pct identical to glt1\_ecoli sw: p41076) (le:9660) (re:10385) (di:complement) AE000169 AE000169 g1786872 Escherichia coli 562 -11533992 5000691726 glt1 glutamate/aspartate transport atp-binding (sr:escherichia coli(strain:k12) dna, clone:kohara clone #170) (db:genpept) (de:escherichia coli genomic dna. (14.6 - 14.9 min).) (nt:orf\_id:o170#6; similar to swissprot accession) (le:7014) (re:7739) (di:complement) D90705 D90705 gl651271 Escherichia coli 562 -11533992

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501838974	9404	31560	936	311

# Description

6500730135 gltk:b0653 glutamate/aspartate transport system permease protein gltk (gtcfc:12.1:5.1) (keggfc:11.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0653 b0653 Escherichia coli 562 -11533993 74125 gltk (de:glutamate/aspartate transport system permease protein gltk) (db:swissprot) GLTK\_ECOLI P41075 ESCHERICHIA COLI 562 -11533993 7000685426 gltk glutamate/aspartate transport protein gltk:glutamate/aspartate transport system permease gltk (cl:histidine permease protein m) (db:pir2.dat) C64800 C64800 Escherichia coli 562 -11533993 223130 gltk glutamate/aspartate transport system permease (sr:escherichia coli(strain:k12) dna, clone:kohara clone #170) (db:genpept-bct1) (de:escherichia coli genomic dna. (14.6 - 14.9 min).) (le:7739) (re:8413) (di:complement) D90705 D90705 g1651272 Escherichia coli 562 -11533993 240167 gltk gltk (db:genpept-bct1) (de:escherichia coli k12-bk9mdg glutamate-aspartate bindingprotein-dependent transport system membrane bound components gltj(gltj), gltk(gltk), and glt1(glt1) genes, complete cds.) (nt:membrane bound component of a glutamate-asparta... ECU10981 U10981 g624631 Escherichia coli 562 -11533993 7500882558 gltk glutamate/aspartate transport system permease (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (le:125885) (re:126559) (di:complement) ECU82598 U82598 g1778571 Escherichia coli 562 -11533993 238595 gltk glutamate/aspartate transport system permease (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 59 of 400 of the completegenome.) (nt:f224; 100 pct identical to gltk\_ecoli sw: p41075) (le:10385) (re:11059) (di:complement) AE000169 AE000169 g1786873 Escherichia coli 562 -11533993 5000691727 gltk glutamate/aspartate transport system permease (sr:escherichia coli(strain:k12) dna, clone:kohara clone #170) (db:genpept) (de:escherichia coli genomic dna. (14.6 - 14.9 min).) (nt:orf\_id:o170#7; similar to swissprot accession) (le:7739) (re:8413) (di:complement) D90705 D90705 g1651272 Escherichia coli 562 -11533993

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501839007	9405	31561	348	115

# Description

6500730136 gltj:b0654 glutamate/aspartate transport system permease protein gltj (gtcfc:12.1:5.1) (keggfc:11.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0654 b0654 Escherichia coli 562 -11533994 74124 gltj (de:glutamate/aspartate transport system permease protein gltj) (db:swissprot) GLTJ\_ECOLI P41074 ESCHERICHIA COLI 562 -11533994 7000685425 gltj glutamate/aspartate transport protein gltj:glutamate/aspartate transport system permease gltj (cl:histidine permease protein m) (db:pir2.dat) D64800 D64800 Escherichia coli 562 -11533994 223131 gltj glutamate/aspartate transport system permease (sr:escherichia coli(strain:k12) dna, clone:kohara clone #170) (db:genpept-bct1) (de:escherichia coli genomic dna. (14.6 - 14.9 min).) (le:8413) (re:9153) (di:complement) D90705 D90705 g1651273 Escherichia coli 562 -11533994 240168 gltj gltj (db:genpept-bct1) (de:escherichia coli k12-bk9mdg glutamate-aspartate bindingprotein-dependent transport system membrane bound components gltj(gltj), gltk (gltk), and glt1 (glt1) genes, complete cds.) (nt:membrane bound component of a glutamate-asparta... ECU10981 U10981 g624630 Escherichia coli 562 -11533994 7500882557 gltj glutamate/aspartate transport system permease (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (le:126559) (re:127299) (di:complement) ECU82598 U82598 g1778572 Escherichia coli 562 -11533994 238594 gltj glutamate/aspartate transport system permease (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 59 of 400 of the completegenome.) (nt:f246; 99 pct identical to gltj\_ecoli sw: p41074) (le:11059) (re:11799) (di:complement) AE000169 AE000169 g1786874 Escherichia coli 562 -11533994 5000691728 gltj glutamate/aspartate transport system permease (sr:escherichia coli(strain:k12) dna, clone:kohara clone #170) (db:genpept) (de:escherichia coli genomic dna. (14.6 - 14.9 min).) (nt:orf\_id:o170#8; similar to swissprot accession) (le:8413) (re:9153) (di:complement) D90705 D90705 g1651273 Escherichia coli 562 -11533994

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501839020	9406	31562	669	223

#### Description

6500730137 sapd:b1291 peptide transport system atp-binding protein sapd (gtcfc:12.1) (keggfc:11.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1291 b1291 Escherichia coli 562 -11533995 97925 sapd (de:peptide transport system atp-binding protein sapd) (db:swissprot) SAPD\_ECOLI P36635 ESCHERICHIA COLI 562 -11533995 7000686559 sapd peptide transport system atp-binding protein sapd (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) F64877 F64877 Escherichia coli 562 -11533995 223518 sapd peptide transport system atp-binding protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #255(28.8-29.2 min.)) (nt:orf\_id:o255#19; similar to (swissprot accession) (le:14904) (re:15896) (di:complement) D90766 D90766 g1742104 Escherichia coli 562 -11533995 223526 sapd peptide transport system atp-binding protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #256(29.0-29.4 min.)) (nt:orf\_id:o255#19; similar to (swissprot accession) (le:8299) (re:9291) (di:complement) D90767 D90767 g1742113 Escherichia coli 562 -11533995 300324 sapd peptide transport system atp-binding protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #257(29.1-29.6 min.)) (nt:orf\_id:o255#19; similar to (swissprot accession) (le:8) (re:1000) (di:complement) D90768 D90768 g1742122 Escherichia coli 562 -11533995 300321 sapd sapd protein (db:genpept-bct1) (de:e.coli sapabcdf operon.) (le:3716) (re:4708) (di:direct) ECSAPABCD X97282 g1279403 Escherichia coli 562 -11533995 238202 sapd putative atp-binding protein of peptide (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 117 of 400 of the completegenome.) (nt:f330; 100 pct identical to 30 aa fragment) (le:3720) (re:4712) (di:complement) AE000227 AE000227 g1787548 Escherichia coli 562 -11533995 223534 sapd peptide transport system atp-binding protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #257(29.1-29.6 min.)) (nt:orf\_id:o255#19; similar to (swissprot accession) (le:8) (re:1000) (di:complement) D90768 D90768 g1742122 Escherichia coli 562 -11533995 5000692108 (de:(ecoli\_1251) (pn:peptide transport system atp-binding protein sapd:fragment) (gn:sapd) (gtcfc:13.7:14.1) (ec:) (sapd\_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_1251 ECOLI\_1251 Escherichia coli 562 10119504

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501839039	9407	31563	324	107

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839048	9408	31564	864	287

Description

GTC ORF with score 154 to: (sr:thale cress) (db:genpept-pln1) (de:sequence of bac f7g19 from arabidopsis thaliana chromosome 1,complete sequence.)  
(nt:contains similarity to bos beta-mannosidase)  
(le:43900:44515:44824:44926) ...

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839056	9409	31565	276	91

Description

Hypothetical protein

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839061	9410	31566	597	198

#### Description

6500730138 sapc:b1292 peptide transport system permease protein sapc (gtcfc:12.1) (keggfc:11.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1292 b1292 Escherichia coli 562 -11533996 121664 sapc (de:peptide transport system permease protein sapc) (db:swissprot) SAPC\_ECOLI Q47624 ESCHERICHIA COLI 562 -11533996 7000686558 sapc peptide transport system permease protein sapc (cl:oligopeptide permease protein oppb) (db:pir2.dat) G64877 G64877 Escherichia coli 562 -11533996 223519 peptide transport system permease protein sapc. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #255(28.8-29.2 min.)) (nt:orf\_id:o255#20; similar to (swissprot accession) (le:15896) (re:16786) (di:complement) D90766 D90766 g1742105 Escherichia coli 562 -11533996 223527 peptide transport system permease protein sapc. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #256(29.0-29.4 min.)) (nt:orf\_id:o255#20; similar to (swissprot accession) (le:9291) (re:10181) (di:complement) D90767 D90767 g1742114 Escherichia coli 562 -11533996 300325 peptide transport system permease protein sapc. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #257(29.1-29.6 min.)) (nt:orf\_id:o255#20; similar to (swissprot accession) (le:1000) (re:1890) (di:complement) D90768 D90768 g1742123 Escherichia coli 562 -11533996 300322 sapc sapc protein (db:genpept-bct1) (de:e.coli sapabcdf operon.) (le:2826) (re:3716) (di:direct) ECSAPABCD X97282 g1279402 Escherichia coli 562 -11533996 238201 sapc homolog of salmonella peptide transport permease (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 117 of 400 of the completegenome.) (nt:f296; 100 pct identical to gb:) (le:4712) (re:5602) (di:complement) AE000227 AE000227 g1787549 Escherichia coli 562 -11533996 223535 peptide transport system permease protein sapc. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #257(29.1-29.6 min.)) (nt:orf\_id:o255#20; similar to (swissprot accession) (le:1000) (re:1890) (di:complement) D90768 D90768 g1742123 Escherichia coli 562 -11533996 5000692109 (de:(ecoli\_1252) (pn:peptide transport system permease protein sapc) (gn:sapc) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_1252 ECOLI\_1252 Escherichia coli 562 10065106

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839066	9411	31567	192	63

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839068	9412	31568	561	186

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839094	9413	31569	438	145

Description

6500730139 sapb:b1293 peptide transport system permease protein sapb (gtcfc:12.1) (keggfc:11.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1293 b1293 Escherichia coli 562 -11533997 121663 sapb (de:peptide transport system permease protein sapb) (db:swissprot) SAPB\_ECOLI Q47623 ESCHERICHIA COLI 562 -11533997 7000686557 sapb peptide transport system permease protein sapb (cl:transmembrane protein dppb) (db:pir2.dat) H64877 H64877 Escherichia coli 562 -11533997 223528 peptide transport system permease protein sapb. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #256(29.0-29.4 min.)) (nt:orf\_id:o257#1; similar to (swissprot accession) (le:10168) (re:11133) (di:complement) D90767 D90767 g1742115 Escherichia coli 562 -11533997 223536 peptide transport system permease protein sapb. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #257(29.1-29.6 min.)) (nt:orf\_id:o257#1; similar to (swissprot accession) (le:1877) (re:2842) (di:complement) D90768 D90768 g1742124 Escherichia coli 562 -11533997 300326 sapb sapb protein (db:genpept-bct1) (de:e.coli sapabcdf operon.) (le:1874) (re:2839) (di:direct) ECSAPABCD X97282 g1279401 Escherichia coli 562 -11533997 238200 sapb homolog of salmonella peptide transport permease (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 117 of 400 of the completegenome.) (nt:f321; 100 pct identical to gb:) (le:5589) (re:6554) (di:complement) AE000227 AE000227 g1787550 Escherichia coli 562 -11533997 5000692110 (de:(ecoli\_1253) (pn:peptide transport system permease protein sapb) (gn:sapb) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_1253 ECOLI\_1253 Escherichia coli 562 10065105

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839100	9414	31570	441	146

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839105	9415	31571	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839118	9416	31572	375	124

Description

6500730140 sapa:b1294 peptide transport periplasmic protein sapa precursor (gtcfc:12.1) (keggfc:11.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1294 b1294 Escherichia coli 562 -11533998 121357 sapa (de:peptide transport periplasmic protein sapa precursor) (db:swissprot) SAPA\_ECOLI\_Q47622 ESCHERICHIA COLI 562 -11533998 7000686555 sapa peptide transport periplasmic protein sapa precursor (cl:dipeptide transport protein) (db:pir2.dat) A64878 A64878 Escherichia coli 562 -11533998 7500891308 sapa sapa protein (db:genpept-bct1) (de:e.coli sapabcdf operon.) (le:234) (re:1877) (di:direct) ECSAPABCD X97282 g1279400 Escherichia coli 562 -11533998 238199 sapa homolog of salmonella peptide transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 117 of 400 of the completegenome.) (nt:f547; 100 pct identical to gb:) (le:6551) (re:8194) (di:complement) AE000227 AE000227 g1787551 Escherichia coli 562 -11533998 5000692111 (de:(ecoli\_1254) (pn:peptide transport periplasmic protein sapa precursor) (gn:sapa) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_1254 ECOLI\_1254 Escherichia coli 562 10064674

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839119	9417	31573	465	154

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839128	9418	31574	324	107

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501839139	9419	31575	507	168

# Description

6500730141 btud:b1709 vitamin b12 transport atp-binding protein btud (gtcfc:12.6:9.9) (keggfc:11.1) (rileyfc:4.1.6) (db:gtc-escherichia coli) (gtcfc:cell processes-transporters of unknown specificity (abc\_atpases\_drug) or metals:metabolism of cofactors and vitamins-cobalamin (vitamin b12)) b1709 b1709 Escherichia coli 562 -11533999 62075 btud (de:vitamin b12 transport atp-binding protein btud) (db:swissprot) BTUD\_ECOLI P06611 ESCHERICHIA COLI 562 -11533999 130713 btud vitamin b12 transport atp-binding protein btud (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir1.dat) (mp:37 min) QRECB D24498 Escherichia coli 562 -11533999 224156 btud vitamin b12 transport protein btud (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #322(38.4-38.8 min.)) (nt:orf\_id:o322#10; similar to (pir accession number) (le:9554) (re:10303) (di:complement) D90813 D90813 g1742789 Escherichia coli 562 -11533999 224168 btud vitamin b12 transport protein btud (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #323(38.6-39.0 min.)) (nt:orf\_id:o322#10; similar to (pir accession number) (le:2394) (re:3143) (di:complement) D90814 D90814 g1742802 Escherichia coli 562 -11533999 300825 btud peripheral membrane component (sr:e.coli (k12) dna, clone plcd25) (db:genpept-bct1) (de:e.coli btuced genes encoding vitamin b12 transport mechanisms,complete cds, orf17 encoding a protein of unknown function, andhima gene encoding integration host factor (ihf) alpha-subunit,partia... ECOBTUCED M14031 g145445 Escherichia coli 562 -11533999 233925 btud atp-binding component of vitamin b12 transport (fn:transport; transport of small molecules: other) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 156 of 400 of the completegenome.) (nt:f249; 100 pct identical to btud\_ecoli sw: p06611;) (le:3292) (re:4041) (di:complement) AE000266 AE000266 g1788002 Escherichia coli 562 -11533999 5000691250 (de:(ecoli\_1666) (pn:vitamin b12 transport, membrane-associated protein) (gn:btud) (gtcfc:12.6) (ec:) (btud\_ecoli) (keggfc:11.2) (rileyfc:4.1.6) (db:gtc-escherichia coli)) ECOLI\_1666 ECOLI\_1666 Escherichia coli 562 10004775

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839145	9420	31576	831	277

Description

6500730142 btue:b1710 vitamin b12 transport periplasmic protein btue (gtcfc:12.6:9.9) (keggfc:11.1) (rileyfc:4.1.6) (db:gtc-escherichia coli) (gtcfc:cell processes-transporters of unknown specificity (abc\_atpases\_drug) or metals:metabolism of cofactors and vitamins-cobalamin (vitamin b12)) b1710 b1710 Escherichia coli 562 -11534000 62076 btue (de:vitamin b12 transport periplasmic protein btue) (db:swissprot) BTUE\_ECOLI P06610 ESCHERICHIA COLI 562 -11534000 7000684734 btue vitamin b12 transport periplasmic protein btue (cl:glutathione peroxidase) (db:pir1.dat) (mp:37 min) QRECBF F64929 Escherichia coli 562 -11534000 224157 btue vitamin b12 transport periplasmic protein btue. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #322(38.4-38.8 min.).) (nt:orf\_id:o322#11; similar to (swissprot accession) (le:10303) (re:10854) (di:complement) D90813 D90813 g1742790 Escherichia coli 562 -11534000 224169 btue vitamin b12 transport periplasmic protein btue. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #323(38.6-39.0 min.).) (nt:orf\_id:o322#11; similar to (swissprot accession) (le:3143) (re:3694) (di:complement) D90814 D90814 g1742803 Escherichia coli 562 -11534000 300826 btue periplasmic protein (sr:e.coli (k12) dna, clone plcd25) (db:genpept-bct1) (de:e.coli btuced genes encoding vitamin b12 transport mechanisms,complete cds, orf17 encoding a protein of unknown function, andhima gene encoding integration host factor (ihf) alpha-subunit,partia... ECOBTUCED M14031 g145444 Escherichia coli 562 -11534000 233924 btue vitamin b12 transport (fn:transport; transport of small molecules: other) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 156 of 400 of the completegenome.) (nt:f183; 100 pct identical to btue\_ecoli sw: p06610;) (le:4041) (re:4592) (di:complement) AE000266 AE000266 g1788003 Escherichia coli 562 -11534000 5000691251 (de:(ecoli\_1667) (pn:vitamin b12 transport) (gn:btue) (gtcfc:12.6) (ec:) (btue\_ecoli) (keggfc:11.2) (rileyfc:4.1.6) (db:gtc-escherichia coli)) ECOLI\_1667 ECOLI\_1667 Escherichia coli 562 10004776

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839150	9421	31577	420	139

Description

6500730143 btuc:b1711 vitamin b12 transport system permease protein btuc (gtcfc:12.6:9.9) (keggfc:11.1) (rileyfc:4.1.6) (db:gtc-escherichia coli) (gtcfc:cell processes-transporters of unknown specificity (abc\_atpases\_drug) or metals:metabolism of cofactors and vitamins-cobalamin (vitamin b12)) b1711 b1711 Escherichia coli 562 -11534001 62074 btuc (de:vitamin b12 transport system permease protein btuc) (db:swissprot) BTUC\_ECOLI P06609 ESCHERICHIA COLI 562 -11534001 7000684733 btuc vitamin b12 transport protein btuc (cl:vitamin b12 transport protein btuc) (db:pir1.dat) (mp:37 min) QRECBC G64929 Escherichia coli 562 -11534001 224158 btuc vitamin b12 transport system permease protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #322(38.4-38.8 min.)) (nt:orf\_id:o322#12; similar to (swissprot accession) (le:10917) (re:11897) (di:complement) D90813 D90813 g1742791 Escherichia coli 562 -11534001 224170 btuc vitamin b12 transport system permease protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #323(38.6-39.0 min.)) (nt:orf\_id:o322#12; similar to (swissprot accession) (le:3757) (re:4737) (di:complement) D90814 D90814 g1742804 Escherichia coli 562 -11534001 300827 btuc vitamin b12 transport permease protein (fn:transport; transport of small molecules: other) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 156 of 400 of the completegenome.) (nt:f326; 99 pct identical to btuc\_ecoli sw: p06609; cg) (le:4655) (re:5635) (di:complement) AE000266 AE000266 g1788004 Escherichia coli 562 -11534001 5000691252 (de:(ecoli\_1668) (pn:vitamin b12 transport) (gn:btuc) (gtcfc:12.6) (ec:) (btuc\_ecoli) (keggfc:11.2) (rileyfc:4.1.6) (db:gtc-escherichia coli)) ECOLI\_1668 ECOLI\_1668 Escherichia coli 562 10119785

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839162	9422	31578	279	92

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839172	9423	31579	375	124

Description

6500730144 hisq:b2308 histidine transport system permease protein hisq (gtcfc:12.1:11.1:5.11) (keggfc:11.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2308 b2308 Escherichia coli 562 -11534002 77071 hisq (de:histidine transport system permease protein hisq) (db:swissprot) HISQ\_ECOLI P52094 ESCHERICHIA COLI 562 -11534002 7000685534 hisq histidine transport system permease protein hisq (cl:histidine permease protein m) (db:pir2.dat) B65003 B65003 Escherichia coli 562 -11534002 224841 hisq histidine transport system permease protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #406(52.2-52.5 min.)) (nt:similar to (swissprot accession number p52094)) (le:8807) (re:9493) (di:complement) D90862 D90862 g1799689 Escherichia coli 562 -11534002 7500883338 hisq histidine transport system permease protein (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 209 of 400 of the completegenome.) (nt:f228; 96 pct identical to hisq\_ecoli sw: p52094) (le:10551) (re:11237) (di:complement) AE000319 AE000319 g1788646 Escherichia coli 562 -11534002 5000692841 (de:(ecoli\_2257) (pn:histidine transport system permease protein hisq) (gn:hisq) (gtcfc:13.7:14.1) (ec:) (hisq\_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2257 ECOLI\_2257 Escherichia coli 562 10120105

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839180	9424	31580	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839193	9425	31581	984	327

Description

6500730145 cysu:cyst:b2424 sulfate transport system permease protein cyst (gtcfc:12.4:11.1) (keggfc:11.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of anions (cl\_so4\_po4\_etc\_):cell envelope-membrane proteins--porins--and lipoproteins) b2424 b2424 Escherichia coli 562 -11534003 67710 cysu:cyst (de:sulfate transport system permease protein cyst) (db:swissprot) CYST\_ECOLI P16701 ESCHERICHIA COLI 562 -11534003 130789 cysu:cyst sulfate/thiosulfate transport protein cyst:sulfate transport system permease protein cyst (cl:maltose transport protein malg) (db:pir1.dat) (mp:52 min) QRECST A35402 Escherichia coli 562 -11534003 224986 cyst sulfate transport system permease protein cyst. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #418(54.6-54.9 min.)) (nt:similar to (swissprot accession number p16701)) (le:10047) (re:10880) (di:complement) D90871 D90871 g1799843 Escherichia coli 562 -11534003 224995 cyst sulfate transport system permease protein cyst. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #419(54.7-55.1 min.)) (nt:similar to (swissprot accession number p16701)) (le:4808) (re:5641) (di:complement) D90872 D90872 g1799853 Escherichia coli 562 -11534003 7500879927 cyst (sr:e.coli k12 dna) (db:genpept-bct1) (de:e.coli thiosulfate binding protein (cysp), sulfate permease (cyst,cysw, cysa) and o-acetylserine (thiol)-lyase-b (cysm) genes,complete cds.) (le:1575) (re:2408) (di:direct) ECOCYS M32101 g145659 Escherichia coli 562 -11534003 234093 cysu sulfate:thiosulfate transport system permease t (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 220 of 400 of the completegenome.) (nt:f277; 93 pct identical to cyst\_ecoli sw: p16701;) (le:243) (re:1076) (di:complement) AE000330 AE000330 g1788764 Escherichia coli 562 -11534003 5000692918 (de:(ecoli\_2364) (pn:sulfate, thiosulfate transport system) (gn:cysu) (gtcfc:13.7:14.1) (ec:) (cyst\_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_2364 ECOLI\_2364 Escherichia coli 562 10010308

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839198	9426	31582	201	66

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839213	9427	31583	525	174

Description

6500730146 dppf:dppe:b3540 dipeptide transport atp-binding protein dppf (gtcfc:12.1) (keggfc:11.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3540 b3540 Escherichia coli 562 -11534004 69238 dppf:dppe (de:dipeptide transport atp-binding protein dppf) (db:swissprot) DPPF\_ECOLI P37313 ESCHERICHIA COLI 562 -11534004 162968 dppf:dppe dipeptide transport protein dppf (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) S47762 S47762 Escherichia coli 562 -11534004 7500880599 dppf (fn:transport of dipeptides) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:was dppe) (le:116117) (re:117121) (di:complement) ECOUW76 U00039 g466679 Escherichia coli 562 -11534004 236778 dppf putative atp-binding component of dipeptide (fn:transport; protein, peptide secretion) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 321 of 400 of the completegenome.) (nt:f334; 100 pct identical amino acid sequence and) (le:5620) (re:6624) (di:complement) AE000431 AE000431 g1789962 Escherichia coli 562 -11534004 5000693640 (de:(ecoli\_3461) (pn:dipeptide transport atp-binding protein dppf) (gn:dppf) (gtcfc:13.7:14.1) (ec:) (dppf\_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_3461 ECOLI\_3461 Escherichia coli 562 10011821

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839216	9428	31584	714	237

Description

6500730147 dppd:b3541 dipeptide transport atp-binding protein dppd (gtcfc:12.1) (keggfc:11.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3541 b3541 Escherichia coli 562 -11534005 69235 dppd (de:dipeptide transport atp-binding protein dppd) (db:swissprot) DPPD\_ECOLI P37314 ESCHERICHIA COLI 562 -11534005 164263 dppd dipeptide transport protein dppd:peripheral membrane protein dppd (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) S61404 S61404 Escherichia coli 562 -11534005 236779 dppd peripheral membrane protein (sr:escherichia coli (sub\_species mm500, strain k-12) dna) (db:genpept-bct1) (de:escherichia coli dpp locus encoding dipeptide transporter, chemotaxis, dipeptide-binding protein, transmembrane proteins, and peripheral membrane proteins, complete cds.) (n... ECODPP L08399 g349228 Escherichia coli 562 -11534005 7500880597 dppd (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:117118) (re:118101) (di:complement) ECOUW76 U00039 g466680 Escherichia coli 562 -11534005 234200 dppd putative atp-binding component of dipeptide (fn:transport; protein, peptide secretion) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 321 of 400 of the complete genome.) (nt:f327; 100 pct identical amino acid sequence and) (le:6621) (re:7604) (di:complement) AE000431 AE000431 g1789963 Escherichia coli 562 -11534005 5000693641 (de:(ecoli\_3462) (pn:dipeptide transport atp-binding protein dppd) (gn:dppd) (gtcfc:13.7:14.1) (ec:) (dppd\_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_3462 ECOLI\_3462 Escherichia coli 562 10011818

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839221	9429	31585	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839227	9430	31586	423	140

Description

6500730148 dppc:b3542 dipeptide transport system permease protein dppc (gtcfc:12.1) (keggfc:11.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3542 b3542 Escherichia coli 562 -11534006 69232 dppc (de:dipeptide transport system permease protein dppc) (db:swissprot) DPPC\_ECOLI P37315 ESCHERICHIA COLI 562 -11534006 164744 dppc dipeptide transport system permease protein dppc (cl:oligopeptide permease protein oppb) (db:pir2.dat) S47764 S47764 Escherichia coli 562 -11534006 236780 dppc transmembrane protein (sr:escherichia coli (sub\_species mm500, strain k-12) dna) (db:genpept-bct1) (de:escherichia coli dpp locus encoding dipeptide transporter, chemotaxis, dipeptide-binding protein, transmembrane proteins, and peripheral membrane proteins, complete cds.) (n... ECODPP L08399 g349227 Escherichia coli 562 -11534006 7500880594 dppc (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:118112) (re:119014) (di:complement) ECOUW76 U00039 g466681 Escherichia coli 562 -11534006 234199 dppc dipeptide transport system permease protein 2 (fn:transport; protein, peptide secretion) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 321 of 400 of the complete genome.) (nt:f300; 100 pct identical amino acid sequence and) (le:7615) (re:8517) (di:complement) AE000431 AE000431 g1789964 Escherichia coli 562 -11534006 5000693642 (de:(ecoli\_3463) (pn:dipeptide transport system permease protein dppc) (gn:dppc) (gtcfc:13.7:14.1) (ec:) (dppc\_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_3463 ECOLI\_3463 Escherichia coli 562 10011815

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839230	9431	31587	405	134

Description

6500730149 dppb:b3543 dipeptide transport system permease protein dppb (gtcfc:12.1) (keggfc:11.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3543 b3543 Escherichia coli 562 -11534007 69229 dppb (de:dipeptide transport system permease protein dppb) (db:swissprot) DPPB\_ECOLI P37316 ESCHERICHIA COLI 562 -11534007 164743 dppb dipeptide transport system permease protein dppb (cl:transmembrane protein dppb) (db:pir2.dat) S47765 S47765 Escherichia coli 562 -11534007 236781 dppb transmembrane protein (sr:escherichia coli (sub\_species mm500, strain k-12) dna) (db:genpept-bct1) (de:escherichia coli dpp locus encoding dipeptide transporter, chemotaxis, dipeptide-binding protein, transmembrane proteins, and peripheral membrane proteins, complete cds.) (n... ECODPP L08399 g349226 Escherichia coli 562 -11534007 7500880592 dppb (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:119024) (re:120043) (di:complement) ECOUW76 U00039 g466682 Escherichia coli 562 -11534007 234198 dppb dipeptide transport system permease protein 1 (fn:transport; protein, peptide secretion) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 321 of 400 of the complete genome.) (nt:f339; 100 pct identical amino acid sequence and) (le:8527) (re:9546) (di:complement) AE000431 AE000431 g1789965 Escherichia coli 562 -11534007 5000693643 (de:(ecoli\_3464) (pn:dipeptide transport system permease protein dppb) (gn:dppb) (gtcfc:13.7:14.1) (ec:) (dppb\_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI\_3464 ECOLI\_3464 Escherichia coli 562 10011812

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839231	9432	31588	273	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839233	9433	31589	291	96

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839245	9434	31590	1131	376

Description

5000691254 phne (gtcfc:12.6) (keggfc:11.1) (rileyfc:4.1.6)  
(db:gtc-escherichia coli) b4104 b4104 Escherichia coli 562 -11534008 237312  
phne (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from  
92.8 to 00.1 minutes.) (le:13589) (re:14209) (di:complement) ECOUW93 U14003  
g536948 Escherichia coli 562 -11534008 7500974872 phne membrane channel  
protein component of pn (fn:transport; transport of small molecules:)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 372 of 400 of the  
completegenome.) (nt:f206; this 206 aa orf is 100 pct identical (0 gaps))  
(le:18308) (re:18928) (di:complement) AE000482 AE000482 g1790542 Escherichia  
coli 562 -11534008 6500730150 phne (gtcfc:12.6) (keggfc:11.1)  
(rileyfc:4.1.6) (db:gtc-escherichia coli) b4104 b4104 Escherichia coli 562  
-11534008 154759 (de:phne protein - escherichia coli) S56332 S56332  
Escherichia coli 562 -11534008

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839246	9435	31591	402	133

Description

6500730151 phnd:psid:b4105 carbon phosphorus lyase:phosphonates-binding  
periplasmic protein precursor (gtcfc:12.6) (keggfc:11.1) (rileyfc:4.1.6)  
(db:gtc-escherichia coli) b4105 b4105 Escherichia coli 562 -11534009 89594  
phnd:psid (de:phosphonates-binding periplasmic protein precursor)  
(db:swissprot) PHND\_ECOLI P16682 ESCHERICHIA COLI 562 -11534009 162795 phnd  
carbon phosphorus lyase (db:pir2.dat) S56333 S56333 Escherichia coli 562  
-11534009 237313 phnd periplasmic protein (sr:escherichia coli  
(strain:k-12, sub\_strain:w3110) dna) (db:genpept-bct1) (de:escherichia coli  
phn operon genes.) (le:912) (re:1928) (di:direct) ECOPHN D90227 g216592  
Escherichia coli 562 -11534009 7500888026 phnd carbon phosphorus lyase  
(db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to  
00.1 minutes.) (nt:cg site no. 17638; alternate gene name psid;) (le:14264)  
(re:15280) (di:complement) ECOUW93 U14003 g536949 Escherichia coli 562  
-11534009 235417 phnd periplasmic binding protein component of pn  
(fn:transport; transport of small molecules:) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 372 of 400 of the completegenome.)  
(nt:f338; 100 pct identical to phnd\_ecoli sw: p16682;) (le:18983) (re:19999)  
(di:complement) AE000482 AE000482 g1790543 Escherichia coli 562 -11534009  
5000691255 (de:(ecoli\_3991) (pn:periplasmic binding protein component of pn  
transporter) (gn:phnd) (gtcfc:12.6) (ec:) (phnd\_ecoli) (keggfc:11.2)  
(rileyfc:4.1.6) (db:gtc-escherichia coli)) ECOLI\_3991 ECOLI\_3991 Escherichia  
coli 562 10031716

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839247	9436	31592	735	244

Description

GTC ORF with score 101 to: (sr:human) (db:genpept) (de:human dna sequence from clone 283e3 on chromosome 1p36.21-36.33.contains the alternatively spliced gene for matrixmetalloproteinase in the female reproductive tract mifr1, -2,mmp21/22a, -b and -c, ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839249	9437	31593	690	229

Description

6500730152 phnc:b4106 phosphonates transport atp-binding protein:phosphonates transport atp-binding protein phnc (gtcfc:12.4) (keggfc:11.1) (rileyfc:4.1.6) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of anions (cl\_so4\_po4\_etc\_)) b4106 b4106 Escherichia coli 562 -11534010 89593 phnc (de:phosphonates transport atp-binding protein phnc) (db:swissprot) PHNC\_ECOLI P16677 ESCHERICHIA COLI 562 -11534010 7000686133 phnc phosphonates transport atp-binding protein phnc (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) A65220 A65220 Escherichia coli 562 -11534010 237314 phnc atp-binding protein (sr:escherichia coli (strain:k-12, sub\_strain:w3110) dna) (db:genpept-bct1) (de:escherichia coli phn operon genes.) (le:99) (re:887) (di:direct) ECOPHN D90227 g216591 Escherichia coli 562 -11534010 7500888025 phnc (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:hisp-like nucleotide binding protein (atp-binding) (le:15305) (re:16093) (di:complement) ECOUW93 U14003 g536950 Escherichia coli 562 -11534010 235416 phnc atp-binding component of phosphonate transport (fn:transport; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 372 of 400 of the completegenome.) (nt:f262; 100 pct identical amino acid sequence and) (le:20024) (re:20812) (di:complement) AE000482 AE000482 g1790544 Escherichia coli 562 -11534010 5000691256 (de:(ecoli\_3992) (pn:abc permease component of pn transporter) (gn:phnc) (gtcfc:12.6) (ec:) (phnc\_ecoli) (keggfc:11.2) (rileyfc:4.1.6) (db:gtc-escherichia coli)) ECOLI\_3992 ECOLI\_3992 Escherichia coli 562 10031715

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839289	9438	31594	1239	413

#### Description

6500730153 htre:b0139 outer membrane usher protein htre precursor:heat shock protein e (gtcfc:11.3:12.6:12.7) (keggfc:14.2) (rileyfc:4.1.6) (db:gtc-escherichia coli) b0139 b0139 Escherichia coli 562 -11534011 78036 htre (de:outer membrane usher protein htre precursor (heat shock protein e)) (db:swissprot) HTRE\_ECOLI P33129 ESCHERICHIA COLI 562 -11534011 7000685570 htre outer membrane usher protein htre precursor:fimbriae biogenesis protein homolog:pilin porin homolog htre precursor (cl:outer membrane usher protein fimd) (db:pir2.dat) C64737 C64737 Escherichia coli 562 -11534011 7500883609 htre probable outer membrane porin protein involved (fn:putative membrane; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 13 of 400 of the completegenome.) (nt:f865; 99 pct identical to htre\_ecoli sw: p33129) (le:3201) (re:5798) (di:complement) AE000123 AE000123 g1786332 Escherichia coli 562 -11534011 5000691242 (de:(ecoli\_139) (pn:outer membrane usher protein htre precursor) (gn:htre) (gtcfc:12.6) (ec:) (htre\_ecoli) (keggfc:11.2) (rileyfc:4.1.6) (db:gtc-escherichia coli)) ECOLI\_139 ECOLI\_139 Escherichia coli 562 10122678

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839290	9439	31595	207	68

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839296	9440	31596	294	97

#### Description

6500730154 abc:b0199 abc:atp-binding protein (gtcfc:12.6) (keggfc:14.2) (rileyfc:4.1.6) (db:gtc-escherichia coli) b0199 b0199 Escherichia coli 562 -11534012 57913 abc (de:atp-binding protein abc) (db:swissprot) ABC\_ECOLI P30750 ESCHERICHIA COLI 562 -11534012 7000684481 abc probable abc-type transport protein abc (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) G64744 G64744 Escherichia coli 562 -11534012 7500876261 abc atp-binding protein (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:52689) (re:53720) (di:complement) ECU70214 U70214 g1552775 Escherichia coli 562 -11534012 239826 abc atp-binding component of a transporter (fn:transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 19 of 400 of the completegenome.) (nt:f343; 98 pct identical to fragment (231) (le:1590) (re:2621) (di:complement) AE000129 AE000129 g1786398 Escherichia coli 562 -11534012 5000691243 (de:(ecoli\_199) (pn:abc transporter) (gn:abc) (gtcfc:12.6) (ec:) (abc\_ecoli) (keggfc:11.2) (rileyfc:4.1.6) (db:gtc-escherichia coli)) ECOLI\_199 ECOLI\_199 Escherichia coli 562 10122703

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839299	9441	31597	408	135

Description

6500730155 bett:b0314 high-affinity choline transport protein (gtcfc:12.1) (keggfc:14.2) (rileyfc:4.1.6) (db:gtc-escherichia coli) b0314 b0314 Escherichia coli 562 -11534013 239933 bett (de:high-affinity choline transport protein) (db:swissprot) BETT\_ECOLI P17447 ESCHERICHIA COLI 562 -11534013 162787 bett choline transport protein bett:high-affinity (cl:choline transport protein bett) (db:pir2.dat) (mp:7.5 min) S15179 S15179 Escherichia coli 562 -11534013 5000691244 (db:genpept-bct1) (de:escherichia coli bett, beti, betb and beta genes.) (nt:bett gene product (aa 1-677)) (le:1254) (re:3287) (di:complement) ECBET X52905 g48716 Escherichia coli 562 -11534013 7500877762 bett high-affinity choline transport protein (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (le:37260) (re:39293) (di:direct) ECU73857 U73857 g1657512 Escherichia coli 562 -11534013 232445 bett high-affinity choline transport (fn:transport; transport of small molecules: other) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 28 of 400 of the completegenome.) (nt:o677; 100 pct identical to bett\_ecoli sw: p17447) (le:4835) (re:6868) (di:direct) AE000138 AE000138 g1786506 Escherichia coli 562 -11534013 61590 bett (de:high-affinity choline transport protein) (db:swissprot) BETT\_ECOLI P17447 ESCHERICHIA COLI 562 -11534013

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839303	9442	31598	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839309	9443	31599	216	71

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839314	9444	31600	567	189

#### Description

5000691245 mdla (gtcfc:12.6) (keggfc:14.2) (rileyfc:4.1.6)  
(db:gtc-escherichia coli) b0448 b0448 Escherichia coli 562 -11534014  
7000691860 mdla abc-type transport protein mdla:mdla protein (cl:unassigned  
atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat)  
H64774 H64774 Escherichia coli 562 -11534014 7500960380 mdl multidrug  
resistance-like atp-binding protein (db:genpept-bct1) (de:escherichia coli  
minutes 9 to 11 genomic sequence.) (le:48321) (re:50093) (di:direct)  
ECU82664 U82664 g1773132 Escherichia coli 562 -11534014 240225 mdla  
atp-binding component of a transport system (fn:transport; not classified)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 41 of 400 of the  
completegenome.) (nt:o590; 98 pct identical to residues 1-516) (le:3322)  
(re:5094) (di:direct) AE000151 AE000151 g1786653 Escherichia coli 562  
-11534014 6500730156 mdla (gtcfc:12.6) (keggfc:14.2) (rileyfc:4.1.6)  
(db:gtc-escherichia coli) b0448 b0448 Escherichia coli 562 -11534014

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839341	9445	31601	408	135

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839355	9446	31602	483	161

#### Description

5000691246 mdlb (gtcfc:12.6) (keggfc:14.2) (rileyfc:4.1.6)  
(db:gtc-escherichia coli) b0449 b0449 Escherichia coli 562 -11534015  
7000691861 mdlb abc-type transport protein mdlb:mdlb protein (cl:unassigned  
atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat)  
A64775 A64775 Escherichia coli 562 -11534015 7500960381 mdlb putative  
atp-binding component of a transport (fn:putative transport; not classified)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 41 of 400 of the  
completegenome.) (nt:o593; 97 pct identical (1 gap) to residues) (le:5087)  
(re:6868) (di:direct) AE000151 AE000151 g1786654 Escherichia coli 562  
-11534015 6500730157 mdlb (gtcfc:12.6) (keggfc:14.2) (rileyfc:4.1.6)  
(db:gtc-escherichia coli) b0449 b0449 Escherichia coli 562 -11534015

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839358	9447	31603	204	67

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839363	9448	31604	1209	402

Description

6500730158 cydc:mdra:mdrh:surb:b0886 transport atp-binding protein cydc (gtcfc:12.6) (keggfc:14.2) (rileyfc:4.1.6) (db:gtc-escherichia coli) b0886 b0886 Escherichia coli 562 -11534016 67472 cydc:mdra:mdrh:surb (de:transport atp-binding protein cydc) (db:swissprot) CYDC\_ECOLI P23886 ESCHERICHIA COLI 562 -11534016 164407 cydc:mdrh:mdra:surb abc-type transport protein cydc:atp-binding cassette transporter chain cydc (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) (mp:20 min) B36888 B36888 Escherichia coli 562 -11534016 223247 cydc transport atp-binding protein cydc (sr:escherichia coli(strain:k12) dna, clone:kohara clone #214) (db:genpept-bct1) (de:escherichia coli genomic dna. (19.9 - 20.2 min).) (le:3354) (re:5075) (di:complement) D90726 D90726 g1651408 Escherichia coli 562 -11534016 7500879837 mdrh (fn:unknown) (sr:escherichia coli dna) (db:genpept-bct1) (de:e. coli leucyl/phenylalanyl trna protein transferase (aat) gene,mdrh gene, initiation factor (infa) gene, and serine transfer rna(serw) gene, complete cds's.) (nt:putative) (le:24) (re:1745) ... ECOAAT L10383 g145165 Escherichia coli 562 -11534016 233703 cydc atp-binding component of cytochrome-related (fn:transport; transport of small molecules: other) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 80 of 400 of the completegenome.) (nt:f573; 100 pct identical to cydc\_ecoli sw: p23886) (le:5175) (re:6896) (di:complement) AE000190 AE000190 g1787112 Escherichia coli 562 -11534016 5000691247 cydc probable transport protein mdrh (sr:escherichia coli(strain:k12) dna, clone:kohara clone #214) (db:genpept) (de:escherichia coli genomic dna. (19.9 - 20.3 min).) (nt:orf\_id:o214#5; similar to pir accession number) (le:3354) (re:5075) (di:complement) D90726 D90726 g1651408 Escherichia coli 562 -11534016

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839366	9449	31605	960	319

Description

6500730159 cydd:htrd:b0887 transport atp-binding protein cydd (gtcfc:12.6) (keggfc:14.2) (rileyfc:4.1.6) (db:gtc-escherichia coli) b0887 b0887 Escherichia coli 562 -11534017 67474 cydd:htrd (de:transport atp-binding protein cydd) (db:swissprot) CYDD\_ECOLI P29018 ESCHERICHIA COLI 562 -11534017 7000684960 cydd:htrd abc-type transport protein cydd:probable abc transporter cydd:probable atp-binding cassette transporter cydd (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) F64827 F64827 Escherichia coli 562 -11534017 223248 cydd transport atp-binding protein cydd (sr:escherichia coli(strain:k12) dna, clone:kohara clone #214) (db:genpept-bct1) (de:escherichia coli genomic dna. (19.9 - 20.2 min).) (le:5076) (re:6842) (di:complement) D90726 D90726 g1651409 Escherichia coli 562 -11534017 7500879839 cydd atp-binding component of cytochrome-related (fn:transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 80 of 400 of the completegenome.) (nt:f588; 99 pct identical to cydd\_ecoli sw: p29018) (le:6897) (re:8663) (di:complement) AE000190 AE000190 g1787113 Escherichia coli 562 -11534017 5000691248 cydd transport atp-binding protein cydd. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #214) (db:genpept) (de:escherichia coli genomic dna. (19.9 - 20.3 min).) (nt:orf\_id:o214#6; similar to swissprot accession) (le:5076) (re:6842) (di:complement) D90726 D90726 g1651409 Escherichia coli 562 -11534017

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839368	9450	31606	915	304

Description

6500730160 msba:b0914 probable transport atp-binding protein msba (gtcfc:12.6) (keggfc:14.2) (rileyfc:4.1.6) (db:gtc-escherichia coli) b0914 b0914 Escherichia coli 562 -11534018 7500885915 msba (de:probable transport atp-binding protein msba) (db:swissprot) MSBA\_ECOLI P27299 ESCHERICHIA COLI 562 -11534018 164105 msba probable abc-type transport protein msba (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) (mp:20.5 min) S27998 S27998 Escherichia coli 562 -11534018 223277 msba msba protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #217) (db:genpept-bct1) (de:escherichia coli genomic dna. (20.4 - 20.8 min).) (le:14781) (re:16529) (di:direct) D90729 D90729 g1651441 Escherichia coli 562 -11534018 5000691249 msba (db:genpept-bct1) (de:e.coli msba gene.) (nt:member of atp-dependent transport family, very) (le:562) (re:2310) (di:direct) ECMSBAG Z11796 g42023 Escherichia coli 562 -11534018 233410 msba atp-binding transport protein:multicopy (fn:transport; transport of small molecules: other) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 83 of 400 of the completegenome.) (nt:o582; 100 pct identical to msba\_ecoli sw: p27299) (le:9950) (re:11698) (di:direct) AE000193 AE000193 g1787143 Escherichia coli 562 -11534018 7502851983 msba msba protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #217) (db:genpept) (de:escherichia coli genomic dna. (20.5 - 20.9 min).) (nt:orf\_id:o217#11; similar to pir accession number) (le:14781) (re:16529) (di:direct) D90729 D90729 g1651441 Escherichia coli 562 -11534018 84287 msba (de:probable transport atp-binding protein msba) (db:swissprot) MSBA\_ECOLI P27299 ESCHERICHIA COLI 562 -11534018

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839369	9451	31607	588	195

Description

GTC ORF with score 134 to: (or:Boreogadus saida) (db:genpept-vrt) (de:boreogadus saida antifreeze glycopeptide afgp polyprotein precursorgene, complete cds.) (nt:cleavage of polyprotein at conserved spacers r or) (le:209:281) (re:211:1801) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839375	9452	31608	1893	630
<u>Description</u>				
6500730161 btub:bfe:cer:b3966 vitamin b12 receptor precursor (gtcfc:12.6) (keggfc:14.2) (rileyfc:4.1.6) (db:gtc-escherichia coli) b3966 b3966 Escherichia coli 562 -11534019 62072 btub:bfe:cer (de:vitamin b12 receptor precursor) (db:swissprot) BTUB_ECOLI P06129 ESCHERICHIA COLI 562 -11534019 7000684732 btub vitamin b12 receptor precursor (cl:vitamin b12 receptor:tonb-dependent receptor amino-terminal homology:tonb-dependent receptor carboxyl-terminal homology) (db:pir1.dat) (mp:90 min) QRECBT A65204 Escherichia coli 562 -11534019 237184 btub outer membrane receptor for transport of vitamin (fn:membrane; outer membrane constituents) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 361 of 400 of the completegenome.) (nt:o614; 100 pct identical amino acid sequence and) (le:224) (re:2068) (di:direct) AE000471 AE000471 g1790405 Escherichia coli 562 -11534019 7500877961 btub (fn:receptor for vitamin b12, e colicins, and phage) (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 946) (le:28881) (re:30725) (di:dir... ECOUW89 U00006 g396313 Escherichia coli 562 -11534019 5000691253 (de:(ecoli_3864) (pn:outer membrane receptor for transport of vitamin b12, e colicins, and bacteriophage bf23) (gn:btub) (gtcfc:12.6) (ec:) (btub_ecoli) (keggfc:11.2) (rileyfc:4.1.6) (db:gtc-escherichia coli)) ECOLI_3864 ECOLI_3864 Escherichia coli 562 10004772				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839376	9453	31609	213	70

Description

6500730162 dnak:grpfgrop:seg:b0014 dnak protein:heat shock protein 70:hsp70 (gtcfc:12.7) (keggfc:14.2) (rileyfc:4.2.0) (db:gtc-escherichia coli) b0014 b0014 Escherichia coli 562 -11534020 130454 dnak dnak-type molecular chaperone dnak:heat shock protein:70k:hsp70 protein (cl:heat shock protein 70) (db:pir1.dat) (mp:0 min) IQECDK A03311 Escherichia coli 562 -11534020 234186 dnak hsp70 protein (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (le:11812) (re:13728) (di:direct) ECODNAK D10483 g216440 Escherichia coli 562 -11534020 234187 dnak (sr:escherichia coli dna (lambda-dnak dna)) (db:genpept-bct1) (de:e.coli dnak gene encoding the heat shock 70 protein.) (nt:hsp70 protein (dnak gene)) (le:1) (re:1917) (di:direct) ECODNAK K01298 g145774 Escherichia coli 562 -11534020 7500953588 dnak dnak protein homolog (sr:escherichia coli b (h/r30rt) genomic dna) (db:genpept-bct1) (de:escherichia coli b, dnak gene, complete cds.) (le:194) (re:2110) (di:direct) ECODNAKB D10765 g216546 Escherichia coli 562 -11534020 233550 dnak chaperone hsp70:dna biosynthesis:autoregulated (fn:factor; chaperones) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 2 of 400 of the completegenome.) (nt:o638; 100 pct identical to dnak\_ecoli sw: p04475) (le:1625) (re:3541) (di:direct) AE000112 AE000112 g1786196 Escherichia coli 562 -11534020 5000691257 (de:(ecoli\_14) (pn:chaperone hsp70; dna biosynthesis; autoregulated heat shock proteins) (gn:dnak) (gtcfc:12.7) (ec:) (dnak\_ecoli) (keggfc:11.2) (rileyfc:4.2.0) (db:gtc-escherichia coli)) ECOLI\_14 ECOLI\_14 Escherichia coli 562 10067857

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839377	9454	31610	480	159

Description

6500730163 dnaj:grop:b0015 dnaj protein (gtcfc:12.7) (keggfc:14.2) (rileyfc:4.2.0) (db:gtc-escherichia coli) b0015 b0015 Escherichia coli 562 -11534021 130464 dnaj heat shock protein dnaj (cl:heat shock protein dnaj:dnaj amino-terminal homology) (db:pir1.dat) (mp:0 min) HHECDJ A92572 Escherichia coli 562 -11534021 234185 dnaj dnaj protein (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (le:13817) (re:14947) (di:direct) ECO110K D10483 g216441 Escherichia coli 562 -11534021 7500880420 dnaj (sr:e.coli dna) (db:genpept-bct1) (de:e. coli k12 dnaj gene encoding a heat shock protein, complete cds.) (nt:heat shock protein dnaj) (le:127) (re:1257) (di:direct) ECODNAJ M12565 g145769 Escherichia coli 562 -11534021 233551 dnaj chaperone with dnak:heat shock protein (fn:factor; chaperones) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 2 of 400 of the completegenome.) (nt:o376; 100 pct identical to dnaj\_ecoli sw: p08622) (le:3630) (re:4760) (di:direct) AE000112 AE000112 g1786197 Escherichia coli 562 -11534021 68871 dnaj:grop (de:dnaj protein) (db:swissprot) DNAJ\_ECOLI P08622 ESCHERICHIA COLI 562 -11534021 5000691258 (de:(ecoli\_15) (pn:chaperone with dnak; heat shock protein) (gn:dnaj) (gtcfc:12.7) (ec:) (dnaj\_ecoli) (keggfc:11.2) (rileyfc:4.2.0) (db:gtc-escherichia coli)) ECOLI\_15 ECOLI\_15 Escherichia coli 562 10011456

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839378	9455	31611	603	200

Description

6500730164 httpg:b0473 heat shock protein httpg:high temperature protein  
g:heat shock protein c62.5 (gtcfc:12.7) (keggfc:14.2) (rileyfc:4.2.0)  
(db:gtc-escherichia coli) b0473 b0473 Escherichia coli 562 -11534022 78021  
httpg (de:protein c62.5)) (db:swissprot) HTPG\_ECOLI P10413 ESCHERICHIA COLI  
562 -11534022 130463 httpg heat shock protein c62.5:high temperature protein  
g (cl:heat shock protein 90) (db:pir1.dat) (mp:11 min) HHEC62 A28324  
Escherichia coli 562 -11534022 240248 (sr:e.coli dna) (db:genpept-bct1)  
(de:e.coli sequence of the apt-adk region.) (nt:httpg orf) (le:3898)  
(re:5772) (di:direct) ECOAPTADK M38777 g145300 Escherichia coli 562  
-11534022 7500883599 httpg heat shock protein httpg (db:genpept-bct1)  
(de:escherichia coli minutes 9 to 11 genomic sequence.) (le:74568)  
(re:76442) (di:direct) ECU82664 U82664 g1773155 Escherichia coli 562  
-11534022 233819 httpg chaperone hsp90:heat shock protein c 62.5 (fn:factor;  
chaperones) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 43 of  
400 of the completegenome.) (nt:o624; 100 pct identical to httpg\_ecoli sw:  
p10413) (le:5146) (re:7020) (di:direct) AE000153 AE000153 g1786679  
Escherichia coli 562 -11534022 5000691259 (de:(ecoli\_456) (pn:heat shock  
protein httpg:high temperature protein g:heat shock protein c62) (gn:httpg)  
(gtcfc:12.7) (ec:) (httpg\_ecoli) (keggfc:11.2) (rileyfc:4.2.0)  
(db:gtc-escherichia coli)) ECOLI\_456 ECOLI\_456 Escherichia coli 562 10020360



ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501839383	9456	31612	813	270

#### Description

6500730165 cbpa:b1000 curved dna-binding protein (gtcfc:12.7) (keggfc:14.2) (rileyfc:4.2.0) (db:gtc-escherichia coli) b1000 b1000 Escherichia coli 562 -11534023 63232 cbpa (de:curved dna-binding protein) (db:swissprot) CBPA\_ECOLI P36659 ESCHERICHIA COLI 562 -11534023 7000684762 cbpa curved dna-binding protein cbpa (cl:dnaJ amino-terminal homology) (db:pir2.dat) F64841 F64841 Escherichia coli 562 -11534023 223321 cbpa curved dna-binding protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept-bct1) (de:escherichia coli genomic dna. (22.5 - 22.9 min).) (le:17350) (re:18270) (di:complement) D90736 D90736 g1651491 Escherichia coli 562 -11534023 223326 cbpa curved dna-binding protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #227) (db:genpept-bct1) (de:escherichia coli genomic dna. (22.7 - 23.0 min).) (le:8352) (re:9272) (di:complement) D90737 D90737 g1651497 Escherichia coli 562 -11534023 7500878279 cbpa curved dna-binding protein:functions closely (fn:factor; chaperones) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 92 of 400 of the completegenome.) (nt:f306; 100 pct identical to 293 residues) (le:411) (re:1331) (di:complement) AE000202 AE000202 g1787235 Escherichia coli 562 -11534023 5000691260 cbpa curved dna-binding protein cbpa (sr:escherichia coli(strain:k12) dna, clone:kohara clone #227) (db:genpept) (de:escherichia coli genomic dna. (22.8 - 23.1 min).) (nt:orf\_id:o227#7; similar to pir accession number) (le:8352) (re:9272) (di:complement) D90737 D90737 g1651497 Escherichia coli 562 -11534023 7502851984 cbpa curved dna-binding protein cbpa (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept) (de:escherichia coli genomic dna. (22.6 - 23.0 min).) (nt:orf\_id:o227#7; similar to pir accession number) (le:17350) (re:18270) (di:complement) D90736 D90736 g1651491 Escherichia coli 562 -11534023

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501839390	9457	31613	354	117

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839396	9458	31614	834	277

Description

6500730166 hsca:hsc:b2526 heat shock protein hsca:hsc66 (gtcfc:12.7)  
 (keggfc:14.2) (rileyfc:4.2.0) (db:gtc-escherichia coli) b2526 b2526  
 Escherichia coli 562 -11534024 77868 hsca:hsc (de:chaperone protein hsca  
 (hsc66)) (db:swissprot) HSCA\_ECOLI P36541 ESCHERICHIA COLI 562 -11534024  
 7000685562 hsca heat shock cognate protein 66 (cl:heat shock protein 70)  
 (db:pir2.dat) E65029 E65029 Escherichia coli 562 -11534024 225109 heat  
 shock cognate protein 66 (sr:escherichia coli (strain:k12) dna,  
 clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
 kohara clone #430(57.2-57.5 min.)) (nt:similar to (pir accession number  
 a53488)) (le:848) (re:2698) (di:complement) D90883 D90883 g1799934  
 Escherichia coli 562 -11534024 7500883558 hsca heat shock  
 protein:chaperone:member of hsp70 (fn:factor; chaperones) (db:genpept-bct2)  
 (de:escherichia coli k-12 mg1655 section 229 of 400 of the completegenome.)  
 (nt:f616; 98 pct identical (1 gap) to hsca\_ecoli) (le:3367) (re:5217)  
 (di:complement) AE000339 AE000339 g1788875 Escherichia coli 562 -11534024  
 5000691261 (de:(ecoli\_2466) (pn:heat shock protein, member of hsp70 protein  
 family) (gn:hsca) (gtcfc:12.7) (ec:) (hsca\_ecoli) (keggfc:11.2)  
 (rileyfc:4.2.0) (db:gtc-escherichia coli)) ECOLI\_2466 ECOLI\_2466 Escherichia  
 coli 562 10120246

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839400	9459	31615	423	140

Description

GTC ORF with score 132 to: (fn:transport; transport of small molecules:)  
 (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 254 of 400 of the  
 completegenome.) (nt:o438; 100 pct identical to fucp\_ecoli sw: p11551;)  
 (le:304) (re:1620) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839423	9460	31616	1326	442

Description

6500730167 mopb:groes:b4142 groes protein:10 kd chaperonin:protein  
cpn10:protein groes (gtcfc:12.7) (keggfc:14.2) (rileyfc:4.2.0)  
(db:gtc-escherichia coli) b4142 b4142 Escherichia coli 562 -11534025 237350  
groes:mopb:groes (de:10 kd chaperonin (protein cpn10) (protein groes))  
(db:swissprot) CH10\_ECOLI P05380 ESCHERICHIA COLI 562 -11534025 131358  
mopb:groes chaperonin groes:heat shock protein groes (cl:chaperonin groes)  
(db:pir1.dat) (mp:94 min) BVECGS S03931 Escherichia coli 562 -11534025  
5000691262 (db:genpept-bct1) (de:e. coli groe operon.) (nt:groes protein  
(aa 1-97)) (le:134) (re:427) (di:direct) ECGROESL X07850 g41616 Escherichia  
coli 562 -11534025 7500878584 mopb groes protein (db:genpept-bct1)  
(de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.)  
(nt:cg site no. 492; alternate gene names groe, groes,) (le:61516)  
(re:61809) (di:direct) ECOUW93 U14003 g536986 Escherichia coli 562 -11534025  
233034 mopb groes:10 kd chaperone binds to hsp60 in pres. (fn:factor;  
chaperones) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 377  
of 400 of the completegenome.) (nt:o97; 100 pct identical to ch10\_ecoli sw:  
p05380; cg) (le:2178) (re:2471) (di:direct) AE000487 AE000487 g1790585  
Escherichia coli 562 -11534025 64043 mopb:groes (de:10 kd chaperonin  
(protein cpn10) (protein groes)) (db:swissprot) CH10\_ECOLI P05380  
ESCHERICHIA COLI 562 -11534025

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839434	9461	31617	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839438	9462	31618	1332	444
<u>Description</u>				
6500730168 mopa:groel:b4143 60 kd chaperonin:protein cpn60:groel protein:ams (gtcfc:12.7) (keggfc:14.2) (rileyfc:4.2.0) (db:gtc-escherichia coli) b4143 b4143 Escherichia coli 562 -11534026 154558 mopa:groel:ams chaperonin groel:heat shock protein groel:hsp60:ribosomal protein a misnomer (cl:chaperonin groel) (db:pir1.dat) (mp:94 min) BVECGL S56371 Escherichia coli 562 -11534026 7500953641 mopa groel protein (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 493; alternate gene names groe, groel,) (le:61853) (re:63499) (di:direct) ECOUW93 U14003 g536987 Escherichia coli 562 -11534026 237351 mopa groel:chaperone hsp60:peptide-dependent (fn:factor; chaperones) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 377 of 400 of the completegenome.) (nt:o548; cg site no. 493; alternate gene names) (le:2515) (re:4161) (di:direct) AE000487 AE000487 g1790586 Escherichia coli 562 -11534026 5000691263 (de:(ecoli_4029) (pn:groel, chaperone hsp60, peptide-dependent atpase, heat shock protein) (gn:mopa) (gtcfc:12.7) (ec:) (ch60_ecoli) (keggfc:11.2) (rileyfc:4.2.0) (db:gtc-escherichia coli)) ECOLI_4029 ECOLI_4029 Escherichia coli 562 10081604				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839444	9463	31619	510	169

Description

6500730169 ftsl:mrar:b0083 cell division protein ftsl (gtcfc:12.8) (keggfc:14.2) (rileyfc:4.3.0) (db:gtc-escherichia coli) b0083 b0083 Escherichia coli 562 -11534027 227990 ftsl:mrar (de:cell division protein ftsl) (db:swissprot) FTSL\_ECOLI P22187 ESCHERICHIA COLI 562 -11534027 162807 mrar:ftsl cell division protein ftsl (db:pir2.dat) (mp:2 min) A45278 A45278 Escherichia coli 562 -11534027 5000691264 orfa protein (db:genpept-bct1) (de:e. coli 2 minute region.) (le:7562) (re:7927) (di:direct) EC2MIN X55034 g40851 Escherichia coli 562 -11534027 258425 (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli pbpb gene (ftsi) coding for penicillin-binding protein 3.) (nt:orfa gene) (le:247) (re:612) (di:direct) ECOPBPB K00137 g147110 Escherichia coli 562 -11534027 258428 mrar mrar (db:genpept-bct1) (de:murein synthesis gene cluster a: mrar=cell cycle regulator, ftsi(escherichia coli, genomic, 840 nt).) (nt:cell cycle regulator; this sequence comes from fig.) (le:247) (re:612) (di:direct) S49802 S49802 g260730 Escherichia coli 562 -11534027 304527 ftsl ftsl (db:genpept-bct1) (de:ftsl=cytoplasmic membrane cell division protein, ftsi=ftsi(escherichia coli, genomic, 607 nt).) (nt:cytoplasmic membrane cell division protein; this) (le:102) (re:467) (di:direct) S49875 S49875 g260716 Escherichia coli 562 -11534027 235360 ftsl cell division protein:ingrowth of wall at (fn:phenotype; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 8 of 400 of the completegenome.) (nt:o121; 100 pct identical to ftsl\_ecoli sw: p22187) (le:7487) (re:7852) (di:direct) AE000118 AE000118 g1786271 Escherichia coli 562 -11534027 72459 ftsl:mrar (de:cell division protein ftsl) (db:swissprot) FTSL\_ECOLI P22187 ESCHERICHIA COLI 562 -11534027

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839446	9464	31620	270	89

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839447	9465	31621	405	134
<u>Description</u>				
6500730170 ftsw:b0089 cell division protein ftsw (gtcfc:12.8) (keggfc:14.2) (rileyfc:4.3.0) (db:gtc-escherichia coli) b0089 b0089 Escherichia coli 562 -11534028 227996 ftsw (de:cell division protein ftsw) (db:swissprot) FTSW_ECOLI P16457 ESCHERICHIA COLI 562 -11534028 131643 ftsw cell division protein ftsw (cl:rod shape-determining protein) (db:pir1.dat) (mp:2 min) CEEFCW A32581 Escherichia coli 562 -11534028 5000691265 ftsw ftsw protein (db:genpept-bct1) (de:e. coli 2 minute region.) (le:14933) (re:16177) (di:direct) EC2MIN X55034 g40857 Escherichia coli 562 -11534028 234413 ftsw cell division protein ftsw (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (le:98057) (re:99301) (di:direct) ECO110K D10483 g216503 Escherichia coli 562 -11534028 304533 ftsw cell division protein (sr:escherichia coli (strain jlb17) dna) (db:genpept-bct1) (de:escherichia coli cell division protein gene (ftsw) gene, completecds.) (le:192) (re:1436) (di:direct) ECOFTSW M30807 g146039 Escherichia coli 562 -11534028 233613 ftsw cell division:membrane protein involved in (fn:membrane; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 8 of 400 of the completegenome.) (nt:o414; 100 pct identical to ftsw_ecoli sw: p16457) (le:14858) (re:16102) (di:direct) AE000118 AE000118 g1786277 Escherichia coli 562 -11534028 72467 ftsw (de:cell division protein ftsw) (db:swissprot) FTSW_ECOLI P16457 ESCHERICHIA COLI 562 -11534028				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839450	9466	31622	471	156

Description

6500730171 ftsq:b0093 cell division protein ftsq (gtcfc:12.8) (keggfc:14.2) (rileyfc:4.3.0) (db:gtc-escherichia coli) b0093 b0093 Escherichia coli 562 -11534029 233617 ftsq (de:cell division protein ftsq) (db:swissprot) FTSQ\_ECOLI P06136 ESCHERICHIA COLI 562 -11534029 131337 ftsq cell division protein ftsq (cl:cell division protein ftsq) (db:pir1.dat) (mp:2 min) CEECQ S10852 Escherichia coli 562 -11534029 228000 ftsq ftsq protein (db:genpept-bct1) (de:e. coli 2 minute region.) (le:19685) (re:20515) (di:direct) EC2MIN X55034 g40861 Escherichia coli 562 -11534029 304537 ftsa put. ftsa protein (db:genpept-bct1) (de:e. coli cell division genes ftsq, ftsa and ftsz (5' end).) (le:223) (re:1053) (di:direct) ECFTSQA X02821 g41493 Escherichia coli 562 -11534029 234409 ftsq cell division protein ftsq (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (le:102809) (re:103639) (di:direct) ECO110K D10483 g216507 Escherichia coli 562 -11534029 5000691266 ftsq (sr:e.coli dna, clone lambda-16-2) (db:genpept-bct1) (de:e. coli ddl gene encoding d-alanine:d-alanine ligase and ftsq andfts a genes, complete cds, and ftsz gene, 5' end.) (nt:ftsq protein) (le:1068) (re:1898) (di:direct) ECOFTSQA K02668 g146031 Escherichia coli 562 -11534029 232922 ftsq cell division protein:ingrowth of wall at (fn:phenotype; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 8 of 400 of the completegenome.) (nt:o276; 100 pct identical to ftsq\_ecoli sw: p06136) (le:19610) (re:20440) (di:direct) AE000118 AE000118 g1786281 Escherichia coli 562 -11534029 72462 ftsq (de:cell division protein ftsq) (db:swissprot) FTSQ\_ECOLI P06136 ESCHERICHIA COLI 562 -11534029

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839465	9467	31623	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839472	9468	31624	2157	718

Description

6500730172 ftsa:diva:b0094 cell division protein ftsa (gtcfc:12.8)  
 (keggfc:14.2) (rileyfc:4.3.0) (db:gtc-escherichia coli) b0094 b0094  
 Escherichia coli 562 -11534030 233618 ftsa:diva (de:cell division protein  
 ftsa) (db:swissprot) FTSA\_ECOLI P06137 ESCHERICHIA COLI 562 -11534030  
 131349 ftsa cell division protein ftsa (cl:cell division protein ftsa)  
 (db:pir1.dat) (mp:2 min) CEECA B23318 Escherichia coli 562 -11534030 228001  
 ftsa ftsa protein (db:genpept-bct1) (de:e. coli 2 minute region.) (le:20512)  
 (re:21774) (di:direct) EC2MIN X55034 g40862 Escherichia coli 562 -11534030  
 5000691267 ftsa ftsa protein (db:genpept-bct1) (de:e. coli cell division  
 genes ftsq, ftsa and ftsz (5' end).) (le:1050) (re:2312) (di:direct) ECFTSQA  
 X02821 g41494 Escherichia coli 562 -11534030 304538 ftsa cell division  
 protein ftsa (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1)  
 (de:e.coli k12 genome, 0-2.4min. region.) (le:103636) (re:104898)  
 (di:direct) ECO110K D10483 g216508 Escherichia coli 562 -11534030 232923  
 ftsa atp-binding cell division protein:septation (fn:phenotype; cell  
 division) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 8 of  
 400 of the completegenome.) (nt:o420; 100 pct identical to ftsa\_ecoli sw:  
 p06137) (le:20437) (re:21699) (di:direct) AE000118 AE000118 g1786282  
 Escherichia coli 562 -11534030 72441 ftsa:diva (de:cell division protein  
 ftsa) (db:swissprot) FTSA\_ECOLI P06137 ESCHERICHIA COLI 562 -11534030

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839475	9469	31625	204	67

Description

Hypothetical protein



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839488	9470	31626	1320	439

Description

6500730173 tig:b0436 trigger factor:tf (gtcfc:12.8) (keggfc:14.2) (rileyfc:4.3.0) (db:gtc-escherichia coli) b0436 b0436 Escherichia coli 562 -11534031 101511 tig (de:trigger factor (tf)) (db:swissprot) TIG\_ECOLI P22257 ESCHERICHIA COLI 562 -11534031 7000686798 tig trigger factor (cl:trigger factor) (db:pir2.dat) (mp:10 min) D64773 D64773 Escherichia coli 562 -11534031 7500893180 tig trigger factor (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:34583) (re:35881) (di:direct) ECU82664 U82664 g1773120 Escherichia coli 562 -11534031 240213 tig trigger factor:a molecular chaperone involved (fn:factor; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 40 of 400 of the completegenome.) (nt:o432; 97 pct identical to tig\_ecoli sw: p22257) (le:202) (re:1500) (di:direct) AE000150 AE000150 g1786640 Escherichia coli 562 -11534031 5000691269 (de:(ecoli\_420) (pn:trigger factor; a molecular chaperone involved in cell division) (gn:tig) (gtcfc:12.8) (ec:) (tig\_ecoli) (keggfc:11.2) (rileyfc:4.3.0) (db:gtc-escherichia coli)) ECOLI\_420 ECOLI\_420 Escherichia coli 562 10122827

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839498	9471	31627	939	312

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839504	9472	31628	324	107

Description

5000691270 mukb (gtcfc:12.8) (keggfc:14.2) (rileyfc:4.3.0)  
(db:gtc-escherichia coli) b0924 b0924 Escherichia coli 562 -11534032  
7500886079 mukb (de:cell division protein mukb) (db:swissprot) MUKB\_ECOLI  
P22523 ESCHERICHIA COLI 562 -11534032 7000691867 mukb cell division protein  
mukb (cl:escherichia coli mukb protein) (sr:strain k-12, substrain mg1655, ,  
strain k-12, substrain mg1655) (sr:strain k-12, substrain mg1655, )  
(db:pir2.dat) C64832 C64832 Escherichia coli 562 -11534032 223283 mukb mukb  
protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #218)  
(db:genpept-bct1) (de:escherichia coli genomic dna. (20.8 - 21.2 min).)  
(le:8680) (re:13140) (di:direct) D90730 D90730 g1651448 Escherichia coli 562  
-11534032 7500886082 mukb kinesin-like cell division protein involved in  
(fn:structural component; cell division) (db:genpept-bct2) (de:escherichia  
coli k-12 mg1655 section 84 of 400 of the completegenome.) (nt:o1486; this  
1486 aa orf is 97 pct identical (3) (le:4681) (re:9141) (di:direct) AE000194  
AE000194 g1787154 Escherichia coli 562 -11534032 6500730174 mukb mukb  
protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #218)  
(db:genpept) (de:escherichia coli genomic dna. (20.9 - 21.3 min).)  
(nt:orf\_id:o218#10; similar to pir accession number) (le:8680) (re:13140)  
(di:direct) D90730 D90730 g1651448 Escherichia coli 562 -11534032

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839524	9473	31629	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839531	9474	31630	390	129

Description

6500730175 sula:sfia:b0958 cell division inhibitor (gtcfc:12.8)  
 (keggfc:14.2) (rileyfc:4.3.0) (db:gtc-escherichia coli) b0958 b0958  
 Escherichia coli 562 -11534033 99847 sula:sfia (de:cell division inhibitor)  
 (db:swissprot) SULA\_ECOLI P08846 ESCHERICHIA COLI 562 -11534033 131335  
 sula:sfia cell division inhibitor sula (cl:cell division inhibitor sula)  
 (db:pir1.dat) (mp:22 min) QQECA1 A29016 Escherichia coli 562 -11534033  
 223299 sula cell division inhibitor (sr:escherichia coli(strain:k12) dna,  
 clone:kohara clone #222) (db:genpept-bct1) (de:escherichia coli genomic dna.  
 (21.6 - 22.0 min).) (le:13762) (re:14271) (di:complement) D90733 D90733  
 g1651466 Escherichia coli 562 -11534033 223302 sula cell division inhibitor  
 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #223)  
 (db:genpept-bct1) (de:escherichia coli genomic dna. (21.9 - 22.2 min).)  
 (le:1933) (re:2442) (di:complement) D90734 D90734 g1651470 Escherichia coli  
 562 -11534033 7500892255 sula suppressor of lon:inhibits cell division and  
 (fn:phenotype; cell division) (db:genpept-bct2) (de:escherichia coli k-12  
 mg1655 section 88 of 400 of the completegenome.) (nt:f169; 100 pct identical  
 to sula\_ecoli sw: p08846) (le:2048) (re:2557) (di:complement) AE000198  
 AE000198 g1787192 Escherichia coli 562 -11534033 5000691271 sfia cell  
 division inhibitor. (sr:escherichia coli(strain:k12) dna, clone:kohara clone  
 #222) (db:genpept) (de:escherichia coli genomic dna. (21.7 - 22.1 min).)  
 (nt:orf\_id:o223#3; similar to swissprot accession) (le:13762) (re:14271)  
 (di:complement) D90733 D90733 g1651466 Escherichia coli 562 -11534033  
 7502851985 sfia cell division inhibitor. (sr:escherichia coli(strain:k12)  
 dna, clone:kohara clone #223) (db:genpept) (de:escherichia coli genomic dna.  
 (22.0 - 22.3 min).) (nt:orf\_id:o223#3; similar to swissprot accession)  
 (le:1933) (re:2442) (di:complement) D90734 D90734 g1651470 Escherichia coli  
 562 -11534033

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839535	9475	31631	564	187

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839536	9476	31632	612	203

Description

6500730176 mine:b1174 cell division topological specificity factor (gtcfc:12.8) (keggfc:14.2) (rileyfc:4.3.0) (db:gtc-escherichia coli) b1174 b1174 Escherichia coli 562 -11534034 83732 mine (de:cell division topological specificity factor) (db:swissprot) MINE\_ECOLI P18198 ESCHERICHIA COLI 562 -11534034 131336 mine cell division topological specificity factor (cl:cell division topological specificity factor) (db:pir1.dat) (mp:26 min) CEECTF C31877 Escherichia coli 562 -11534034 223389 mine cell division topological specificity factor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #242) (db:genpept-bct1) (de:escherichia coli genomic dna. (26.1 - 26.5 min).) (le:10614) (re:10880) (di:complement) D90751 D90751 g1651573 Escherichia coli 562 -11534034 223392 mine cell division topological specificity factor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #243) (db:genpept-bct1) (de:escherichia coli genomic dna. (26.2 - 26.6 min).) (le:6170) (re:6436) (di:complement) D90752 D90752 g1651577 Escherichia coli 562 -11534034 7500885649 mine (sr:e.coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli minicell (minb) locus encoding minc, mind, and mine genes, (required for the proper placement of the division septum) completecds.) (nt:mine protein) (le:1731) (re:1997) (di:direct) ECOMINB J03153 g146868 Escherichia coli 562 -11534034 235148 mine cell division topological specificity factor (fn:factor; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 106 of 400 of the completegenome.) (nt:f88; 100 pct identical to mine\_ecoli sw: p18198) (le:3146) (re:3412) (di:complement) AE000216 AE000216 g1787422 Escherichia coli 562 -11534034 5000691272 mine cell division topological specificity factor. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #242) (db:genpept) (de:escherichia coli genomic dna. (26.2 - 26.6 min).) (nt:orf\_id:o243#6; similar to swissprot accession) (le:10614) (re:10880) (di:complement) D90751 D90751 g1651573 Escherichia coli 562 -11534034 7502851986 mine cell division topological specificity factor. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #243) (db:genpept) (de:escherichia coli genomic dna. (26.3 - 26.7 min).) (nt:orf\_id:o243#6; similar to swissprot accession) (le:6170) (re:6436) (di:complement) D90752 D90752 g1651577 Escherichia coli 562 -11534034

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839560	9477	31633	381	126

Description

6500730177 mind:b1175 cell division inhibitor mind (gtcfc:12.8)  
(keggfc:14.2) (rileyfc:4.3.0) (db:gtc-escherichia coli) b1175 b1175  
Escherichia coli 562 -11534035 131331 mind cell division inhibitor  
mind:septum site-determining protein mind (cl:cell division inhibitor mind)  
(db:pir1.dat) (mp:26 min) CCECID B31877 Escherichia coli 562 -11534035  
223390 mind cell division inhibitor mind (sr:escherichia coli(strain:k12)  
dna, clone:kohara clone #242) (db:genpept-bct1) (de:escherichia coli genomic  
dna. (26.1 - 26.5 min).) (le:10884) (re:11696) (di:complement) D90751 D90751  
g1651574 Escherichia coli 562 -11534035 223393 mind cell division inhibitor  
mind (sr:escherichia coli(strain:k12) dna, clone:kohara clone #243)  
(db:genpept-bct1) (de:escherichia coli genomic dna. (26.2 - 26.6 min).)  
(le:6440) (re:7252) (di:complement) D90752 D90752 g1651578 Escherichia coli  
562 -11534035 7500953638 mind (sr:e.coli (strain k-12) dna)  
(db:genpept-bct1) (de:e.coli minicell (minb) locus encoding minc, mind, and  
mine genes, (required for the proper placement of the division septum)  
completecds.) (nt:mind protein) (le:915) (re:1727) (di:direct) ECOMINB  
J03153 g146867 Escherichia coli 562 -11534035 235147 mind cell division  
inhibitor:a membrane atpase (fn:enzyme; cell division) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 106 of 400 of the completegenome.)  
(nt:f270; 100 pct identical to mind\_ecoli sw: p18197) (le:3416) (re:4228)  
(di:complement) AE000216 AE000216 g1787423 Escherichia coli 562 -11534035  
5000691273 mind cell division inhibitor mind. (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #242) (db:genpept) (de:escherichia  
coli genomic dna. (26.2 - 26.6 min).) (nt:orf\_id:o243#7; similar to pir  
accession number) (le:10884) (re:11696) (di:complement) D90751 D90751  
g1651574 Escherichia coli 562 -11534035 7502851987 mind cell division  
inhibitor mind. (sr:escherichia coli(strain:k12) dna, clone:kohara clone  
#243) (db:genpept) (de:escherichia coli genomic dna. (26.3 - 26.7 min).)  
(nt:orf\_id:o243#7; similar to pir accession number) (le:6440) (re:7252)  
(di:complement) D90752 D90752 g1651578 Escherichia coli 562 -11534035

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839561	9478	31634	318	105

# Description

6500730178 minc:b1176 cell division inhibitor minc (gtcfc:12.8)  
(keggfc:14.2) (rileyfc:4.3.0) (db:gtc-escherichia coli) b1176 b1176  
Escherichia coli 562 -11534036 83729 minc (de:cell division inhibitor minc)  
(db:swissprot) MINC\_ECOLI P18196 ESCHERICHIA COLI 562 -11534036 131330 minc  
cell division inhibitor minc (cl:cell division inhibitor minc) (db:pir1.dat)  
(mp:26 min) CEECIC A31877 Escherichia coli 562 -11534036 223391 minc cell  
division inhibitor minc (sr:escherichia coli(strain:k12) dna, clone:kohara  
clone #242) (db:genpept-bct1) (de:escherichia coli genomic dna. (26.1 - 26.5  
min).) (le:11720) (re:12415) (di:complement) D90751 D90751 g1651575  
Escherichia coli 562 -11534036 223394 minc cell division inhibitor minc  
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #243)  
(db:genpept-bct1) (de:escherichia coli genomic dna. (26.2 - 26.6 min).)  
(le:7276) (re:7971) (di:complement) D90752 D90752 g1651579 Escherichia coli  
562 -11534036 7500885639 minc (sr:e.coli (strain k-12) dna)  
(db:genpept-bct1) (de:e.coli minicell (minb) locus encoding minc, mind, and  
mine genes, (required for the proper placement of the division septum)  
completecds.) (nt:minc protein) (le:196) (re:891) (di:direct) ECOMINB J03153  
g146866 Escherichia coli 562 -11534036 235146 minc cell division  
inhibitor:inhibits ftsz ring (fn:factor; cell division) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 106 of 400 of the completegenome.)  
(nt:f231; 100 pct identical to minc\_ecoli sw: p18196) (le:4252) (re:4947)  
(di:complement) AE000216 AE000216 g1787424 Escherichia coli 562 -11534036  
5000691274 minc cell division inhibitor minc. (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #242) (db:genpept) (de:escherichia  
coli genomic dna. (26.2 - 26.6 min).) (nt:orf\_id:o243#8; similar to pir  
accession number) (le:11720) (re:12415) (di:complement) D90751 D90751  
g1651575 Escherichia coli 562 -11534036 7502851988 minc cell division  
inhibitor minc. (sr:escherichia coli(strain:k12) dna, clone:kohara clone  
#243) (db:genpept) (de:escherichia coli genomic dna. (26.3 - 26.7 min).)  
(nt:orf\_id:o243#8; similar to pir accession number) (le:7276) (re:7971)  
(di:complement) D90752 D90752 g1651579 Escherichia coli 562 -11534036

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839562	9479	31635	822	273

Description

6500730179 dicc:b1569 repressor protein of division inhibition gene dicb (gtcfc:12.8) (keggfc:14.2) (rileyfc:4.3.0) (db:gtc-escherichia coli) b1569 b1569 Escherichia coli 562 -11534037 300671 dicc (de:repressor protein of division inhibition gene dicb) (db:swissprot) DICC\_ECOLI P06965 ESCHERICHIA COLI 562 -11534037 131328 dicc cell division control protein dicc gene dicb repressor (cl:cell division control protein dicc) (db:pir1.dat) (mp:35 min) CEECDC A24328 Escherichia coli 562 -11534037 223952 dicc cell division control protein dicc (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #308(35.3-35.7 min.)) (nt:orf\_id:o309#1; similar to (pir accession number) (le:9587) (re:9817) (di:complement) D90799 D90799 g1742571 Escherichia coli 562 -11534037 300693 dicc cell division control protein dicc (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #309(35.4-35.7 min.)) (nt:orf\_id:o309#1; similar to (pir accession number) (le:6363) (re:6593) (di:complement) D90800 D90800 g1742594 Escherichia coli 562 -11534037 5000691275 (db:genpept-bct1) (de:e. coli genes dica, dicb, dicc and dicf.) (nt:dicc polypeptide) (le:39) (re:269) (di:complement) ECDICABC X07465 g41277 Escherichia coli 562 -11534037 232678 dicc regulator of dicb (fn:regulator; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 143 of 400 of the completegenome.) (nt:f76; 100 pct identical to dicc\_ecoli sw: p06965; cg) (le:5372) (re:5602) (di:complement) AE000253 AE000253 g1787852 Escherichia coli 562 -11534037 68649 dicc (de:repressor protein of division inhibition gene dicb) (db:swissprot) DICC\_ECOLI P06965 ESCHERICHIA COLI 562 -11534037 223974 dicc cell division control protein dicc (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #309(35.4-35.7 min.)) (nt:orf\_id:o309#1; similar to (pir accession number) (le:6363) (re:6593) (di:complement) D90800 D90800 g1742594 Escherichia coli 562 -11534037

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839563	9480	31636	363	120

# Description

6500730180 dica:b1570 repressor protein of division inhibition gene dicb (gtcfc:12.8) (keggfc:14.2) (rileyfc:4.3.0) (db:gtc-escherichia coli) b1570 b1570 Escherichia coli 562 -11534038 300672 dica (de:repressor protein of division inhibition gene dicb) (db:swissprot) DICA\_ECOLI P06966 ESCHERICHIA COLI 562 -11534038 131547 dica cell division control protein dica gene dicb repressor (cl:dica protein) (db:pir1.dat) (mp:35 min) BVEFDA S05260 Escherichia coli 562 -11534038 223953 dica dica protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #308(35.3-35.7 min.)) (nt:orf\_id:o309#2; similar to (pir accession number) (le:9901) (re:10308) (di:direct) D90799 D90799 g1742572 Escherichia coli 562 -11534038 300694 dica dica protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #309(35.4-35.7 min.)) (nt:orf\_id:o309#2; similar to (pir accession number) (le:6677) (re:7084) (di:direct) D90800 D90800 g1742595 Escherichia coli 562 -11534038 5000691276 (db:genpept-bct1) (de:e. coli genes dica, dicb, dicc and dicf.) (nt:dica polypeptide) (le:353) (re:760) (di:direct) ECDICABC X07465 g41278 Escherichia coli 562 -11534038 232679 dica regulator of dicb (fn:regulator; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 143 of 400 of the completegenome.) (nt:o135; 100 pct identical to dica\_ecoli sw: p06966;) (le:5686) (re:6093) (di:direct) AE000253 AE000253 g1787853 Escherichia coli 562 -11534038 68647 dica (de:repressor protein of division inhibition gene dicb) (db:swissprot) DICA\_ECOLI P06966 ESCHERICHIA COLI 562 -11534038 223975 dica dica protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #309(35.4-35.7 min.)) (nt:orf\_id:o309#2; similar to (pir accession number) (le:6677) (re:7084) (di:direct) D90800 D90800 g1742595 Escherichia coli 562 -11534038



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839578	9481	31637	429	142

Description

6500730181 dicb:b1575 division inhibition protein dicb (gtcfc:12.8)  
(keggfc:14.2) (rileyfc:4.3.0) (db:gtc-escherichia coli) b1575 b1575  
Escherichia coli 562 -11534039 68648 dicb (de:division inhibition protein  
dicb) (db:swissprot) DICB\_ECOLI P09557 ESCHERICHIA COLI 562 -11534039  
7000685049 dicb cell division inhibitor dicb (cl:cell division inhibitor  
dicb) (db:pir1.dat) (mp:35 min) CEECDB A64913 Escherichia coli 562 -11534039  
223957 dicb division inhibition protein dicb. (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #308(35.3-35.7 min..))  
(nt:orf\_id:o309#6; similar to (swissprot accession) (le:11576) (re:11764)  
(di:direct) D90799 D90799 g1742576 Escherichia coli 562 -11534039 300698  
dicb division inhibition protein dicb. (sr:escherichia coli (strain:k12)  
dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic  
dna, kohara clone #309(35.4-35.7 min..)) (nt:orf\_id:o309#6; similar to  
(swissprot accession) (le:8352) (re:8540) (di:direct) D90800 D90800 g1742599  
Escherichia coli 562 -11534039 300676 dicb inhibition of cell division  
(fn:regulator; cell division) (db:genpept-bct2) (de:escherichia coli k-12  
mg1655 section 143 of 400 of the completegenome.) (nt:o62; 98 pct identical  
to dicb\_ecoli sw: p09557; cg) (le:7361) (re:7549) (di:direct) AE000253  
AE000253 g1787857 Escherichia coli 562 -11534039 223979 dicb division  
inhibition protein dicb. (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #309(35.4-35.7 min..)) (nt:orf\_id:o309#6; similar to (swissprot  
accession) (le:8352) (re:8540) (di:direct) D90800 D90800 g1742599  
Escherichia coli 562 -11534039 5000691277 (de:(ecoli\_1534) (pn:inhibition  
of cell division) (gn:dicb) (gtcfc:12.8) (ec:) (dicb\_ecoli) (keggfc:11.2)  
(rileyfc:4.3.0) (db:gtc-escherichia coli)) ECOLI\_1534 ECOLI\_1534 Escherichia  
coli 562 10119705

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839593	9482	31638	801	266

Description

6500730182 sdia:b1916 regulatory protein:sdia regulatory protein (gtcfc:12.8) (keggfc:14.2) (rileyfc:4.3.0) (db:gtc-escherichia coli) b1916 b1916 Escherichia coli 562 -11534040 98271 sdia (de:sdia regulatory protein) (db:swissprot) SDIA\_ECOLI P07026 ESCHERICHIA COLI 562 -11534040 7000686581 sdia sdia regulatory protein (cl:sdia regulatory protein) (db:pir1.dat) (mp:68 min) QQECU1 A64955 Escherichia coli 562 -11534040 224419 sdia sdia regulatory protein. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #341(42.7-43.1 min.)) (nt:orf\_id:o341#13; similar to (swissprot accession) (le:12640) (re:13362) (di:complement) D90832 D90832 g1736575 Escherichia coli 562 -11534040 301059 sdia transcriptional regulator of ftsqaz gene (fn:regulator; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 174 of 400 of the completegenome.) (nt:f240; 95 pct identical (1 gap) to sdia\_ecoli) (le:8138) (re:8860) (di:complement) AE000284 AE000284 g1788224 Escherichia coli 562 -11534040 5000691278 (de:(ecoli\_1870) (pn:regulator of transcription of ftsqaz gene cluster) (gn:sdia) (gtcfc:12.8) (ec:) (sdia\_ecoli) (keggfc:11.2) (rileyfc:4.3.0) (db:gtc-escherichia coli)) ECOLI\_1870 ECOLI\_1870 Escherichia coli 562 10119908

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839602	9483	31639	288	95

Description

6500730183 tolcb:mtcb:muka:refi:b3035 tolcb:outer membrane protein tolcb precursor (gtcfc:12.8:11.3) (keggfc:14.2) (rileyfc:4.3.0) (db:gtc-escherichia coli) b3035 b3035 Escherichia coli 562 -11534041 7000688976 tolcb outer membrane protein tolcb precursor (cl:outer membrane protein tolcb) (db:pir1.dat) (mp:66 min) MMECTC A65091 Escherichia coli 562 -11534041 7500953618 tolcb (fn:specific tolerance to colicin e1; expression of) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:cg site no. 97; alternate names cole1-i, mtcb,) (le:132497) (re:133984) (di:direct) ECU28377 U28377 g882565 Escherichia coli 562 -11534041 239249 tolcb outer membrane channel:specific tolerance to (fn:putative membrane; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 275 of 400 of the completegenome.) (nt:o495; 99 pct identical to tolcb\_ecoli sw: p02930; cg) (le:5769) (re:7256) (di:direct) AE000385 AE000385 g1789413 Escherichia coli 562 -11534041 5000691279 (de:(ecoli\_2958) (pn:outer membrane channel; specific tolerance to colicin e1; segregation of daughter chromosomes) (gn:tolcb) (gtcfc:12.8) (ec:) (tolcb\_ecoli) (keggfc:11.2) (rileyfc:4.3.0) (db:gtc-escherichia coli)) ECOLI\_2958 ECOLI\_2958 Escherichia coli 562 10123955

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839606	9484	31640	261	86

Description

6500730184 ftsj:mrsf:b3179 cell division protein ftsj (gtcfc:12.8)  
(keggfc:14.2) (rileyfc:4.3.0) (db:gtc-escherichia coli) b3179 b3179  
Escherichia coli 562 -11534042 72453 ftsj:mrsf (de:cell division protein  
ftsj) (db:swissprot) FTSJ\_ECOLI P28692 ESCHERICHIA COLI 562 -11534042  
163086 ftsj cell division protein ftsj (cl:cell division protein j)  
(db:pir2.dat) S35108 S35108 Escherichia coli 562 -11534042 236416 ftsj  
(sr:escherichia coli (sub\_strain w3110, strain k-12) dna) (db:genpept-bct1)  
(de:e.coli ftsh and ftsj genes, complete cds.) (le:138) (re:767) (di:direct)  
ECOFTSHJA M83138 g146027 Escherichia coli 562 -11534042 267284 ftsj  
(db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to  
76.0 minutes.) (le:107787) (re:108416) (di:complement) ECOUW67 U18997  
g606117 Escherichia coli 562 -11534042 7500881831 mrsf regulatory protein  
(db:genpept-bct1) (de:escherichia coli k12 ampicillin-binding protein  
(dacb),transcription elongation factor (grea), regulatory protein  
(mrsf),atp-binding protein (mrsc), dihydropteroate synthase,  
regulatoryprotein (mrsc), and membrane protein genes, c... U01376 U01376  
g746400 Escherichia coli 562 -11534042 234405 ftsj cell division protein  
(fn:phenotype; cell division) (db:genpept-bct2) (de:escherichia coli k-12  
mg1655 section 288 of 400 of the completegenome.) (nt:f209; 100 pct  
identical amino acid sequence and) (le:8896) (re:9525) (di:complement)  
AE000398 AE000398 g1789569 Escherichia coli 562 -11534042 5000691280  
(de:(ecoli\_3101) (pn:cell division protein) (gn:ftsj) (gtcfc:12.8) (ec:)  
(ftsj\_ecoli) (keggfc:11.2) (rileyfc:4.3.0) (db:gtc-escherichia coli))  
ECOLI\_3101 ECOLI\_3101 Escherichia coli 562 10015004

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839622	9485	31641	420	140

Description

6500730185 cafa:b3247 cytoplasmic axial filament protein (gtcfc:12.8) (keggfc:14.2) (rileyfc:4.3.0) (db:gtc-escherichia coli) b3247 b3247 Escherichia coli 562 -11534043 7000690868 cafa cytosolic axial filament protein cafa (db:pir2.dat) A65117 A65117 Escherichia coli 562 -11534043 7500959719 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf\_f495; orff of ecmred, uses 2nd start) (le:177071) (re:178558) (di:complement) ECOUW67 U18997 g606187 Escherichia coli 562 -11534043 236486 cafa bundles of cytoplasmic filaments (fn:structural component; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 294 of 400 of the completegenome.) (nt:f495; f495; orff of ecmred, uses 2nd start; 100 pct) (le:64) (re:1551) (di:complement) AE000404 AE000404 g1789645 Escherichia coli 562 -11534043 5000691281 (de:(ecoli\_3171) (pn:bundles of cytoplasmic filaments) (gn:cafa) (gtcfc:12.8) (ec:) (cafa\_ecoli) (keggfc:11.2) (rileyfc:4.3.0) (db:gtc-escherichia coli)) ECOLI\_3171 ECOLI\_3171 Escherichia coli 562 10123998

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839623	9486	31642	423	140

Description

GTC ORF with score 128 to: (fn:mitochondrial matrix -associated,) (sr:human) (db:genpept-pri2) (de:homo sapiens dna from chromosome 19p13.2 cosmids r31240, r30272 andr28549 containing the ek1f, gcdh, crtc, and rad23a genes, genomicsequence.) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839625	9487	31643	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839636	9488	31644	576	191

Description

6500730186 fic:b3361 cell filamentation protein (gtcfc:12.8) (keggfc:14.2) (rileyfc:4.3.0) (db:gtc-escherichia coli) b3361 b3361 Escherichia coli 562 -11534044 71673 fic (de:cell filamentation protein fic) (db:swissprot) FIC\_ECOLI P20605 ESCHERICHIA COLI 562 -11534044 7000685248 fic cell filamentation protein fic (db:pir2.dat) (mp:74 min) D65130 D65130 Escherichia coli 562 -11534044 7500881455 fic (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 18361; filamentation in presence of) (le:271608) (re:272210) (di:complement) ECOUW67 U18997 g606295 Escherichia coli 562 -11534044 236594 fic induced in stationary phase:recognized by rpos (fn:phenotype; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 302 of 400 of the completegenome.) (nt:f200; cg site no. 18361; filamentation in) (le:1965) (re:2567) (di:complement) AE000412 AE000412 g1789761 Escherichia coli 562 -11534044 5000691282 (de:(ecoli\_3279) (pn:induced in stationary phase, recognized by rpos, affects cell division) (gn:fic) (gtcfc:12.8) (ec:) (fic\_ecoli) (keggfc:11.2) (rileyfc:4.3.0) (db:gtc-escherichia coli)) ECOLI\_3279 ECOLI\_3279 Escherichia coli 562 10014231

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839638	9489	31645	876	291

Description

6500730187 ftsx:ftss:b3462 cell division protein ftsx (gtcfc:12.8) (keggfc:14.2) (rileyfc:4.3.0) (db:gtc-escherichia coli) b3462 b3462 Escherichia coli 562 -11534045 236697 ftsx:ftss (de:cell division protein ftsx) (db:swissprot) FTSX\_ECOLI P10122 ESCHERICHIA COLI 562 -11534045 131338 ftsx cell division protein ftsx (cl:cell division protein ftsx) (db:pir1.dat) (mp:76 min) CEECFX S03132 Escherichia coli 562 -11534045 5000691283 (db:genpept-bct1) (de:e.coli ftsyex genes for cell division control.) (nt:orf 3 (aa 1-352); 38 kd (put. ftsx)) (le:3304) (re:4362) (di:direct) ECFTSYEX X04398 g41500 Escherichia coli 562 -11534045 7500881850 ftsx (fn:cell division) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 18298; f352; upstream starts for o357) (le:15290) (re:16348) (di:com... ECOUW76 U00039 g466598 Escherichia coli 562 -11534045 232928 ftsx cell division membrane protein (fn:membrane; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 312 of 400 of the completegenome.) (nt:f352; 100 pct identical to ftsx\_ecoli sw: p10122;) (le:3148) (re:4206) (di:complement) AE000422 AE000422 g1789872 Escherichia coli 562 -11534045 72469 ftsx:ftss (de:cell division protein ftsx) (db:swissprot) FTSX\_ECOLI P10122 ESCHERICHIA COLI 562 -11534045

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839652	9490	31646	1218	405

Description

6500730188 ftse:b3463 cell division atp-binding protein ftse (gtcfc:12.8) (keggfc:14.2) (rileyfc:4.3.0) (db:gtc-escherichia coli) b3463 b3463 Escherichia coli 562 -11534046 236698 ftse (de:cell division atp-binding protein ftse) (db:swissprot) FTSE\_ECOLI P10115 ESCHERICHIA COLI 562 -11534046 130727 ftse cell division atp-binding protein ftse (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir1.dat) (mp:76 min) CEECFE S03131 Escherichia coli 562 -11534046 5000691284 (db:genpept-bct1) (de:e.coli ftsyex genes for cell division control.) (nt:orf 2 (aa 1-222); 25 kd (put. ftse)) (le:2643) (re:3311) (di:direct) ECFTSYEX X04398 g41499 Escherichia coli 562 -11534046 7500881814 ftse (fn:cell division) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 736) (le:16341) (re:17009) (di:complement) ECOUW76 U00039 g466599 Escherichia coli 562 -11534046 232927 ftse atp-binding component of a membrane-associated (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 312 of 400 of the completegenome.) (nt:f222; 100 pct identical to ftse\_ecoli sw: p10115;) (le:4199) (re:4867) (di:complement) AE000422 AE000422 g1789873 Escherichia coli 562 -11534046 72444 ftse (de:cell division atp-binding protein ftse) (db:swissprot) FTSE\_ECOLI P10115 ESCHERICHIA COLI 562 -11534046

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839660	9491	31647	1053	351

Description

6500730189 ftsy:b3464 cell division protein ftsy (gtcfc:12.8) (keggfc:14.2) (rileyfc:4.3.0) (db:gtc-escherichia coli) b3464 b3464 Escherichia coli 562 -11534047 236699 ftsy (de:cell division protein ftsy) (db:swissprot) FTSY\_ECOLI P10121 ESCHERICHIA COLI 562 -11534047 131339 ftsy cell division protein ftsy (cl:cell division protein ftsy) (db:pir1.dat) (mp:76 min) CEECFY S03130 Escherichia coli 562 -11534047 5000691285 (db:genpept-bct1) (de:e.coli ftsyex genes for cell division control.) (nt:orf 1 (aa 1-497); 48 kd (put. ftsy)) (le:1147) (re:2640) (di:direct) ECFTSYEX X04398 g41498 Escherichia coli 562 -11534047 7500881852 ftsy (fn:cell division) (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 18295) (le:17012) (re:18505) (di:complement) ECOUW76 U00039 g466600 Escherichia coli 562 -11534047 232926 ftsy cell division membrane protein (fn:membrane; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 312 of 400 of the completegenome.) (nt:f497; 100 pct identical to ftsy\_ecoli sw: p10121;) (le:4870) (re:6363) (di:complement) AE000422 AE000422 g1789874 Escherichia coli 562 -11534047 72472 ftsy (de:cell division protein ftsy) (db:swissprot) FTSY\_ECOLI P10121 ESCHERICHIA COLI 562 -11534047

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839664	9492	31648	285	94

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839672	9493	31649	738	245

Description

6500730190 ftsn:msga:b3933 cell division protein ftsn (gtcfc:12.8)  
(keggfc:14.2) (rileyfc:4.3.0) (db:gtc-escherichia coli) b3933 b3933  
Escherichia coli 562 -11534048 164667 ftsn cell division protein  
ftsn:suppressor protein (db:pir2.dat) S40876 S40876 Escherichia coli 562  
-11534048 7500959708 msga suppressor protein (sr:escherichia coli  
(sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e.  
coli chromosomal region from 87.2 to 89.2 minutes.) (nt:suppressor specific  
for grpe280 and ftsa12 ts) (le:84013) (re:84972) (di:complement) ECOUW87  
L19201 g305036 Escherichia coli 562 -11534048 237150 ftsn essential cell  
division protein (fn:phenotype; cell division) (db:genpept-bct2)  
(de:escherichia coli k-12 mg1655 section 357 of 400 of the completegenome.)  
(nt:f319; 99 pct identical amino acid sequence and) (le:9506) (re:10465)  
(di:complement) AE000467 AE000467 g1790368 Escherichia coli 562 -11534048  
5000691286 (de:(ecoli\_3831) (pn:essential cell division protein) (gn:ftsn)  
(gtcfc:12.8) (ec:) (ftsn\_ecoli) (keggfc:11.2) (rileyfc:4.3.0)  
(db:gtc-escherichia coli)) ECOLI\_3831 ECOLI\_3831 Escherichia coli 562  
10087417

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839677	9494	31650	525	174

Description

6500730191 trg:b1421 methyl-accepting chemotaxis protein iii:mcp-iii:ribose and galactose chemoreceptor protein (gtcfc:12.9) (keggfc:12.2) (rileyfc:4.4.0) (db:gtc-escherichia coli) b1421 b1421 Escherichia coli 562 -11534049 83197 trg (de:galactose chemoreceptor protein)) (db:swissprot) MCP3\_ECOLI P05704 ESCHERICHIA COLI 562 -11534049 7000685800 trg methyl-accepting chemotaxis protein iii:mcp-iii protein:ribose and galactose chemoreceptor protein (cl:methyl-accepting chemotaxis protein) (db:pir1.dat) (mp:31 min) QREC3M H64893 Escherichia coli 562 -11534049 223719 trg methyl-accepting chemotaxis protein iii (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #270(32.0-32.3 min.)) (nt:orf\_id:o270#12; similar to (swissprot accession) (le:8141) (re:9781) (di:direct) D90781 D90781 g1742320 Escherichia coli 562 -11534049 300494 trg methyl-accepting chemotaxis protein iii (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #271(32.1-32.5 min.)) (nt:orf\_id:o270#12; similar to (swissprot accession) (le:880) (re:2520) (di:direct) D90782 D90782 g1742331 Escherichia coli 562 -11534049 300484 trg methyl-accepting chemotaxis protein iii:ribose (fn:regulator; chemotaxis and mobility) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 129 of 400 of the completgenome.) (nt:o546; residues 1-534 are 100 pct identical) (le:5401) (re:7041) (di:direct) AE000239 AE000239 g1787690 Escherichia coli 562 -11534049 223729 trg methyl-accepting chemotaxis protein iii (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #271(32.1-32.5 min.)) (nt:orf\_id:o270#12; similar to (swissprot accession) (le:880) (re:2520) (di:direct) D90782 D90782 g1742331 Escherichia coli 562 -11534049 5000691287 (de:(ecoli\_1381) (pn:methyl-accepting chemotaxis protein iii, ribose receptor, sensory transducer for ribose) (gn:trg) (gtcfc:12.9) (ec:) (mcp3\_ecoli) (keggfc:11.2) (rileyfc:4.4.0) (db:gtc-escherichia coli)) ECOLI\_1381 ECOLI\_1381 Escherichia coli 562 10119599

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839678	9495	31651	858	286

Description

6500730192 chez:b1881 chemotaxis protein chez (gtcfc:12.9) (keggfc:12.2) (rileyfc:4.4.0) (db:gtc-escherichia coli) b1881 b1881 Escherichia coli 562 -11534050 64246 chez (de:chemotaxis protein chez) (db:swissprot) CHEZ\_ECOLI P07366 ESCHERICHIA COLI 562 -11534050 130896 chez chemotaxis protein chez (cl:chemotaxis chez protein) (db:pir1.dat) (mp:42 min) QRECCZ F25195 Escherichia coli 562 -11534050 224380 chez chemotaxis protein chez (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #338(42.1-42.5 min.)) (nt:orf\_id:o338#3; similar to (pir accession number) (le:10760) (re:11404) (di:complement) D90830 D90830 g1736534 Escherichia coli 562 -11534050 301020 chez chemotactic response:chey protein phosphatase (fn:regulator; chemotaxis and mobility) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 172 of 400 of the completegenome.) (nt:f214; 100 pct identical to chez\_ecoli sw: p07366;) (le:131) (re:775) (di:complement) AE000282 AE000282 g1788190 Escherichia coli 562 -11534050 5000691288 (de:(ecoli\_1838) (pn:chemotactic response; chey protein phosphatase; antagonist of chey as switch regulator) (gn:chez) (gtcfc:12.9) (ec:) (chez\_ecoli) (keggfc:11.2) (rileyfc:4.4.0) (db:gtc-escherichia coli)) ECOLI\_1838 ECOLI\_1838 Escherichia coli 562 10006910

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839686	9496	31652	402	133

Description

6500730193 chey:b1882 chemotaxis protein chey (gtcfc:12.9) (keggfc:12.2) (rileyfc:4.4.0) (db:gtc-escherichia coli) b1882 b1882 Escherichia coli 562 -11534051 130884 chey chemotaxis protein chey (cl:chemotaxis chey protein:response regulator homology) (db:pir1.dat) (mp:42 min) QRECCY E25195 Escherichia coli 562 -11534051 224381 chey chemotaxis protein chey (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #338(42.1-42.5 min.)) (nt:orf\_id:o338#4; similar to (pir accession number) (le:11415) (re:11804) (di:complement) D90830 D90830 g1736535 Escherichia coli 562 -11534051 301021 (sr:e. coli dna, genomic library of clarket carbon, clones plc128) (db:genpept-bct1) (de:e. coli chey gene with 3' end of cheb and 5' end of chez genes.) (nt:chey protein (chey)) (le:38) (re:427) (di:direct) ECOCHey K02175 g145534 Escherichia coli 562 -11534051 233986 chey chemotaxis regulator transmits chemoreceptor (fn:regulator; chemotaxis and mobility) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 172 of 400 of the completegenome.) (nt:f129; 100 pct identical to chey\_ecoli sw: p06143;) (le:786) (re:1175) (di:complement) AE000282 AE000282 g1788191 Escherichia coli 562 -11534051 5000691289 (de:(ecoli\_1839) (pn:chemotaxis protein transmits chemoreceptor signals to flagelllar motors) (gn:chey) (gtcfc:12.9) (ec:) (chey\_ecoli) (keggfc:11.2) (rileyfc:4.4.0) (db:gtc-escherichia coli)) ECOLI\_1839 ECOLI\_1839 Escherichia coli 562 10067981

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839690	9497	31653	807	268

Description

6500730194 cheb:b1883 protein-glutamate methylesterase (gtcfc:12.9)  
(ec:3.1.1.61) (keggfc:12.2) (rileyfc:4.4.0) (db:gtc-escherichia coli) b1883  
b1883 Escherichia coli 562 -11534052 64230 cheb (ec:3.1.1.61)  
(de:protein-glutamate methylesterase,) (db:swissprot) CHEB\_ECOLI P07330  
ESCHERICHIA COLI 562 -11534052 124254 cheb protein-glutamate  
methylesterase::chemotaxis-specific methylesterase (cl:protein-glutamate  
methylesterase:response regulator homology) (ec:3.1.1.61) (db:pir1.dat)  
(mp:42 min) XYECEB D25195 Escherichia coli 562 -11534052 224382 cheb  
protein-glutamate methylesterase ec 3.1.1.61 . (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #338(42.1-42.5 min..))  
(nt:orf\_id:o338#5; similar to (swissprot accession) (le:11819) (re:12868)  
(di:complement) D90830 D90830 g1736536 Escherichia coli 562 -11534052  
301022 cheb response regulator for chemotaxis chea sensor (fn:enzyme;  
chemotaxis and mobility) (db:genpept-bct2) (ec:3.1.1.61) (de:escherichia  
coli k-12 mg1655 section 172 of 400 of the completegenome.) (nt:f349; 99 pct  
identical to cheb\_ecoli sw: p07330; cg) (le:1190) (re:2239) (di:complement)  
AE000282 AE000282 g1788192 Escherichia coli 562 -11534052 5000691290  
(de:(ecoli\_1840) (pn:response regulator for chemotaxis:chea sensor; protein  
methylesterase) (gn:cheb) (gtcfc:12.9) (ec:3.1.1.61) (cheb\_ecoli)  
(keggfc:11.1) (rileyfc:4.4.0) (db:gtc-escherichia coli)) ECOLI\_1840  
ECOLI\_1840 Escherichia coli 562 10066061

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839695	9498	31654	390	129

# Description

6500730195 cher:chex:b1884 chemotaxis protein methyltransferase (gtcfc:12.9) (ec:2.1.1.80) (keggfc:12.2) (rileyfc:4.4.0) (db:gtc-escherichia coli) b1884 b1884 Escherichia coli 562 -11534053 64235 cher:chex (ec:2.1.1.80) (de:chemotaxis protein methyltransferase,) (db:swissprot) CHER\_ECOLI P07364 ESCHERICHIA COLI 562 -11534053 7000684808 cher protein-glutamate o-methyltransferase::methyl-accepting chemotaxis protein o-methyltransferase:protein methylase ii:protein-glutamate methyltransferase (cl:protein-glutamate o-methyltransferase:protein-glutamate o-methyltransferase homology) (ec:2.1.1.80) (db:pir1.dat) (mp:42 min) XYECCR D64951 Escherichia coli 562 -11534053 224383 cher:chex chemotaxis protein methyltransferase ec (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #338(42.1-42.5 min.)) (nt:orf\_id:o338#6; similar to (swissprot accession) (le:12871) (re:13731) (di:complement) D90830 D90830 g1736537 Escherichia coli 562 -11534053 301023 cher response regulator for chemotaxis:protein (fn:enzyme; chemotaxis and mobility) (db:genpept-bct2) (ec:2.1.1.80) (de:escherichia coli k-12 mg1655 section 172 of 400 of the completegenome.) (nt:f286; 100 pct identical to cher\_ecoli sw: p07364;) (le:2242) (re:3102) (di:complement) AE000282 AE000282 g1788193 Escherichia coli 562 -11534053 5000691291 (de:(ecoli\_1841) (pn:response regulator for chemotaxis; protein glutamate methyltransferase) (gn:cher) (gtcfc:12.9) (ec:2.1.1.80) (cher\_ecoli) (keggfc:11.1) (rileyfc:4.4.0) (db:gtc-escherichia coli)) ECOLI\_1841 ECOLI\_1841 Escherichia coli 562 10119892

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839703	9499	31655	540	179

Description

6500730196 tap:b1885 methyl-accepting chemotaxis protein iv:mcp-iv:dipeptide chemoreceptor protein (gtcfc:12.9) (keggfc:12.2) (rileyfc:4.4.0) (db:gtc-escherichia coli) b1885 b1885 Escherichia coli 562 -11534054 83200 tap (de:chemoreceptor protein)) (db:swissprot) MCP4\_ECOLI P07018 ESCHERICHIA COLI 562 -11534054 7000685801 tap methyl-accepting chemotaxis protein ii:mcp-ii (cl:methyl-accepting chemotaxis protein) (db:pir1.dat) (mp:42 min) QRECM2 E64951 Escherichia coli 562 -11534054 224384 tap methyl-accepting chemotaxis protein iv mcp-iv (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #338(42.1-42.5 min.)) (nt:orf\_id:o338#7; similar to (swissprot accession) (le:13750) (re:15351) (di:complement) D90830 D90830 g1736538 Escherichia coli 562 -11534054 301029 tap methyl-accepting chemotaxis protein iv mcp-iv (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #339(42.4-42.8 min.)) (nt:orf\_id:o338#7; similar to (swissprot accession) (le:700) (re:2301) (di:complement) D90831 D90831 g1736544 Escherichia coli 562 -11534054 301024 tap methyl-accepting chemotaxis protein iv:peptide (fn:regulator; chemotaxis and mobility) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 172 of 400 of the completegenome.) (nt:f533; 99 pct identical to mcp4\_ecoli sw: p07018) (le:3121) (re:4722) (di:complement) AE000282 AE000282 g1788194 Escherichia coli 562 -11534054 224389 tap methyl-accepting chemotaxis protein iv mcp-iv (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #339(42.4-42.8 min.)) (nt:orf\_id:o338#7; similar to (swissprot accession) (le:700) (re:2301) (di:complement) D90831 D90831 g1736544 Escherichia coli 562 -11534054 5000691292 (de:(ecoli\_1842) (pn:methyl-accepting chemotaxis protein iv, peptide receptor, dipeptide sensory transducer) (gn:tap) (gtcfc:12.9) (ec:)(mcp4\_ecoli) (keggfc:11.2) (rileyfc:4.4.0) (db:gtc-escherichia coli)) ECOLI\_1842 ECOLI\_1842 Escherichia coli 562 10119893

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839717	9500	31656	297	98

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839718	9501	31657	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839722	9502	31658	333	110

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839730	9503	31659	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839732	9504	31660	417	138

Description

GTC ORF with score 116 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839733	9505	31661	507	168

#### Description

6500730197 tar:chem:b1886 methyl-accepting chemotaxis protein  
ii:mcp-ii:aspartate chemoreceptor protein (gtcfc:12.9) (keggfc:12.2)  
(rileyfc:4.4.0) (db:gtc-escherichia coli) b1886 b1886 Escherichia coli 562  
-11534055 83190 tar:chem (de:chemoreceptor protein)) (db:swissprot)  
MCP2\_ECOLI P07017 ESCHERICHIA COLI 562 -11534055 7000685798 tar aspartate  
chemoreceptor protein:methyl-accepting chemotaxis protein iv mcp-iv  
(cl:methyl-accepting chemotaxis protein) (db:pir1.dat) (mp:42 min) QRECM4  
F64951 Escherichia coli 562 -11534055 224385 tar:chem methyl-accepting  
chemotaxis protein ii mcp-ii (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #338(42.1-42.5 min.)) (nt:orf\_id:o338#8; similar to (swissprot  
accession) (le:15397) (re:17058) (di:complement) D90830 D90830 g1736539  
Escherichia coli 562 -11534055 301030 tar:chem methyl-accepting chemotaxis  
protein ii mcp-ii (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara  
lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#339(42.4-42.8 min.)) (nt:orf\_id:o338#8; similar to (swissprot accession)  
(le:2347) (re:4008) (di:complement) D90831 D90831 g1736545 Escherichia coli  
562 -11534055 301025 tar methyl-accepting chemotaxis protein ii  
(fn:regulator; chemotaxis and mobility) (db:genpept-bct2) (de:escherichia  
coli k-12 mg1655 section 172 of 400 of the completegenome.) (nt:f553; 99 pct  
identical to mcp2\_ecoli sw: p07017; cg) (le:4768) (re:6429) (di:complement)  
AE000282 AE000282 g1788195 Escherichia coli 562 -11534055 224390 tar:chem  
methyl-accepting chemotaxis protein ii mcp-ii (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #339(42.4-42.8 min.))  
(nt:orf\_id:o338#8; similar to (swissprot accession) (le:2347) (re:4008)  
(di:complement) D90831 D90831 g1736545 Escherichia coli 562 -11534055  
5000691293 (de:(ecoli\_1843) (pn:methyl-accepting chemotaxis protein ii,  
chemoreceptor for aspartate, aspartate sensory transducer) (gn:tar)  
(gtcfc:12.9) (ec:) (mcp2\_ecoli) (keggfc:11.2) (rileyfc:4.4.0)  
(db:gtc-escherichia coli)) ECOLI\_1843 ECOLI\_1843 Escherichia coli 562  
10119894

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839739	9506	31662	1854	617

#### Description

GTC ORF with score 207 to: (fn:involved in production of the virulence  
factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide  
synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703)  
(re:1524:2083:2661:3353) (di:directjoin)



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839741	9507	31663	585	194

Description

6500730198 chew:b1887 purine binding chemotaxis protein:purine-binding chemotaxis protein (gtcfc:12.9) (keggfc:12.2) (rileyfc:4.4.0) (db:gtc-escherichia coli) b1887 b1887 Escherichia coli 562 -11534056 64240 chew (de:purine-binding chemotaxis protein) (db:swissprot) CHEW\_ECOLI P07365 ESCHERICHIA COLI 562 -11534056 130883 chew purine binding chemotaxis protein chew (cl:chemotaxis chew protein) (db:pir1.dat) (mp:42 min) QRECCW B25195 Escherichia coli 562 -11534056 224386 chew chemotaxis protein chew (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #338(42.1-42.5 min.)) (nt:orf\_id:o338#9; similar to (pir accession number) (le:17203) (re:17706) (di:complement) D90830 D90830 g1736540 Escherichia coli 562 -11534056 301031 chew chemotaxis protein chew (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #339(42.4-42.8 min.)) (nt:orf\_id:o338#9; similar to (pir accession number) (le:4153) (re:4656) (di:complement) D90831 D90831 g1736546 Escherichia coli 562 -11534056 301026 chew (sr:e.coli dna, clone pak108) (db:genpept-bct1) (de:e.coli chea gene (3' end) and chew gene, encoding chemotaxisproteins.) (nt:chew peptide) (le:701) (re:1204) (di:direct) ECOCHE1 M13462 g145520 Escherichia coli 562 -11534056 233974 chew positive regulator of chea protein activity (fn:regulator; chemotaxis and mobility) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 172 of 400 of the completegenome.) (nt:f167; 100 pct identical to chew\_ecoli sw: p07365;) (le:6574) (re:7077) (di:complement) AE000282 AE000282 g1788196 Escherichia coli 562 -11534056 224391 chew chemotaxis protein chew (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #339(42.4-42.8 min.)) (nt:orf\_id:o338#9; similar to (pir accession number) (le:4153) (re:4656) (di:complement) D90831 D90831 g1736546 Escherichia coli 562 -11534056 5000691294 (de:(ecoli\_1844) (pn:positive regulator of chea protein activity) (gn:chew) (gtcfc:12.9) (ec:) (chew\_ecoli) (keggfc:11.2) (rileyfc:4.4.0) (db:gtc-escherichia coli)) ECOLI\_1844 ECOLI\_1844 Escherichia coli 562 10006904

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839765	9508	31664	231	76

Description

6500730199 chea:b1888 chemotaxis protein chea (gtcfc:12.9) (ec:2.7.3.-) (keggfc:12.2) (rileyfc:4.4.0) (db:gtc-escherichia coli) b1888 b1888 Escherichia coli 562 -11534057 64226 chea (ec:2.7.3.-) (de:chemotaxis protein chea,) (db:swissprot) CHEA\_ECOLI P07363 ESCHERICHIA COLI 562 -11534057 7000684806 chea chemotaxis protein chea:histidine autokinase (cl:chemotaxis protein chea) (db:pir1.dat) (mp:42 min) QRECCS H64951 Escherichia coli 562 -11534057 224392 chea chemotaxis protein chea ec 2.7.3.-. (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #339(42.4-42.8 min.)) (nt:orf\_id:o339#1; similar to (swissprot accession) (le:4677) (re:6641) (di:complement) D90831 D90831 g1736547 Escherichia coli 562 -11534057 301032 chea sensory transducer kinase between chemo-signal (fn:enzyme; chemotaxis and mobility) (db:genpept-bct2) (ec:2.7.3.-) (de:escherichia coli k-12 mg1655 section 172 of 400 of the completegenome.) (nt:f654; 99 pct identical to chea\_ecoli sw: p07363) (le:7098) (re:9062) (di:complement) AE000282 AE000282 g1788197 Escherichia coli 562 -11534057 5000691295 (de:(ecoli\_1845) (pn:chemotaxis protein) (gn:chea) (gtcfc:12.9) (ec:2.7.3.-) (chea\_ecoli) (keggfc:11.1) (rileyfc:4.4.0) (db:gtc-escherichia coli)) ECOLI\_1845 ECOLI\_1845 Escherichia coli 562 10119897

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839766	9509	31665	648	215

Description

6500730200 motb:b1889 chemotaxis motb protein:motility protein b  
 (gtcfc:12.9) (keggfc:12.2) (rileyfc:4.4.0) (db:gtc-escherichia coli) b1889  
 b1889 Escherichia coli 562 -11534058 84047 motb (de:chemotaxis motb protein  
 (motility protein b)) (db:swissprot) MOTB\_ECOLI P09349 ESCHERICHIA COLI 562  
 -11534058 7000685864 motb chemotaxis protein motb:motility protein b  
 (cl:motb protein) (db:pir1.dat) (mp:42 min) QRECMB A64952 Escherichia coli  
 562 -11534058 224393 motb chemotaxis motb protein motility protein b .  
 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise)  
 (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #339(42.4-42.8  
 min.)) (nt:orf\_id:o339#2; similar to (swissprot accession) (le:6646)  
 (re:7572) (di:complement) D90831 D90831 g1736548 Escherichia coli 562  
 -11534058 301033 (sr:escherichia coli (strain cs520) dna library of clarke  
 and carbon) (db:genpept-bct1) (de:e. coli mocha promoter, mota and motb  
 genes encoding integralmembrane proteins, and start of chea gene.) (nt:motb  
 protein for chemotaxis) (le:1061) (re:1987) (d... ECOMOTAB J01652 g146883  
 Escherichia coli 562 -11534058 235163 motb enables flagellar motor  
 rotation:linking torque (fn:structural component; chemotaxis and mobility)  
 (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 172 of 400 of the  
 completegenome.) (nt:f308; 100 pct identical to motb\_ecoli sw: p09349;)  
 (le:9067) (re:9993) (di:complement) AE000282 AE000282 g1788198 Escherichia  
 coli 562 -11534058 5000691296 (de:(ecoli\_1846) (pn:enables flagellar motor  
 rotation, linking torque machinery to cell wall; no effect on switching)  
 (gn:motb) (gtcfc:12.9) (ec:) (motb\_ecoli) (keggfc:11.2) (rileyfc:4.4.0)  
 (db:gtc-escherichia coli)) ECOLI\_1846 ECOLI\_1846 Escherichia coli 562  
 10026249

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839780	9510	31666	474	157

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839794	9511	31667	834	277

Description

6500730201 mota:b1890 chemotaxis mota protein:motility protein a (gtcfc:12.9) (keggfc:12.2) (rileyfc:4.4.0) (db:gtc-escherichia coli) b1890 b1890 Escherichia coli 562 -11534059 84044 mota (de:chemotaxis mota protein (motility protein a)) (db:swissprot) MOTA\_ECOLI P09348 ESCHERICHIA COLI 562 -11534059 130897 mota chemotaxis protein mota:motility protein a (cl:mota protein) (db:pir1.dat) (mp:42 min) QRECMA A30279 Escherichia coli 562 -11534059 224394 mota chemotaxis protein mota (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #339(42.4-42.8 min..)) (nt:orf\_id:o339#3; similar to (pir accession number) (le:7569) (re:8456) (di:complement) D90831 D90831 g1736549 Escherichia coli 562 -11534059 301034 (sr:escherichia coli (strain cs520) dna library of clarke and carbon) (db:genpept-bct1) (de:e. coli mocha promoter, mota and motb genes encoding integralmembrane proteins, and start of chea gene.) (nt:mota protein for chemotaxis (gtg start codon)) (le:... ECOMOTAB J01652 g146882 Escherichia coli 562 -11534059 235162 mota proton conductor component of motor:no effect (fn:phenotype; chemotaxis and mobility) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 172 of 400 of the completegenome.) (nt:f295; 100 pct identical to mota\_ecoli sw: p09348;) (le:9990) (re:10877) (di:complement) AE000282 AE000282 g1788199 Escherichia coli 562 -11534059 5000691297 (de:(ecoli\_1847) (pn:proton conductor component of motor; no effect on switching) (gn:mota) (gtcfc:12.9) (ec:) (mota\_ecoli) (keggfc:11.2) (rileyfc:4.4.0) (db:gtc-escherichia coli)) ECOLI\_1847 ECOLI\_1847 Escherichia coli 562 10026246

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839808	9512	31668	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839813	9513	31669	1047	348

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839819	9514	31670	540	179

Description

6500730202 tsr:ched:b4355 methyl-accepting chemotaxis protein i:mcp-i:serine chemoreceptor protein (gtcfc:12.9) (keggfc:12.2) (rileyfc:4.4.0) (db:gtc-escherichia coli) b4355 b4355 Escherichia coli 562 -11534060 83183 tsr:ched (de:protein) (db:swissprot) MCP1\_ECOLI P02942 ESCHERICHIA COLI 562 -11534060 7000685797 tsr serine chemoreceptor protein:methyl-accepting chemotaxis protein i mcp-i (cl:methyl-accepting chemotaxis protein) (db:pir1.dat) (mp:99 min) QRECS E65250 Escherichia coli 562 -11534060 7500885384 tsr (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli tsr gene coding for methyl-accepting chemotaxis protein i,sensory transducer protein.) (nt:methyl-accepting chemotaxis protein i) (le:61) (re:1716) (di:direct) ECOTSR J01718 g148077 Escherichia coli 562 -11534060 236227 tsr methyl-accepting chemotaxis protein i:serine (fn:regulator; chemotaxis and mobility) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 396 of 400 of the completegenome.) (nt:o551; 99 pct identical amino acid sequence and) (le:4805) (re:6460) (di:direct) AE000506 AE000506 g2367378 Escherichia coli 562 -11534060

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839822	9515	31671	702	233

Description

6500730203 nmmpc:b0553 outer membrane porin protein nmmpc precursor (gtcfc:11.3) (keggfc:14.2) (rileyfc:5.1.0) (db:gtc-escherichia coli) b0553 b0553 Escherichia coli 562 -11534061 240062 nmmpc outer membrane porin protein (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (le:16389) (re:17516) (di:complement) ECU82598 U82598 g1778466 Escherichia coli 562 -11534061 7500974858 nmmpc outer membrane porin protein:locus of qsr (fn:is, phage, tn; phage-related functions and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 50 of 400 of the completegenome.) (nt:f375; 99 pct identical to nmmpc\_ecoli sw: p21420) (le:9106) (re:10233) (di:complement) AE000160 AE000160 g1786765 Escherichia coli 562 -11534061 5000691299 (de:(ecoli\_535) (pn:outer membrane porin protein; locus of qsr prophage) (gn:nmmpc) (gtcfc:13.1) (ec:) (nmmpc\_ecoli) (keggfc:11.2) (rileyfc:5.1.0) (db:gtc-escherichia coli) ECOLI\_535 ECOLI\_535 Escherichia coli 562 -11534061 7000691877 g64787 (de:(pn:outer membrane porin protein nmmpc precursor) (gn:nmmpc) (db:pir)) G64787 G64787 Escherichia coli 562 10122891

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839824	9516	31672	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839829	9517	31673	645	214

Description

6500730204 nfra:b0568 bacteriophage n4 adsorption protein a (gtcfc:13.1) (keggfc:14.2) (rileyfc:5.1.0) (db:gtc-escherichia coli) b0568 b0568 Escherichia coli 562 -11534062 85728 nfra (de:bacteriophage n4 adsorption protein a precursor) (db:swissprot) NFRA\_ECOLI P31600 ESCHERICHIA COLI 562 -11534062 163295 nfra bacteriophage n4 adsorption protein nfra precursor:bacteriophage n4 receptor protein a (db:pir2.dat) B49351 B49351 Escherichia coli 562 -11534062 223100 nfra bacteriophage n4 adsorptopn protein a (sr:escherichia coli(strain:k12) dna, clone:kohara clone #162) (db:genpept-bct1) (de:escherichia coli genomic dna. (12.6 - 12.9 min).) (le:2397) (re:5369) (di:complement) D90699 D90699 g1651236 Escherichia coli 562 -11534062 240079 nfra (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical bacteriophage n4 receptor protein) (le:28613) (re:31585) (di:complement) ECU82598 U82598 g1778483 Escherichia coli 562 -11534062 235237 nfra bacteriophage n4 receptor:outer membrane (fn:membrane; phage-related functions and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 51 of 400 of the completegenome.) (nt:f990; 100 pct identical to nfra\_ecoli sw: p31600) (le:10871) (re:13843) (di:complement) AE000161 AE000161 g1786780 Escherichia coli 562 -11534062 7500886403 nfra (fn:bacteriophage n4 adsorption) (sr:escherichia coli (strain k-12) dna) (db:genpept-bct2) (de:escherichia coli nfra and nfrb genes, complete cds's.) (le:2454) (re:5426) (di:direct) ECONFRAB L16945 g290460 Escherichia coli 562 -11534062 5000691300 nfra hypothetical bacteriophage n4 receptor protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #162) (db:genpept) (de:escherichia coli genomic dna. (12.6 - 12.9 min).) (nt:orf\_id:ol62#3; similar to pir accession number) (le:2397) (re:5369) (di:complement) D90699 D90699 g1651236 Escherichia coli 562 -11534062

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839848	9518	31674	237	78

Description

6500730205 nfrb:b0569 bacteriophage n4 adsorption protein b precursor  
(gtcfc:13.1) (keggfc:14.2) (rileyfc:5.1.0) (db:gtc-escherichia coli) b0569  
b0569 Escherichia coli 562 -11534063 85729 nfrb (de:bacteriophage n4  
adsorption protein b) (db:swissprot) NFRB\_ECOLI P31599 ESCHERICHIA COLI 562  
-11534063 162773 nfrb bacteriophage n4 adsorption protein nrfb precursor  
(db:pir2.dat) A49351 A49351 Escherichia coli 562 -11534063 223101 nfrb  
bacteriophage n4 adsorptopn protein b precursor (sr:escherichia  
coli(strain:k12) dna, clone:kohara clone #162) (db:genpept-bct1)  
(de:escherichia coli genomic dna. (12.6 - 12.9 min).) (le:5356) (re:7593)  
(di:complement) D90699 D90699 g1651237 Escherichia coli 562 -11534063  
240080 nfrb bacteriophage n4 adsorption protein b precursor  
(db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.)  
(le:31572) (re:33809) (di:complement) ECU82598 U82598 g1778484 Escherichia  
coli 562 -11534063 235236 nfrb bacteriophage n4 receptor:outer membrane  
(fn:membrane; phage-related functions and) (db:genpept-bct2) (de:escherichia  
coli k-12 mg1655 section 51 of 400 of the completegenome.) (nt:f745; 100 pct  
identical to nfrb\_ecoli sw: p31599) (le:13830) (re:16067) (di:complement)  
AE000161 AE000161 g1786781 Escherichia coli 562 -11534063 7500886404 nfrb  
(fn:bacteriophage n4 adsorption) (sr:escherichia coli (strain k-12) dna)  
(db:genpept-bct2) (de:escherichia coli nfra and nfrb genes, complete cds's.)  
(nt:gtg start codon) (le:230) (re:2467) (di:direct) ECONFRAB L16945 g290459  
Escherichia coli 562 -11534063 5000691301 nfrb bacteriophage n4 adsorption  
inner membrane (sr:escherichia coli(strain:k12) dna, clone:kohara clone  
#162) (db:genpept) (de:escherichia coli genomic dna. (12.6 - 12.9 min).)  
(nt:orf\_id:o162#4; similar to pir accession number) (le:5356) (re:7593)  
(di:complement) D90699 D90699 g1651237 Escherichia coli 562 -11534063

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839849	9519	31675	885	294

Description

6500730206 lit:b1139 bacteriophage t4 late gene expression blocking protein:gplit (gtcfc:13.1) (keggfc:14.2) (rileyfc:5.1.0) (db:gtc-escherichia coli) b1139 b1139 Escherichia coli 562 -11534064 82240 lit (de:bacteriophage t4 late gene expression blocking protein (gplit)) (db:swissprot) LIT\_ECOLI P11072 ESCHERICHIA COLI 562 -11534064 7000685754 lit bacteriophage t4 late gene expression-blocking protein (cl:bacteriophage t4 late gene expression blocking protein) (db:pir1.dat) (mp:25 min) BVECLT H64858 Escherichia coli 562 -11534064 223385 lit lit protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #240) (db:genpept-bct1) (de:escherichia coli genomic dna. (25.6 - 26.0 min).) (le:9246) (re:10139) (di:direct) D90749 D90749 g1651567 Escherichia coli 562 -11534064 7500885071 lit phage t4 late gene expression:at locus of e14 (fn:membrane; phage-related functions and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 104 of 400 of the completgenome.) (nt:o297; 95 pct identical to lit\_ecoli sw: p11072) (le:2105) (re:2998) (di:direct) AE000214 AE000214 g1787385 Escherichia coli 562 -11534064 5000691302 lit lit protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #240) (db:genpept) (de:escherichia coli genomic dna. (25.7 - 26.1 min).) (nt:orf\_id:o240#8; similar to pir accession number) (le:9246) (re:10139) (di:direct) D90749 D90749 g1651567 Escherichia coli 562 -11534064



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839856	9520	31676	414	137

Description

6500730207 pin:b1158 dna-invertase pin:dna-invertase (gtcfc:13.1)  
 (keggfc:14.2) (rileyfc:5.1.0) (db:gtc-escherichia coli) b1158 b1158  
 Escherichia coli 562 -11534065 68965 pin (de:dna-invertase pin)  
 (db:swissprot) DNIV\_ECOLI P03014 ESCHERICHIA COLI 562 -11534065 131388 pin  
 dna-invertase:gene pin protein (cl:transposase repressor) (db:pir1.dat) JWEC  
 A03545 Escherichia coli 562 -11534065 223387 pin dna-invertase  
 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #241)  
 (db:genpept-bct1) (de:escherichia coli genomic dna. (25.8 - 26.2 min).)  
 (le:7883) (re:8437) (di:direct) D90750 D90750 g1651570 Escherichia coli 562  
 -11534065 7500880507 (sr:escherichia coli (strain csh520; clarke and carbon  
 library, clon) (db:genpept-bct1) (de:e.coli pin gene coding for  
 dna-invertase, complete sequence.) (nt:dna-invertase (pin)) (le:166)  
 (re:720) (di:direct) ECOPIN K00676 g147274 Escherichia coli 562 -11534065  
 235496 pin inversion of adjacent dna:at locus of e14 (fn:membrane;  
 phage-related functions and) (db:genpept-bct2) (de:escherichia coli k-12  
 mg1655 section 104 of 400 of the completegenome.) (nt:o184; 99 pct identical  
 to dniv\_ecoli sw: p03014) (le:13095) (re:13649) (di:direct) AE000214  
 AE000214 g1787404 Escherichia coli 562 -11534065 5000691303 pin  
 dna-invertase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #241)  
 (db:genpept) (de:escherichia coli genomic dna. (26.0 - 26.3 min).)  
 (nt:orf\_id:o241#14; similar to pir accession number) (le:7883) (re:8437)  
 (di:direct) D90750 D90750 g1651570 Escherichia coli 562 -11534065

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839857	9521	31677	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839859	9522	31678	645	214

Description

6500730208 racc:b1351 racc protein (gtcfc:13.1) (keggfc:14.2)  
(rileyfc:5.1.0) (db:gtc-escherichia coli) b1351 b1351 Escherichia coli 562  
-11534066 92941 racc (de:racc protein) (db:swissprot) RACC\_ECOLI P15033  
ESCHERICHIA COLI 562 -11534066 131430 racc racc protein (cl:racc protein)  
(db:pir1.dat) (mp:30 min) BVECAC JS0119 Escherichia coli 562 -11534066  
223626 racc racc protein (sr:escherichia coli (strain:k12) dna,  
clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,  
kohara clone #263(30.5-30.9 min.)) (nt:orf\_id:o263#2; similar to (pir  
accession number) (le:3400) (re:3675) (di:complement) D90774 D90774 g1742220  
Escherichia coli 562 -11534066 300399 racc (sr:escherichia coli (strain  
k-12) dna) (db:genpept-bct1) (de:escherichia coli racc and rece genes,  
complete cds and 5' end.) (le:116) (re:391) (di:direct) ECORECEA M24905  
g147535 Escherichia coli 562 -11534066 235718 racc defective prophage  
rac:contains rece and orij (fn:membrane; phage-related functions and)  
(db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 123 of 400 of the  
completegenome.) (nt:f91; 100 pct identical to racc\_ecoli sw: p15033; cg)  
(le:81) (re:356) (di:complement) AE000233 AE000233 g1787614 Escherichia coli  
562 -11534066 5000691304 (de:(ecoli\_1311) (pn:defective prophage rac;  
contains rece and orij) (gn:racc) (gtcfc:13.1) (ec:) (racc\_ecoli)  
(keggfc:11.2) (rileyfc:5.1.0) (db:gtc-escherichia coli)) ECOLI\_1311  
ECOLI\_1311 Escherichia coli 562 10034958

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839860	9523	31679	564	187

Description

6500730209 ogrk:b2082 positive regulator of phage p2 late gene  
transcription:prophage p2 ogr protein (gtcfc:10.2:13.1) (keggfc:14.2)  
(rileyfc:5.1.0) (db:gtc-escherichia coli) b2082 b2082 Escherichia coli 562  
-11534067 87533 ogrk (de:prophage p2 ogr protein) (db:swissprot) OGRK\_ECOLI  
P37057 ESCHERICHIA COLI 562 -11534067 157157 ogrk positive regulator of  
phage p2 late gene transcription:ogr protein (cl:phage p2 ogr protein)  
(db:pir2.dat) A41889 A41889 Escherichia coli 562 -11534067 224620 ogrk ogr  
protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda  
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone  
#357(46.5-46.8 min.)) (nt:orf\_id:o357#7; similar to (pir accession number)  
(le:10054) (re:10272) (di:complement) D90846 D90846 g1736790 Escherichia  
coli 562 -11534067 301271 ogrk ogr protein (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #358(46.6-46.9 min.))  
(nt:orf\_id:o357#7; similar to (pir accession number) (le:4699) (re:4917)  
(di:complement) D90847 D90847 g1736802 Escherichia coli 562 -11534067  
301260 ogrk prophage p2 ogr protein (fn:is, phage, tn; phage-related  
functions and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section  
188 of 400 of the completegenome.) (nt:f72; 98 pct identical to ogrk\_ecoli  
sw: p37057) (le:2258) (re:2476) (di:complement) AE000298 AE000298 g1788398  
Escherichia coli 562 -11534067 224631 ogrk ogr protein (sr:escherichia coli  
(strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1)  
(de:e.coli genomic dna, kohara clone #358(46.6-46.9 min.))  
(nt:orf\_id:o357#7; similar to (pir accession number) (le:4699) (re:4917)  
(di:complement) D90847 D90847 g1736802 Escherichia coli 562 -11534067  
5000691305 (de:(ecoli\_2030) (pn:prophage p2 ogr protein) (gn:ogr)  
(gtcfc:13.1) (ec:) (ogrk\_ecoli) (keggfc:11.2) (rileyfc:5.1.0)  
(db:gtc-escherichia coli)) ECOLI\_2030 ECOLI\_2030 Escherichia coli 562  
10029676

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839900	9524	31680	654	217

Description

6500730210 grpe:b2614 heat shock protein:heat shock protein grpe:heat shock protein b25.3:hsp24 (gtcfc:13.1) (keggfc:14.2) (rileyfc:5.1.0) (db:gtc-escherichia coli) b2614 b2614 Escherichia coli 562 -11534068 7500882747 grpe (de:heat shock protein grpe (heat shock protein b25.3) (hsp24)) (db:swissprot) GRPE\_ECOLI P09372 ESCHERICHIA COLI 562 -11534068 163163 grpe heat shock protein grpe heat shock protein b25.3 hsp24:grpe protein (cl:heat shock protein grpe) (db:pir2.dat) S01240 S01240 Escherichia coli 562 -11534068 225188 grpe heat shock protein b25.3 (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #438(58.9-59.3 min.)) (nt:similar to (pir accession number s01240)) (le:12999) (re:13592) (di:complement) D90888 D90888 g1800018 Escherichia coli 562 -11534068 5000691306 (db:genpept-bct1) (de:e. coli grpe gene.) (nt:grpe protein (aa 1-197)) (le:616) (re:1209) (di:direct) ECGRPE X07863 g41619 Escherichia coli 562 -11534068 233036 grpe phage lambda replication:host dna synthesis (fn:is, phage, tn; phage-related functions and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 237 of 400 of the completegenome.) (nt:f197; 100 pct identical to grpe\_ecoli sw: p09372;) (le:3837) (re:4430) (di:complement) AE000347 AE000347 g1788967 Escherichia coli 562 -11534068 74555 grpe (de:heat shock protein grpe (heat shock protein b25.3) (hsp24)) (db:swissprot) GRPE\_ECOLI P09372 ESCHERICHIA COLI 562 -11534068

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839906	9525	31681	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839928	9526	31682	1599	532

Description

6500730211 hfq:b4172 host factor-i:host factor-i protein:hf-i (gtcfc:13.1) (keggfc:14.2) (rileyfc:5.1.0) (db:gtc-escherichia coli) b4172 b4172  
 Escherichia coli 562 -11534069 163208 hfq host factor i:ndh-binding protein nbp (cl:host factor i) (db:pir2.dat) S56397 S26832 Escherichia coli 562 -11534069 234645 (sr:e.coli genomic dna) (db:genpept-bct1) (de:e.coli host factor-i for bacteriophage q beta gene (hfq) and its 5'and 3' flanking regions.) (nt:host factor-i protein) (le:739) (re:1047) (di:direct) ECOHFQ D00743 g216568 Escherichia coli 562 -11534069 237377 hfq host factor-i hf-i (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:required for bacteriophage q beta rna-directed) (le:91116) (re:91424) (di:direct) ECOUW93 U14003 g537013 Escherichia coli 562 -11534069 234640 hfq host factor i for bacteriophage q beta (fn:putative factor; phage-related functions and) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 379 of 400 of the completegenome.) (nt:ol02; 100 pct identical to hfq\_ecoli sw:) (le:8002) (re:8310) (di:direct) AE000489 AE000489 g1790614 Escherichia coli 562 -11534069 7500959763 hfq host factor-i hf-i (sr:escherichia coli k12) (db:genpept-bct2) (de:e. coli hfla locus encoding the hflx, hflk and hflc genes, hfqgene, complete cds; miaa gene, partial cds.) (nt:required for bacteriophage q beta rna-directed) (le:738) (re:1046) (di:direct) ECOHFLA U00005 g436155 Escherichia coli 562 -11534069 5000691307 (de:(ecoli\_4055) (pn:host factor i for bacteriophage q beta replication, a growth- related protein) (gn:hfq) (gtcfc:13.1) (ec:) (hfq\_ecoli) (keggfc:11.2) (rileyfc:5.1.0) (db:gtc-escherichia coli)) ECOLI\_4055 ECOLI\_4055 Escherichia coli 562 10086807

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839957	9527	31683	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839962	9528	31684	354	117

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839968	9529	31685	222	73

Description

6500730212 psif:b0384 phosphate starvation-inducible protein psif:phosphate starvation-inducible protein psif precursor (gtcfc:13.10) (keggfc:14.2) (rileyfc:1.1.4) (db:gtc-escherichia coli) b0384 b0384 Escherichia coli 562 -11534070 91973 psif (de:phosphate starvation-inducible protein psif precursor) (db:swissprot) PSIF\_ECOLI P27295 ESCHERICHIA COLI 562 -11534070 7000686198 psif phosphate starvation-induced protein psif precursor (db:pir2.dat) H64766 H64766 Escherichia coli 562 -11534070 7500888854 psif phosphate starvation-inducible protein (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (le:110853) (re:111191) (di:direct) ECU73857 U73857 g1657580 Escherichia coli 562 -11534070 240001 psif induced by phosphate starvation (fn:phenotype; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 35 of 400 of the completegenome.) (nt:o112; 100 pct identical to psif\_ecoli sw: p27295) (le:2139) (re:2477) (di:direct) AE000145 AE000145 g1786583 Escherichia coli 562 -11534070 5000690498 (de:(ecoli\_368) (pn:induced by phosphate starvation) (gn:psif) (gtcfc:6.3:13.10) (ec:) (psif\_ecoli) (keggfc:11.2) (rileyfc:1.1.4) (db:gtc-escherichia coli)) ECOLI\_368 ECOLI\_368 Escherichia coli 562 10034007

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501839987	9530	31686	1419	472

# Description

6500730213 phoh:psih:b1020 phoh protein:phosphate starvation-inducible protein psih (gtcfc:13.10) (keggfc:14.2) (rileyfc:1.1.4) (db:gtc-escherichia coli) b1020 b1020 Escherichia coli 562 -11534071 89637 phoh:psih (de:phoh protein (phosphate starvation-inducible protein psih)) (db:swissprot) PHOH\_ECOLI P31544 ESCHERICHIA COLI 562 -11534071 164394 phoh:psih phosphate starvation-inducible protein psih:nucleotide-binding protein phoh:phoh protein (db:pir2.dat) B47065 B47065 Escherichia coli 562 -11534071 223334 phoh phoh protein phosphate starvation-inducible (sr:escherichia coli(strain:k12) dna, clone:kohara clone #229) (db:genpept-bct1) (de:escherichia coli genomic dna. (23.2 - 23.5 min).) (le:4387) (re:5451) (di:direct) D90739 D90739 g1651507 Escherichia coli 562 -11534071 235473 phoh phob-dependent:atp-binding pho regulon (fn:regulator; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 94 of 400 of the completegenome.) (nt:o354; 100 pct identical to phoh\_ecoli sw: p31544) (le:203) (re:1267) (di:direct) AE000204 AE000204 g1787257 Escherichia coli 562 -11534071 7500888042 phoh phoh protein (sr:escherichia coli (strain:k-12) dna, clone\_lib:w3110 clone:10e11) (db:genpept-bct2) (de:escherichia coli gene for phoh protein, complete cds.) (le:1032) (re:2096) (di:direct) ECOPHOH D10391 g285774 Escherichia coli 562 -11534071 5000690499 phoh phoh protein phosphate starvation-inducible (sr:escherichia coli(strain:k12) dna, clone:kohara clone #229) (db:genpept) (de:escherichia coli genomic dna. (23.3 - 23.6 min).) (nt:orf\_id:o229#4; similar to swissprot accession) (le:4387) (re:5451) (di:direct) D90739 D90739 g1651507 Escherichia coli 562 -11534071

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839994	9531	31687	243	80

Description

6500730214 phnp:b4092 phnp protein (gtcfc:13.10) (keggfc:14.2)  
(rileyfc:1.1.4) (db:gtc-escherichia coli) b4092 b4092 Escherichia coli 562  
-11534072 89609 phnp (de:phnp protein) (db:swissprot) PHNP\_ECOLI P16692  
ESCHERICHIA COLI 562 -11534072 164290 phnp phnp protein (db:pir2.dat)  
H35719 H35719 Escherichia coli 562 -11534072 235452 phnp (sr:escherichia  
coli (strain:k-12, sub\_strain:w3110) dna) (db:genpept-bct1) (de:escherichia  
coli phn operon genes.) (le:10162) (re:10920) (di:direct) ECOPHN D90227  
g216605 Escherichia coli 562 -11534072 237300 (sr:e.coli (strain b) dna)  
(db:genpept-bct1) (de:e.coli psid locus containing alkylphosphonate uptake  
(phn) genes athrough q, complete cds.) (nt:phnp protein) (le:14398)  
(re:15156) (di:direct) ECOPHNAQ J05260 g147213 Escherichia coli 562  
-11534072 7500888037 phnp (db:genpept-bct1) (de:escherichia coli k-12  
chromosomal region from 92.8 to 00.1 minutes.) (le:5272) (re:6030)  
(di:complement) ECOUW93 U14003 g536936 Escherichia coli 562 -11534072  
235430 phnp phosphonate metabolism (fn:phenotype; central intermediary  
metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 372  
of 400 of the completegenome.) (nt:f252; 100 pct identical amino acid  
sequence and) (le:9991) (re:10749) (di:complement) AE000482 AE000482  
g1790530 Escherichia coli 562 -11534072 5000690500 (de:(ecoli\_3978)  
(pn:phosphonate metabolism; required for c-p bond cleavage) (gn:phnp)  
(gtcfc:6.3:13.10) (ec:) (phnp\_ecoli) (keggfc:11.2) (rileyfc:1.1.4)  
(db:gtc-escherichia coli)) ECOLI\_3978 ECOLI\_3978 Escherichia coli 562  
10031731



<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501839999	9532	31688	348	115

Description

6500730215 phno:b4093 phno protein (gtcfc:13.10) (keggfc:14.2) (rileyfc:1.1.4) (db:gtc-escherichia coli) b4093 b4093 Escherichia coli 562 -11534073 89608 phno (de:phno protein) (db:swissprot) PHNO\_ECOLI P16691 ESCHERICHIA COLI 562 -11534073 164289 phno phno protein (db:pir2.dat) G35719 G35719 Escherichia coli 562 -11534073 235450 phno (sr:escherichia coli (strain:k-12, sub\_strain:w3110) dna) (db:genpept-bct1) (de:escherichia coli phn operon genes.) (le:9726) (re:10160) (di:direct) ECOPHN D90227 g216604 Escherichia coli 562 -11534073 237301 (sr:e.coli (strain b) dna) (db:genpept-bct1) (de:e.coli psid locus containing alkylphosphonate uptake (phn) genes athrough q, complete cds.) (nt:phno protein) (le:13962) (re:14396) (di:direct) ECOPHNAQ J05260 g147211 Escherichia coli 562 -11534073 7500888036 phno (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:6032) (re:6466) (di:complement) ECOUW93 U14003 g536937 Escherichia coli 562 -11534073 235429 phno putative regulator:phn operon (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 372 of 400 of the completegenome.) (nt:f144; 100 pct identical amino acid sequence and) (le:10751) (re:11185) (di:complement) AE000482 AE000482 g1790531 Escherichia coli 562 -11534073 5000690501 (de:(ecoli\_3979) (pn:phno protein) (gn:phno) (gtcfc:6.3:13.10) (ec:) (phno\_ecoli) (keggfc:11.2) (rileyfc:1.1.4) (db:gtc-escherichia coli)) ECOLI\_3979 ECOLI\_3979 Escherichia coli 562 10031730

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840002	9533	31689	348	115

Description

GTC ORF with score 194 to: (fn:membrane protein mediating transport of) (db:genpept-pln1) (de:candida albicans oligopeptide transporter (opt1) gene, completedcds.) (nt:oligopeptide transporter) (le:482:2166) (re:2107:2891) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501840009	9534	31690	606	201

Description

6500730216 phnn:b4094 phosphonates transport atp-binding protein  
phnn:phosphonates transport atp-binding protein phnm (gtcfc:12.4:13.10)  
(keggfc:14.2) (rileyfc:1.1.4) (db:gtc-escherichia coli) (gtcfc:cell  
processes-transport of anions (cl\_so4\_po4\_etc\_):phosphorus compounds) b4094  
b4094 Escherichia coli 562 -11534074 89607 phnn (de:phosphonates transport  
atp-binding protein phnn) (db:swissprot) PHNN ECOLI P16690 ESCHERICHIA COLI  
562 -11534074 163200 phnn hisp-like nucleotide binding protein phnn  
(db:pir2.dat) F35719 F35719 Escherichia coli 562 -11534074 235449 phnn  
atp-binding protein (sr:escherichia coli (strain:k-12, sub\_strain:w3110)  
dna) (db:genpept-bct1) (de:escherichia coli phn operon genes.) (le:9182)  
(re:9739) (di:direct) ECOPHN D90227 g216603 Escherichia coli 562 -11534074  
237302 (sr:e.coli (strain b) dna) (db:genpept-bct1) (de:e.coli psid locus  
containing alkylphosphonate uptake (phn) genes athrough q, complete cds.)  
(nt:hisp-like nucleotide binding protein (phnn)) (le:13418) (re:13975)  
(di:direct) ECOPHNAQ J05260 g147210 Escherichia coli 562 -11534074  
7500888035 phnn (db:genpept-bct1) (de:escherichia coli k-12 chromosomal  
region from 92.8 to 00.1 minutes.) (nt:hisp-like nucleotide binding protein  
(atp-binding) (le:6453) (re:7010) (di:complement) ECOUW93 U14003 g536938  
Escherichia coli 562 -11534074 235428 phnn atp-binding component of  
phosphonate transport (fn:transport; central intermediary metabolism:)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 372 of 400 of the  
completegenome.) (nt:f185; 100 pct identical amino acid sequence and)  
(le:11172) (re:11729) (di:complement) AE000482 AE000482 g1790532 Escherichia  
coli 562 -11534074 5000690502 (de:(ecoli\_3980) (pn:phosphonate metabolism;  
required for c-p bond cleavage) (gn:phnn) (gtcfc:6.3:13.10) (ec:)  
(phnn\_ecoli) (keggfc:11.2) (rileyfc:1.1.4) (db:gtc-escherichia coli))  
ECOLI\_3980 ECOLI\_3980 Escherichia coli 562 10031729

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840020	9535	31691	711	237

Description

6500730217 phnm:b4095 phnm protein (gtcfc:13.10) (keggfc:14.2) (rileyfc:1.1.4) (db:gtc-escherichia coli) b4095 b4095 Escherichia coli 562 -11534075 89606 phnm (de:phnm protein) (db:swissprot) PHNM\_ECOLI P16689 ESCHERICHIA COLI 562 -11534075 163197 phnm hims-like integral membrane protein phnm (db:pir2.dat) S56323 S56323 Escherichia coli 562 -11534075 237303 phnm (sr:escherichia coli (strain:k-12, sub\_strain:w3110) dna) (db:genpept-bct1) (de:escherichia coli phn operon genes.) (le:8046) (re:9182) (di:direct) ECOPHN D90227 g216602 Escherichia coli 562 -11534075 7500888034 phnm (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:hims-like integral membrane protein) (le:7010) (re:8146) (di:complement) ECOUW93 U14003 g536939 Escherichia coli 562 -11534075 235427 phnm phosphonate metabolism (fn:phenotype; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 372 of 400 of the completegenome.) (nt:f378; 100 pct identical amino acid sequence and) (le:11729) (re:12865) (di:complement) AE000482 AE000482 g1790533 Escherichia coli 562 -11534075 5000690503 (de:(ecoli\_3981) (pn:phosphonate metabolism; required for c-p bond cleavage) (gn:phnm) (gtcfc:6.3:13.10) (ec:) (phnm\_ecoli) (keggfc:11.2) (rileyfc:1.1.4) (db:gtc-escherichia coli)) ECOLI\_3981 ECOLI\_3981 Escherichia coli 562 10031728

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840022	9536	31692	900	300

Description

GTC ORF with score 152 to: (fn:phosphorylates myosin i heavy chain enhancing) (db:genpept-inv) (de:acanthamoeba castellanii myosin i heavy chain kinase mrna, completecds.) (nt:ser/thr protein kinase; mihck; upregulated by) (le:144) (re:2405) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840023	9537	31693	909	303

Description

GTC ORF with score 180 to: (or:Mus musculus) (sr:mouse (strain cd-1) dna, library of o.smithies, clone pump-3 hb) (db:genpept-rod) (de:mouse prp gene encoding proline-rich protein mp-3, exon 2.) (nt:proline-rich protein mp-3) (le:<1) (re:893) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840025	9538	31694	444	147

Description

6500730218 phn1:b4096 phosphonates transport atp-binding protein phn1 (gtcfc:12.4:13.10) (keggfc:14.2) (rileyfc:1.1.4) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of anions (cl\_so4\_po4\_etc\_):phosphorus compounds) b4096 b4096 Escherichia coli 562 -11534076 89605 phn1 (de:phosphonates transport atp-binding protein phn1) (db:swissprot) PHNL\_ECOLI P16679 ESCHERICHIA COLI 562 -11534076 163199 phn1 hisp-like nucleotide binding protein phn1 (cl:atp-binding cassette homology) (db:pir2.dat) D35719 D35719 Escherichia coli 562 -11534076 235446 phn1 atp-binding protein (sr:escherichia coli (strain:k-12, sub\_strain:w3110) dna) (db:genpept-bct1) (de:escherichia coli phn operon genes.) (le:7369) (re:8049) (di:direct) ECOPHN D90227 g216601 Escherichia coli 562 -11534076 237304 (sr:e.coli (strain b) dna) (db:genpept-bct1) (de:e.coli psid locus containing alkylphosphonate uptake (phn) genes athrough q, complete cds.) (nt:hisp-like nucleotide binding protein (phn1)) (le:11605) (re:12285) (di:direct) ECOPHNAQ J05260 g147207 Escherichia coli 562 -11534076 7500888033 phn1 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:hisp-like nucleotide binding protein (atp-binding) (le:8143) (re:8823) (di:complement) ECOUW93 U14003 g536940 Escherichia coli 562 -11534076 235426 phn1 atp-binding component of phosphonate transport (fn:transport; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 372 of 400 of the completegenome.) (nt:f226; 100 pct identical amino acid sequence and) (le:12862) (re:13542) (di:complement) AE000482 AE000482 g1790534 Escherichia coli 562 -11534076 5000690504 (de:(ecoli\_3982) (pn:abc transport of phosphonates) (gn:phn1) (gtcfc:6.3:13.10) (ec:) (phn1\_ecoli) (keggfc:11.2) (rileyfc:1.1.4) (db:gtc-escherichia coli)) ECOLI\_3982 ECOLI\_3982 Escherichia coli 562 10031727

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840038	9539	31695	417	138

Description

6500730219 phnk:b4097 phosphonates transport atp-binding protein phnk (gtcfc:12.4:13.10) (keggfc:14.2) (rileyfc:1.1.4) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of anions (cl\_so4\_po4\_etc\_):phosphorus compounds) b4097 b4097 Escherichia coli 562 -11534077 163198 phnk hisp-like nucleotide binding protein phnk:phosphonates transport atp-binding protein phnk (cl:atp-binding cassette homology) (db:pir2.dat) S56325 S56325 Escherichia coli 562 -11534077 7500959762 phnk (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:hisp-like nucleotide binding protein (atp-binding) (le:8934) (re:9692) (di:complement) ECOUW93 U14003 g536941 Escherichia coli 562 -11534077 237305 phnk atp-binding component of phosphonate transport (fn:transport; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 372 of 400 of the completegenome.) (nt:f252; 99 pct identical amino acid sequence and) (le:13653) (re:14411) (di:complement) AE000482 AE000482 g1790535 Escherichia coli 562 -11534077 5000690505 (de:(ecoli\_3983) (pn:abc transport of phosphonates) (gn:phnk) (gtcfc:6.3:13.10) (ec:) (phnk\_ecoli) (keggfc:11.2) (rileyfc:1.1.4) (db:gtc-escherichia coli)) ECOLI\_3983 ECOLI\_3983 Escherichia coli 562 10086802

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840041	9540	31696	555	185

Description

6500730220 phnj:b4098 phnj protein (gtcfc:13.10) (keggfc:14.2) (rileyfc:1.1.4) (db:gtc-escherichia coli) b4098 b4098 Escherichia coli 562 -11534078 89600 phnj (de:phnj protein) (db:swissprot) PHNJ\_ECOLI P16688 ESCHERICHIA COLI 562 -11534078 7000686136 phnj phnj protein (db:pir2.dat) A65219 A65219 Escherichia coli 562 -11534078 237306 phnj (sr:escherichia coli (strain:k-12, sub\_strain:w3110) dna) (db:genpept-bct1) (de:escherichia coli phn operon genes.) (le:5658) (re:6503) (di:direct) ECOPHN D90227 g216599 Escherichia coli 562 -11534078 7500888031 phnj (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:9689) (re:10534) (di:complement) ECOUW93 U14003 g536942 Escherichia coli 562 -11534078 235424 phnj phosphonate metabolism (fn:putative enzyme; central intermediary) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 372 of 400 of the completegenome.) (nt:f281; 100 pct identical amino acid sequence and) (le:14408) (re:15253) (di:complement) AE000482 AE000482 g1790536 Escherichia coli 562 -11534078 5000690506 (de:(ecoli\_3984) (pn:phosphonate metabolism; required for c-p bond cleavage) (gn:phnj) (gtcfc:6.3:13.10) (ec:) (phnj\_ecoli) (keggfc:11.2) (rileyfc:1.1.4) (db:gtc-escherichia coli)) ECOLI\_3984 ECOLI\_3984 Escherichia coli 562 10031722

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840042	9541	31697	2475	825

Description

6500730221 phni:b4099 phni protein (gtcfc:13.10) (keggfc:14.2)  
(rileyfc:1.1.4) (db:gtc-escherichia coli) b4099 b4099 Escherichia coli 562  
-11534079 89599 phni (de:phni protein) (db:swissprot) PHNI\_ECOLI P16687  
ESCHERICHIA COLI 562 -11534079 7000686135 phni phni protein (db:pir2.dat)  
B65219 B65219 Escherichia coli 562 -11534079 237307 phni (sr:escherichia  
coli (strain:k-12, sub\_strain:w3110) dna) (db:genpept-bct1) (de:escherichia  
coli phn operon genes.) (le:4601) (re:5665) (di:direct) ECOPHN D90227  
g216598 Escherichia coli 562 -11534079 7500888030 phni (db:genpept-bct1)  
(de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.)  
(le:10527) (re:11591) (di:complement) ECOUW93 U14003 g536943 Escherichia  
coli 562 -11534079 235423 phni phosphonate metabolism (fn:phenotype;  
central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli  
k-12 mg1655 section 372 of 400 of the completegenome.) (nt:f354; 100 pct  
identical amino acid sequence and) (le:15246) (re:16310) (di:complement)  
AE000482 AE000482 g1790537 Escherichia coli 562 -11534079 5000690507  
(de:(ecoli\_3985) (pn:phosphonate metabolism; required for c-p bond cleavage)  
(gn:phni) (gtcfc:6.3:13.10) (ec:) (phni\_ecoli) (keggfc:11.2) (rileyfc:1.1.4)  
(db:gtc-escherichia coli)) ECOLI\_3985 ECOLI\_3985 Escherichia coli 562  
10031721

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840056	9542	31698	573	190

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840063	9543	31699	513	170

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840070	9544	31700	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840071	9545	31701	690	229

#### Description

6500730222 phnh:b4100 phnh protein (gtcfc:13.10) (keggfc:14.2)  
(rileyfc:1.1.4) (db:gtc-escherichia coli) b4100 b4100 Escherichia coli 562  
-11534080 89598 phnh (de:phnh protein) (db:swissprot) PHNH\_ECOLI P16686  
ESCHERICHIA COLI 562 -11534080 164284 phnh phnh protein (db:pir2.dat)  
I35718 I35718 Escherichia coli 562 -11534080 235441 phnh (sr:escherichia  
coli (strain:k-12, sub\_strain:w3110) dna) (db:genpept-bct1) (de:escherichia  
coli phn operon genes.) (le:4017) (re:4601) (di:direct) ECOPHN D90227  
g216597 Escherichia coli 562 -11534080 237308 (sr:e.coli (strain b) dna)  
(db:genpept-bct1) (de:e.coli psid locus containing alkylphosphonate uptake  
(phn) genes athrough g, complete cds.) (nt:phnh protein) (le:8253) (re:8837)  
(di:direct) ECOPHNAQ J05260 g147202 Escherichia coli 562 -11534080  
7500888029 phnh (db:genpept-bct1) (de:escherichia coli k-12 chromosomal  
region from 92.8 to 00.1 minutes.) (le:11591) (re:12175) (di:complement)  
ECOUW93 U14003 g536944 Escherichia coli 562 -11534080 235422 phnh  
phosphonate metabolism (fn:phenotype; central intermediary metabolism:)  
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 372 of 400 of the  
completegenome.) (nt:f194) (le:16310) (re:16894) (di:complement) AE000482  
AE000482 g1790538 Escherichia coli 562 -11534080 5000690508  
(de:(ecoli\_3986) (pn:phosphonate metabolism; required for c-p bond cleavage)  
(gn:phnh) (gtcfc:6.3:13.10) (ec:) (phnh\_ecoli) (keggfc:11.2) (rileyfc:1.1.4)  
(db:gtc-escherichia coli)) ECOLI\_3986 ECOLI\_3986 Escherichia coli 562  
10031720

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840072	9546	31702	1008	336

#### Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840104	9547	31703	690	230

Description

6500730223 phng:b4101 phng protein (gtcfc:13.10) (keggfc:14.2)  
(rileyfc:1.1.4) (db:gtc-escherichia coli) b4101 b4101 Escherichia coli 562  
-11534081 89597 phng (de:phng protein) (db:swissprot) PHNG\_ECOLI P16685  
ESCHERICHIA COLI 562 -11534081 7000686134 phng phng protein (db:pir2.dat)  
D65219 D65219 Escherichia coli 562 -11534081 237309 phng (sr:escherichia  
coli (strain:k-12, sub\_strain:w3110) dna) (db:genpept-bct1) (de:escherichia  
coli phn operon genes.) (le:3568) (re:4020) (di:direct) ECOPHN D90227  
g216596 Escherichia coli 562 -11534081 7500888028 phng (db:genpept-bct1)  
(de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.)  
(le:12172) (re:12624) (di:complement) ECOUW93 U14003 g536945 Escherichia  
coli 562 -11534081 235421 phng phosphonate metabolism (fn:phenotype;  
central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli  
k-12 mg1655 section 372 of 400 of the completegenome.) (nt:f150; 100 pct  
identical amino acid sequence and) (le:16891) (re:17343) (di:complement)  
AE000482 AE000482 g1790539 Escherichia coli 562 -11534081 5000690509  
(de:(ecoli\_3987) (pn:phosphonate metabolism; required for c-p bond cleavage)  
(gn:phng) (gtcfc:6.3:13.10) (ec:) (phng\_ecoli) (keggfc:11.2) (rileyfc:1.1.4)  
(db:gtc-escherichia coli)) ECOLI\_3987 ECOLI\_3987 Escherichia coli 562  
10031719

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840105	9548	31704	984	327

Description

6500730224 phnf:b4102 phnf protein (gtcfc:13.10) (keggfc:14.2) (rileyfc:1.1.4) (db:gtc-escherichia coli) b4102 b4102 Escherichia coli 562 -11534082 89596 phnf (de:phnf protein) (db:swissprot) PHNF\_ECOLI P16684 ESCHERICHIA COLI 562 -11534082 164282 phnf phnf protein (db:pir2.dat) G35718 G35718 Escherichia coli 562 -11534082 235439 phnf (sr:escherichia coli (strain:k-12, sub\_strain:w3110) dna) (db:genpept-bct1) (de:escherichia coli phn operon genes.) (le:2842) (re:3567) (di:direct) ECOPHN D90227 g216595 Escherichia coli 562 -11534082 237310 (sr:e.coli (strain b) dna) (db:genpept-bct1) (de:e.coli psid locus containing alkylphosphonate uptake (phn) genes athrough q, complete cds.) (nt:phnf protein) (le:7078) (re:7803) (di:direct) ECOPHNAQ J05260 g147200 Escherichia coli 562 -11534082 7500888027 phnf (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:12625) (re:13350) (di:complement) ECOUW93 U14003 g536946 Escherichia coli 562 -11534082 235420 phnf putative transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 372 of 400 of the completegenome.) (nt:f241; 100 pct identical amino acid sequence and) (le:17344) (re:18069) (di:complement) AE000482 AE000482 g1790540 Escherichia coli 562 -11534082 5000690510 (de:(ecoli\_3988) (pn:phnf protein) (gn:phnf) (gtcfc:6.3:13.10) (ec:) (phnf\_ecoli) (keggfc:11.2) (rileyfc:1.1.4) (db:gtc-escherichia coli)) ECOLI\_3988 ECOLI\_3988 Escherichia coli 562 10031718

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840120	9549	31705	642	213

Description

6500730225 htga:htpy:b0012 heat shock protein htga:heat shock protein htpy (gtcfc:13.2) (keggfc:14.2) (rileyfc:5.6.0) (db:gtc-escherichia coli) b0012 b0012 Escherichia coli 562 -11534083 78011 htga:htpy (de:heat shock protein htga (heat shock protein htpy)) (db:swissprot) HTGA\_ECOLI P28697 ESCHERICHIA COLI 562 -11534083 163170 htga:htpy heat shock protein htga:heat shock protein y (db:pir2.dat) (mp:0 min) A40623 A40623 Escherichia coli 562 -11534083 7500883596 htga positive regulator for sigma 32 heat shock (fn:regulator; adaptations, atypical conditions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 2 of 400 of the completegenome.) (nt:o196; 100 pct identical to htga\_ecoli sw:) (le:187) (re:777) (di:direct) AE000112 AE000112 g1786194 Escherichia coli 562 -11534083 5000691308 (de:(ecoli\_12) (pn:heat shock protein htga:heat shock protein htpy) (gn:htga) (gtcfc:13.2) (ec:) (htga\_ecoli) (keggfc:11.2) (rileyfc:5.6.0) (db:gtc-escherichia coli)) ECOLI\_12 ECOLI\_12 Escherichia coli 562 10020350

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840124	9550	31706	327	108

Description

6500730226 dps:pexb:vtm:b0812 dna protection during starvation protein (gtcfc:13.2) (keggfc:14.2) (rileyfc:5.6.0) (db:gtc-escherichia coli) b0812 b0812 Escherichia coli 562 -11534084 162952 dps:pexb:vtm dna-binding protein:starvation-inducible (db:pir2.dat) A46401 A46401 Escherichia coli 562 -11534084 223212 dps dps protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #205) (db:genpept-bct1) (de:escherichia coli genomic dna.(18.0 - 18.3 min).) (le:9725) (re:10228) (di:complement) D90718 D90718 g1651366 Escherichia coli 562 -11534084 223217 dps dps protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #206) (db:genpept-bct1) (de:escherichia coli genomic dna.(18.2 - 18.5 min).) (le:2940) (re:3443) (di:complement) D90719 D90719 g1651372 Escherichia coli 562 -11534084 7500959725 dps dps (db:genpept-bct1) (de:e.coli dps gene for binding protein.) (le:296) (re:799) (di:direct) ECDPS X69337 g41295 Escherichia coli 562 -11534084 232703 dps global regulator:starvation conditions (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 73 of 400 of the completegenome.) (nt:fl67; 100 pct identical to dps\_ecoli sw: p27430;) (le:6775) (re:7278) (di:complement) AE000183 AE000183 g1787032 Escherichia coli 562 -11534084 5000691309 dps dna-binding protein dps. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #205) (db:genpept) (de:escherichia coli genomic dna.(18.1 - 18.4 min).) (nt:orf\_id:o206#4; similar to pir accession number) (le:9725) (re:10228) (di:complement) D90718 D90718 g1651366 Escherichia coli 562 -11534084 7502851989 dps dna-binding protein dps. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #206) (db:genpept) (de:escherichia coli genomic dna.(18.2 - 18.6 min).) (nt:orf\_id:o206#4; similar to pir accession number) (le:2940) (re:3443) (di:complement) D90719 D90719 g1651372 Escherichia coli 562 -11534084

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501840130	9551	31707	840	279

# Description

6500730227 cspb:b1557 cold shock-like protein cspb (gtcfc:13.2) (keggfc:14.2) (rileyfc:5.6.0) (db:gtc-escherichia coli) b1557 b1557 Escherichia coli 562 -11534085 66659 cspb (de:cold shock-like protein cspb) (db:swissprot) CSPB\_ECOLI P36995 ESCHERICHIA COLI 562 -11534085 152151 cspb cold shock protein cspb (cl:major cold shock protein:cold shock domain homology) (db:pir2.dat) S43617 S43617 Escherichia coli 562 -11534085 4000707008 cspb cspb (db:genpept-bct1) (de:escherichia coli major cold-shock proteins cspb (cspb) and cspf(cspf) genes, complete cds.) (nt:major cold-shock protein) (le:129) (re:344) (di:complement) AF003590 AF003590 g2226341 Escherichia coli 562 -11534085 223944 cspb cspb protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #307(35.1-35.5 min.)) (nt:orf\_id:o308#13; similar to (pir accession number) (le:13333) (re:13548) (di:complement) D90798 D90798 g1742552 Escherichia coli 562 -11534085 223966 cspb cspb protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #308(35.3-35.7 min.)) (nt:orf\_id:o308#13; similar to (pir accession number) (le:3306) (re:3521) (di:complement) D90799 D90799 g1742563 Escherichia coli 562 -11534085 300685 cspb cspb protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #309(35.4-35.7 min.)) (nt:orf\_id:o308#13; similar to (pir accession number) (le:82) (re:297) (di:complement) D90800 D90800 g1742586 Escherichia coli 562 -11534085 300663 cspb cold-shock protein (sr:escherichia coli (strain tap90) (library: kohara) dna) (db:genpept-bct1) (de:escherichia coli cold-shock protein (cspb) gene, complete cds.) (le:528) (re:743) (di:direct) ECOCSPB L28429 g479003 Escherichia coli 562 -11534085 300653 cspb cold shock protein:may affect transcription (fn:phenotype; adaptations, atypical conditions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 142 of 400 of the completegenome.) (nt:f71; 100 pct identical to cspb\_ecoli sw: p36995; cg) (le:8954) (re:9169) (di:complement) AE000252 AE000252 g1787839 Escherichia coli 562 -11534085 223934 cspb cspb (db:genpept-bct1) (de:escherichia coli major cold-shock proteins cspb (cspb) and cspf(cspf) genes, complete cds.) (nt:major cold-shock protein) (le:129) (re:344) (di:complement) AF003590 AF003590 g2226341 Escherichia coli 562 -11534085 234063 cspb cspb protein (sr:escherichia coli (strain:k12) dna, clone\_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #309(35.4-35.7 min.)) (nt:orf\_id:o308#13; similar to (pir accession number) (le:82) (re:297) (di:complement) D90800 D90800 g1742586 Escherichia coli 562 -11534085 5000691310 (de:(ecoli\_1517) (pn:cold shock protein; may affect transcription) (gn:cspb) (gtcfc:13.2) (ec:) (cspb\_ecoli) (keggfc:11.2) (rileyfc:5.6.0) (db:gtc-escherichia coli)) ECOLI\_1517 ECOLI\_1517 Escherichia coli 562 10009277

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840142	9552	31708	267	88

Description

6500730228 mscl:b3291 large conductance mechanosensitive channel  
 (gtcfc:13.2) (keggfc:14.2) (rileyfc:5.6.0) (db:gtc-escherichia coli) b3291  
 b3291 Escherichia coli 562 -11534086 84292 mscl (de:large conductance  
 mechanosensitive channel) (db:swissprot) MSCL\_ECOLI P23867 ESCHERICHIA COLI  
 562 -11534086 164845 mscl:yhdc yhdc protein:hypothetical protein 3 trka 3  
 region:mscl protein (cl:yhdc protein) (db:pir2.dat) I53826 I53826  
 Escherichia coli 562 -11534086 237654 mscl (fn:large conductance  
 mechanosensitive channel) (db:genpept-bct1) (de:escherichia coli k-12  
 chromosomal region from 67.4 to 76.0 minutes.) (le:218772) (re:219182)  
 (di:direct) ECOUW67 U18997 g606225 Escherichia coli 562 -11534086 238544  
 yhdc (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli  
 (pn02530) yhdc, yhdl, yhdm and yhdn genes,complete cds's.) (le:1) (re:411)  
 (di:direct) ECOYHDM L29458 g473420 Escherichia coli 562 -11534086  
 7500885920 mscl large-conductance mechanosensitive channel  
 (db:genpept-bct1) (de:escherichia coli k-12 large-conductance  
 mechanosensitive channel(mscl) gene, complete cds.) (le:31) (re:441)  
 (di:direct) ECU08371 U08371 g473892 Escherichia coli 562 -11534086 236524  
 mscl mechanosensitive channel (fn:transport; transport of small molecules:  
 other) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 297 of 400  
 of the completegenome.) (nt:o136; 100 pct identical amino acid sequence and)  
 (le:6094) (re:6504) (di:direct) AE000407 AE000407 g1789686 Escherichia coli  
 562 -11534086 5000691311 (de:(ecoli\_3209) (pn:mechanosensitive channel)  
 (gn:mscl) (gtcfc:13.2) (ec:) (mscl\_ecoli) (keggfc:11.2) (rileyfc:5.6.0)  
 (db:gtc-escherichia coli)) ECOLI\_3209 ECOLI\_3209 Escherichia coli 562  
 10026493

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840144	9553	31709	237	78

Description

6500730229 uspa:b3495 universal stress protein a (gtcfc:13.2) (keggfc:14.2) (rileyfc:5.6.0) (db:gtc-escherichia coli) b3495 b3495 Escherichia coli 562 -11534087 164819 uspa universal stress protein a (cl:universal stress protein a) (db:pir2.dat) (mp:77 min) S47715 S47715 Escherichia coli 562 -11534087 7500960476 uspa (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:54370) (re:54804) (di:direct) ECOUW76 U00039 g466632 Escherichia coli 562 -11534087 236731 uspa universal stress protein:broad regulatory (fn:putative regulator; adaptations, atypical) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 315 of 400 of the completegenome.) (nt:ol44; 99 pct identical amino acid sequence and) (le:9372) (re:9806) (di:direct) AE000425 AE000425 g1789909 Escherichia coli 562 -11534087 5000691312 (de:(ecoli\_3414) (pn:universal stress protein; broad regulatory function) (gn:uspa) (gtcfc:13.2) (ec:) (uspa\_ecoli) (keggfc:11.2) (rileyfc:5.6.0) (db:gtc-escherichia coli)) ECOLI\_3414 ECOLI\_3414 Escherichia coli 562 10087479

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840145	9554	31710	489	162

Description

6500730230 cspa:b3556 cold shock protein cspa:7.4 kd cold shock protein:cs7.4 (gtcfc:13.2) (keggfc:14.2) (rileyfc:5.6.0) (db:gtc-escherichia coli) b3556 b3556 Escherichia coli 562 -11534088 130468 cspa major cold shock protein cspa:7.4 kda cytoplasmic protein cs7.4 (cl:major cold shock protein:cold shock domain homology) (db:pir1.dat) (mp:79 min) OCECJ JH0201 Escherichia coli 562 -11534088 234062 cspa cold shock protein (db:genpept-bct1) (de:salmonella enteritidis cold shock protein (cspa) gene, completecds.) (le:643) (re:855) (di:direct) AF017276 AF017276 g2353338 Salmonella enteritidis 592 -11534088 236793 cspa cold shock protein a (db:genpept-bct1) (de:salmonella typhimurium strain 3027 cold shock protein a (cspa)gene, complete cds.) (le:1) (re:213) (di:direct) AF052579 AF052579 g2970683 Salmonella typhimurium 602 -11534088 7000688962 (sr:e.coli (strain sb221) dna) (db:genpept-bct1) (de:e.coli cold shock protein 7.4 (cspa) gene, complete cds.) (nt:cold shock protein (cspa)) (le:621) (re:833) (di:direct) ECOCSPAA M30139 g145633 Escherichia coli 562 -11534088 7500953591 cspa (sr:escherichia coli (sub\_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cold regulated) (le:134300) (re:134512) (di:direct) ECOUW76 U00039 g466694 Escherichia coli 562 -11534088 5500686717 cspa cold shock protein 7.4:transcriptional (fn:regulator; adaptations, atypical conditions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 323 of 400 of the completegenome.) (nt:o70; 100 pct identical amino acid sequence and) (le:748) (re:960) (di:direct) AE000433 AE000433 g1789979 Escherichia coli 562 -11534088 5000691313 (de:(ecoli\_3476) (pn:cold shock protein 7) (gn:cspa) (gtcfc:13.2) (ec:) (cspa\_ecoli) (keggfc:11.2) (rileyfc:5.6.0) (db:gtc-escherichia coli)) ECOLI\_3476 ECOLI\_3476 Escherichia coli 562 10067864

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